

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 18:34:54 ; Search time 246 Seconds  
(without alignments)  
3595.614 Million cell updates/sec

Title: US-09-611-257A-24  
Perfect score: 12028  
Sequence: 1 MLPHRVPRCVTPPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12028	100.0	2287	4	AAB66475 Rat alpha
2	11657	96.9	2254	2	AAY14590 Rat T-typ
3	11626	96.7	2272	2	AAY14592 Rat T-typ
4	11610.5	96.5	2265	2	AAY14591 Rat T-typ
5	11606.5	96.5	2247	2	AAY14593 Rat T-typ
6	11542.5	96.0	2428	3	AAY70720 Rat pancr
7	10857	90.3	2250	2	AAY14586 Human T-t
8	10833	90.1	2268	2	AAY14588 Human T-t
9	10820.5	90.0	2273	4	AAE01019 Human T-t
10	10810.5	89.9	2261	2	AAY14587 Human T-t
11	10806.5	89.8	2243	2	AAY14589 Human T-t
12	10806.5	89.8	2243	7	ADJ68819 Human hea
13	10732.5	89.2	2377	8	ADQ89064 Human uro
	10533	87.6	2266	4	AAB66481 Human alp
	1026.5	51.8	2359	4	AAB66476 Rat alpha
	1022	51.7	2353	2	AAY06299 Human act
		51.7	2353	6	ABP72254 Human T-t
		51.7	2353	7	ADJ69322 Human hea
		7	2353	2	AAY06298 Human act
			2353	5	ABG30840 Human vol
			1207	4	AAU00474 Human T-t
			1207.4	2	AAY14594 Human T-t
				2	AAY14595 Human T-t
				2	AAY06300 Human act
					AAU10535 Human T-t

Mon Apr 18 12:12

Mon Apr 18 12:41

26	5409	45.0	2175	6	ABU08511	Abu08511 Human T-t
27	5409	45.0	2175	8	ADH69265	Adh69265 Human TCC
28	5405.5	44.9	2188	5	AAU10536	Aau10536 Human T-t
29	5405.5	44.9	2188	6	ABU08512	Abu08512 Human T-t
30	5405.5	44.9	2188	8	ADH69267	Adh69267 Human TCC
31	5345	44.4	1835	2	AAAY14597	Aay14597 Rat T-typ
32	5345	44.4	1835	8	ADH69268	Adh69268 Rat T-typ
33	5342.5	44.4	1823	2	AAAY14596	Aay14596 Human T-t
34	5179.5	43.1	1792	4	AAB66477	Aab66477 Rat brain
35	4807	40.0	982	4	AAM23743	Aam23743 Human EST
36	3950	32.8	1854	2	AAW79161	Aaw79161 Human cal
37	3950	32.8	1854	4	AAB66472	Aab66472 Protein e
38	3553	29.5	1657	8	ADN24183	Adn24183 Bacterial
39	3397	28.2	2435	4	ABB60448	Abb60448 Drosophil
40	3125	26.0	644	4	AAB66478	Aab66478 Human alp
41	2975	24.7	1859	4	ABG10954	Abg10954 Novel hum
42	1911.5	15.9	853	4	AAM93437	Aam93437 Human pol
43	1911.5	15.9	853	8	ADL31041	Adl31041 Human pro
44	1686.5	14.0	518	4	AAB66479	Aab66479 Human alp
45	1682	14.0	2339	2	AAR33549	Aar33549 Sequence

ALIGNMENTS

RESULT 1  
AAB66475  
ID AAB66475 standard; protein; 2287 AA.

XX AC AAB66475;

XX XX 09-APR-2001 (first entry)

XX XX Rat alpha-IG calcium channel protein.

KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;  
KW hypotensive; cardiant; nootropic; T-type calcium channel subunit;  
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;  
KW epilepsy; alpha-IG calcium channel.

XX OS Rattus sp.

XX XX WO200102561-A2.

XX XX 11-JAN-2001.

XX PF 04-JUL-2000; 2000WO-CA000794.

XX PR 02-JUL-1999; 99US-00346794.

XX PA (NEUR-) NEUROMED TECHNOLOGIES INC.

XX PI Snutch TP, Baillie DL;

XX DR WPI; 2001-123111/13.

XX DR N-PSDB; AAF31677.

XX PT Novel T-type calcium channel alpha-1 subunit gene useful for treating  
XX PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
XX PT epilepsy.

XX PS Disclosure; Page 63-72; 103pp; English.

XX CC The present sequence is given in a specification providing sequences and  
XX CC partial sequences for three types of mammalian (human and rat) T-type  
XX CC calcium channel subunits. An expression cassette has been generated which  
XX CC comprises a nucleotide sequence encoding a T-type calcium channel alpha\_1  
XX CC subunit operably linked to control sequences to effect its expression.  
XX CC The novel calcium channel nucleic acids and proteins are useful for  
XX CC treating conditions characterised by undesirable levels of T-type calcium  
XX CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
XX CC hypertension, sleep disorder and epilepsy





Qy	2101	IRLPAPCPGLEPSWAKDPPETRRSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVET	2160
Db	2101	IRLPAPCPGLEPSWAKDPPETRRSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVET	2160
Qy	2161	QSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSRPPKKLSPPSI	2220
Db	2161	QSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSRPPKKLSPPSI	2220
Qy	2221	SIDPPESQSRPFCSPGVCLRRRAPASDSKDPVSPLDSTAASPPKDTLSLGLSSD	2280
Db	2221	SIDPPESQSRPFCSPGVCLRRRAPASDSKDPVSPLDSTAASPPKDTLSLGLSSD	2280
Qy	2281	PTDMDPZ	2287
Db	2281	PTDMDPZ	2287

RESULT 2  
AAY14590  
ID AAY14590 standard; protein: 2254 AA.

AC AAY14590:

AA	
DT	07-DEC-1999 (first entry)

DE Rat T-type voltage-gated Ca channel  $\alpha$ -1-G (rCavT1a).

Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy. KW

**Rattus sp.**

PN WO9929847-A1.

17-JUN-1999

30-OCT-1998: 98WO-US023161.

05-DEC-1997: 97US-00985809.

PA (LOYO ) UNIV LOYOLA CHICAGO.

PI Perez-Reves E. Cribbs LL:

DR WPI; 1999-394972/33.

www.1000.com

**PT New T-type voltage-gated calcium channels.**

PS Disclosure; Page 67-76; 138pp; English.

This sequence represents a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCav1.1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

**SQ Sequence 2254 AA;**

Query Match	96.9%;	Score 11657;	DB 2;	Length 2254;
Best Local Similarity	99.7%;	Pred. No. 0;		

Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0	
QY	62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSML 121
DB	30 GROQPGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSML 89
QY	122 VILLNCVTLMGFRPCEDIACDQSQRILQAQDDFIFAFAFVEMVVMKVALGIFGKCKCYLG 181
DB	90 VILLNCVTLMGFRPCEDIACDQSQRILQAQDDFIFAFAFVEMVVMKVALGIFGKCKCYLG 149
QY	182 DTWNRLDFFIVIAAGMLEYSLDLQNVFSFAVRTVRVLRPLRAINRVPSMRILVTLLDLP 241
DB	150 DTWNRLDFFIVIAAGMLEYSLDLQNVFSFAVRTVRVLRPLRAINRVPSMRILVTLLDLP 209
QY	242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDSPF 301
DB	210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDSPF 269
QY	302 ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTTCVMNQYVNTCSAGEHN 361
DB	270 ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTTCVMNQYVNTCSAGEHN 329
QY	362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYFILLIIVGSFFMINL 421
DB	330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYFILLIIVGSFFMINL 389
QY	422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELKYLVIILRKAAR 481
DB	390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELKYLVIILRKAAR 449
QY	482 RLAQVSRATGVRAGLLSSPVARSQQEQPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541
DB	450 RLAQVSRATGVRAGLLSSPVARSQQEQPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 509
QY	542 GTLRVPRASPEIQDRDANGSRRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601
DB	510 GTLRVPRASPEIQDRDANGSRRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 569
QY	602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKD KALVEVAPSPGPPTLTSFNIPGPF 661
DB	570 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKD KALVEVAPSPGPPTLTSFNIPGPF 629
QY	662 SSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721
DB	630 SSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 689
QY	722 SEAVYEFTQDAQHSDLRDPHSRRRQRSILGDDAEPSSVLAFWRLICDTERKIVDSKYFGRG 781
DB	690 SEAVYEFTQDAQHSDLRDPHSRRRQRSILGDDAEPSSVLAFWRLICDTERKIVDSKYFGRG 749
QY	782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPGYIKNPYN 841
DB	750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPGYIKNPYN 809
QY	842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALORQLVVLMTDMNVATF 901
DB	810 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALORQLVVLMTDMNVATF 869
QY	902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 961
DB	870 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 929
QY	962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEDPFSPSVD 1021
DB	930 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEDPFSPSVD 989
QY	1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRRTSS 1081
DB	990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRRTSS 1049
QY	1082 SGSAEPGAHHMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
DB	1050 SGSAEPGAHHMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

QY 2222 IDPPESQSRPPCSPGVCLRRRAPASDSDPSVSSPLDSTAASPSPKOTLSLGLSSDP 2281

Db 2190 IDPPESQSRPPCSPGVCLRRRAPASDSDPSVSSPLDSTAASPSPKOTLSLGLSSDP 2249

QY 2282 TMDMP 2286

Db 2250 TMDMP 2254

RESULT 3

AAAY14592

ID AAY14592 standard; protein; 2272 AA.

XX AAY14592;

AC AAY14592;

XX 07-DEC-1999 (first entry)

DT Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c).

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

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XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

QY 1142 LLSGEGQESODEESSEEDRASPGSDHRRHGLEREAKSSFDLPTDLOVPGHRTASGR 1201

Db 1110 LLSGEGQESODEESSEEDRASPGSDHRRHGLEREAKSSFDLPTDLOVPGHRTASGR 1169

QY 1202 SSASEHQCNGKSASGRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWRSRLPACCRE 1261

Db 1170 SSASEHQCNGKSASGRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWRSRLPACCRE 1229

QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLLVIFLNCITIAMERPKIDHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLLVIFLNCITIAMERPKIDHSAERIFL 1289

QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSWNVDGLLVLSVIDILVMSVDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSWNVDGLLVLSVIDILVMSVDSG 1349

QY 1382 TKILGMLRVLLRLTLRLPLRVISRAQGLKLVVETLMSLSKPIGNIVVICAPFIIFGILG 1441

Db 1350 TKILGMLRVLLRLTLRLPLRVISRAQGLKLVVETLMSLSKPIGNIVVICAPFIIFGILG 1409

QY 1442 VOLFKGKFFVCOGEDTRNITNKSDDCAEASVWRVHKYNFNDLQALMSLFVLASKDQWVD 1501

Db 1410 VOLFKGKFFVCOGEDTRNITNKSDDCAEASVWRVHKYNFNDLQALMSLFVLASKDQWVD 1469

QY 1502 IMYDGLDAVGVDQOPIIMNHNPMWLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQEEE 1561

Db 1470 IMYDGLDAVGVDQOPIIMNHNPMWLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQEEE 1529

QY 1562 EARRREKRLRLLEKRRSKEKQMAEAQCKPYYSYDYSRFRLLVHHLCTSHYLDLFTGVI 1621

Db 1530 EARRREKRLRLLEKRRSKEKQMAEAQCKPYYSYDYSRFRLLVHHLCTSHYLDLFTGVI 1589

QY 1622 GLNVVTMAMEHYQQOILDEALKICNYIFTVIFVFSVFKLVAFARFRFFQDRWNQDLA 1681

Db 1590 GLNVVTMAMEHYQQOILDEALKICNYIFTVIFVFSVFKLVAFARFRFFQDRWNQDLA 1649

QY 1682 IVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHLTHVMOALP 1741

Db 1650 IVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHLTHVMOALP 1709

QY 1742 QVGNLGLLFWLLFFIFAALGVLEFGDLECDTHPCCEGLGRHATFRNFGMAFLTFRVSTG 1801

Db 1710 QVGNLGLLFWLLFFIFAALGVLEFGDLECDTHPCCEGLGRHATFRNFGMAFLTFRVSTG 1769

QY 1802 DNWNGIMKDPDRDCQESTCYNTVISPIYFVSFVLTQAQFVLNVVIVIAVLMKHLSEENKEA 1861

Db 1770 DNWNGIMKDPDRDCQESTCYNTVISPIYFVSFVLTQAQFVLNVVIVIAVLMKHLSEENKEA 1829

QY 1862 KEEAELEAELEEMKTLSPQSPHPLGSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921

Db 1830 KEEAELEAELEEMKTLSPQSPHPLGSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889

QY 1922 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESRSLGHRGWGL 1981

Db 1890 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESRSLGHRGWGL 1949

QY 1982 PKAQSGILSVHSQPADTSCILQPKDVHLLQPHGAPTWGAIPKLPPLPGSPPLAQRPPLR 2041

Db 1950 PKAQSGILSVHSQPADTSCILQPKDVHLLQPHGAPTWGAIPKLPPLPGSPPLAQRPPLR 2009

QY 2042 RQAAIRTDLSLDVQGLSREDLLSEVSGPSCPLTRSSSFVGGSSIQVQORSIGSKVSKHI 2101

Db 2010 RQAAIRTDLSLDVQGLSREDLLSEVSGPSCPLTRSSSFVGGSSIQVQORSIGSKVSKHI 2069

QY 2102 RLPAPCPGLEPSPWAKOPPETRSSLELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVETQ 2161

Db 2070 RLPAPCPGLEPSPWAKOPPETRSSLELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVETQ 2129

QY 2162 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPLCPSPSSLGQPLGPGSRPKKLSPPSIS 2221

Db 2130 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPLCPSPSSLGQPLGPGSRPKKLSPPSIS 2189

QY 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSRCLRTVCNPFERSVSM 121

Db 30 GRQPGSIEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSRCLRTVCNPFERSVSM 89

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

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Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

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Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Db 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIPAFFAVEMVVKMVALGIFGKCYLG 181

Query Match 96.7%; Score 11626; DB 2; Length 2272;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;

Sequence 2272 AA;

Query Match 96.7%; Score 11626; DB 2; Length 2272;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;

Sequence 2272 AA;

Query Match 96.7%; Score 11626; DB 2; Length 2272;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;

Sequence 2272 AA;

Query Match 96.7%; Score 11626; DB 2; Length 2272;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;

Sequence 2272 AA;

Db	90	VILLNCVTLMFRPCEDIAQDSQRCRILOAFDDEIFAFAVEMVVKMVALGIFGKKCYLG	149
Qy	182	DTWNRLDFFIIVIAAGMLEYSLDLQNVSFSAVTRVRLRPLRAINRVPSMRILVTLLDITLP	241
Db	150	DTWNRLDFFIIVIAAGMLEYSLDLQNVSFSAVTRVRLRPLRAINRVPSMRILVTLLDITLP	209
Qy	242	MLGNVLLLCFFVFIFIGIVGVQLWAGLLRNCFLPENFSLPLSDLEPYQ TENEDES PF	301
Db	210	MLGNVLLLCFFVFIFIGIVGVQLWAGLLRNCFLPENFSLPLSDLEPYQ TENEDES PF	269
Qy	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNQYTYNCSAGEHN	361
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNQYTYNCSAGEHN	329
Qy	362	PFKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL	421
Db	330	PFKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL	389
Qy	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEBLLKYLYILRKAAR	481
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEBLLKYLYILRKAAR	449
Qy	482	RLAQVSRAIGVRAGLLSSPVARSQOEPQPSGCTSRSHRRLSVHHLVHHHHHHHHYHLGN	541
Db	450	RLAQVSRAIGVRAGLLSSPVARSQOEPQPSGCTSRSHRRLSVHHLVHHHHHHHHYHLGN	509
Qy	542	GTLRVPRASPEIQDRDANGSRRLMLPPPTSTPSPGGPPRGAESVHSFYHADCHLEPVRCQ	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPTSTPSPGGPPRGAESVHSFYHADCHLEPVRCQ	569
Qy	602	APPPRCPSEASGRVTGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTFNIPPGPF	661
Db	570	APPPRCPSEASGRVTGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTFNIPPGPF	629
Qy	662	SSMHKLLTQSTGACHSSCKISSPCSADSGACGPDSCPYCARTGAGEPESADHVMPDSD	721
Db	630	SSMHKLLTQSTGACHSSCKISSPCSADSGACGPDSCPYCARTGAGEPESADHVMPDSD	689
Qy	722	SEAVYEFTQDAQHSDLRDPHSRRRQORSLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRG	781
Db	690	SEAVYEFTQDAQHSDLRDPHSRRRQORSLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRG	749
Qy	782	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN	841
Db	750	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN	809
Qy	842	IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLKMTMDNVATF	901
Db	810	IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLKMTMDNVATF	869
Qy	902	CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWLAI VTFVQILTQEDWNKV	961
Db	870	CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWLAI VTFVQILTQEDWNKV	929
Qy	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAEGDATKSESEPDFSPSVD	1021
Db	930	LYNGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAEGDATKSESEPDFSPSVD	989
Qy	1022	GDGDRKKRLALVALGEHAELRKSLLPPLIITHAATPMSHPKSSSTGVGEALGSGSRRTSS	1081
Db	990	GDGDRKKRLALVALGEHAELRKSLLPPLIITHAATPMSHPKSSSTGVGEALGSGSRRTSS	1049
Qy	1082	SGSAEPGAHHKEMKCPSPARSPPHSPWASAASWTSSRRSRNSLGRAPSLKRRSPSGERRS	1141
Db	1050	SGSAEPGAHHKEMKCPSPARSPPHSPWASAASWTSSRRSRNSLGRAPSLKRRSPSGERRS	1109
Qy	1142	LLSGEGQESQDEEESSEEDRASDPAGSDHRRGSLEREAKSSFOLDPDLQVPGHLRTASGR	1201
Db	1110	LLSGEGQESQDEEESSEEDRASDPAGSDHRRGSLEREAKSSFOLDPDLQVPGHLRTASGR	1169
Qy	1202	SSASEHQDCNGKSASGRILARTLRDTPQLDGDNDNDEGNLSKGERIQAWVR SRLPACC RE	1261
Db	1170	SSASEHQDCNGKSASGRILARTLRDTPQLDGDNDNDEGNLSKGERIQAWVR SRLPACC RE	1229

Qy	1262	RDSWSAYIFPPQSRFRLLCHRIITHKMPDHVVVLVIIFLNCITIAMERP KIDPHSAERIFL	1321
Db	1230	RDSWSAYIFPPQSRFRLLCHRIITHKMPDHVVVLVIIFLNCITIAMERP KIDPHSAERIFL	1289
Qy	1322	TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG	1381
Db	1290	TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG	1349
Qy	1382	TKILGMLRVLRLLRTRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG	1441
Db	1350	TKILGMLRVLRLLRTRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG	1409
Qy	1442	VQLFKGKFFVCQGEDTRNITNKSDCAEASRVRWHKYNFNDNLGQALMSL FVLASKDGWVD	1501
Db	1410	VQLFKGKFFVCQGEDTRNITNKSDCAEASRVRWHKYNFNDNLGQALMSL FVLASKDGWVD	1469
Qy	1502	IMYDGLDAVGVDQOPI MNHNPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE	1561
Db	1470	IMYDGLDAVGVDQOPI MNHNPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE	1529
Qy	1562	EARRREEKRLRRLKRRSKEKQMA-----EAQCKPYYSYDYSRFRLL	1603
Db	1530	EARRREEKRLRRLKRRSKEKQMA-----EAQCKPYYSYDYSRFRLL	1589
Qy	1604	VHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV	1663
Db	1590	VHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV	1649
Qy	1664	AFAPRRFFQDRWNQDLAIVLLSIMGITLBEIEVNLSPINPTIIRIMRVLR IARVLKLL	1723
Db	1650	AFGFRFFQDRWNQDLAIVLLSIMGITLBEIEVNLSPINPTIIRIMRVLR IARVLKLL	1709
Qy	1724	KMAVGMRALHTVMQALPOVGNLGLLFMLLFFIFAALGVELFGDLECDTHPC EGLGRHA	1783
Db	1710	KMAVGMRALHTVMQALPOVGNLGLLFMLLFFIFAALGVELFGDLECDTHPC EGLGRHA	1769
Qy	1784	TFRNFGMAFLTTLFRVSTGDNWNGIMKDPDRDCDOESTCYNTVISPIYFVSFVLTAQFVLV	1843
Db	1770	TFRNFGMAFLTTLFRVSTGDNWNGIMKDPDRDCDOESTCYNTVISPIYFVSFVLTAQFVLV	1829
Qy	1844	NVVI AVL MKHLEESNKEAEAELEAELEEMKTLS PQPHSPLGSPFLMPGVEGVNSTDS	1903
Db	1830	NVVI AVL MKHLEESNKEAEAELEAELEEMKTLS PQPHSPLGSPFLMPGVEGVNSTDS	1889
Qy	1904	PKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPVPLGPDLLTVRKSGVSRTHSLPNDSYM	1963
Db	1890	PKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPVPLGPDLLTVRKSGVSRTHSLPNDSYM	1949
Qy	1964	CRNGSTAERSLGHRCWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA	2023
Db	1950	CRNGSTAERSLGHRCWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA	2009
Qy	2024	IPKLPPPGRSPLAQRPLRQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGG	2083
Db	2010	IPKLPPPGRSPLAQRPLRQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGG	2069
Qy	2084	SIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL LLPSSQ	2143
Db	2070	SIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL LLPSSQ	2129
Qy	2144	EEPLFPRDLKKCYSVETQSCRRRPGFWLDBQRRHSIAVSCLDGSGQRLCPSPSLGGQP	2203
Db	2130	EEPLFPRDLKKCYSVETQSCRRRPGFWLDBQRRHSIAVSCLDGSGQRLCPSPSLGGQP	2189
Qy	2204	LGGPGSRPKKLSPPSISIDPPESQGSRRPSPGVCLRRRAPASDSKDPSSV SPLDSTAA	2263
Db	2190	LGGPGSRPKKLSPPSISIDPPESQGSRRPSPGVCLRRRAPASDSKDPSSV SPLDSTAA	2249
Qy	2264	SPSPKDTLSLSGLSSDPTMDP 2286	
Db	2250	SPSPKDTLSLSGLSSDPTMDP 2272	

RESULT 4  
AAY14591  
ID AAY14591 standard; protein; 2265 AA.  
XX  
AC AAY14591;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1b).  
XX  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX  
OS Rattus sp.  
XX  
PN WO9929847-A1.  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
DR N-PSDB; AAX83486.  
XX  
PT New T-type voltage-gated calcium channels.

XX Disclosure; Page 76-85; 138pp; English.  
PS  
XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel  
XX alpha-1-G designated rCav1b. Voltage gated channels are membrane bound  
CC glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2265 AA;

Query Match 96.5%; Score 11610.5; DB 2; Length 2265;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 2213; Conservative 1; Mismatches 11; Indels 11; Gaps 1;  
QY 62 GAAGAGSTKDPGSADSEAGLPYPALAPVWFFYLSQDSRPRSWCLRTVCNPFWRVSM 121  
DB 30 GRCQPGSTKDPGSADSEAGLPYPALAPVWFFYLSQDSRPRSWCLRTVCNPFWRVSM 89  
QY 122 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 181  
DB 90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 149  
QY 182 DTWNRLDFFIVIAQMLEYSIDLQNVSFSAVRTVRVLRPLRPLRINRVPMSRILVILLDTLP 241  
DB 150 DTWNRLDFFIVIAQMLEYSIDLQNVSFSAVRTVRVLRPLRPLRINRVPMSRILVILLDTLP 209  
QY 242 MLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQOTENEDESPF 301

DB 210 MLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQOTENEDESPF 269  
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDETNNSSNTTTCVNNQYTNCSAGEHN 361  
DB 270 ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDETNNSSNTTTCVNNQYTNCSAGEHN 329  
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINL 421  
DB 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQESQIMREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 481  
DB 390 CLVVIATQFSETKQESQIMREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 449  
QY 482 RLAQVSRRAIGVRAGLLSVPVARSQEPQPSGCTRSRRRLSVHHLVHHHHHHHHYHLGN 541  
DB 450 RLAQVSRRAIGVRAGLLSVPVARSQEPQPSGCTRSRRRLSVHHLVHHHHHHHHYHLGN 509  
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRQ 601  
DB 510 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTSGGPPRGAESVHSFYHADCHLEPVRQ 569  
QY 602 APPRCPSASGRTVSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSTNIPPGPF 661  
DB 570 APPRCPSASGRTVSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSTNIPPGPF 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD 721  
DB 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD 689  
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
DB 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 749  
QY 782 IMTALLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 841  
DB 750 IMTALLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 809  
QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 901  
DB 810 IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 869  
QY 902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 961  
DB 870 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 929  
QY 962 LYNGMASTSSWAALYFIALMTFNGYVLFNLVAILVEGFOAEGDATKSESEPDFSPSVD 1021  
DB 930 LYNGMASTSSWAALYFIALMTFNGYVLFNLVAILVEGFOAEGDATKSESEPDFSPSVD 989  
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMShPKSSSTGVGEALGSGSRRTSS 1081  
DB 990 GDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMShPKSSSTGVGEALGSGSRRTSS 1049  
QY 1082 SGSAEPGAHHMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141  
DB 1050 SGSAEPGAHHMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109  
QY 1142 LLSGEGQESQDEEESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGR 1201  
DB 1110 LLSGEGQESQDEEESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGR 1169  
QY 1202 SSASEHQDCNGKSAASGLARTLRTDDPQLDGDNDNDEGNLSKGERIQAWVRSRLPACCRE 1261  
DB 1170 SSASEHQDCNGKSAASGLARTLRTDDPQLDGDNDNDEGNLSKGERIQAWVRSRLPACCRE 1229  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321  
DB 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289  
QY 1322 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1381  
DB 1290 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1349



QY 1382 TKILGMLRVLRLLRPLRPLRVISRAOGLKLVVETLMSSSLKPIGNIWVICCAFFIIFGILG 1441  
Db 1350 TKILGMLRVLRLLRPLRPLRVISRAOGLKLVVETLMSSSLKPIGNIWVICCAFFIIFGILG 1409  
QY 1442 VQLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFDFNLGQALMSLFLVASKDGWD 1501  
Db 1410 VQLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFDFNLGQALMSLFLVASKDGWD 1469  
QY 1502 IMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQBEE 1561  
Db 1470 IMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQBEE 1529  
QY 1562 EARRREKRLRLLEKKRR-----SKEKQMAEAQCKPYSDYSRFRLLVHLCST 1610  
Db 1530 EARRREKRLRLLEKKRRNMLDDVIASGSSASASEAQCKPYSDYSRFRLLVHLCST 1589  
QY 1611 HYLDLFIITGVIGLVNVTMAMEHYQQOQILDEALKICNYIFTVIFVFSVFKLVAFARRF 1670  
Db 1590 HYLDLFIITGVIGLVNVTMAMEHYQQOQILDEALKICNYIFTVIFVFSVFKLVAFARRF 1649  
QY 1671 FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGM 1730  
Db 1650 FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGM 1709  
QY 1731 ALLHTVMQALPOVGNLGLLMLFFIFAALGVELFGDLECDTHCEGLGRHATFRNFGM 1790  
Db 1710 ALLHTVMQALPOVGNLGLLMLFFIFAALGVELFGDLECDTHCEGLGRHATFRNFGM 1769  
QY 1791 AFLTLFRVSTGDNWNGIMKDPSPRDCQDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL 1850  
Db 1770 AFLTLFRVSTGDNWNGIMKDTLRDCQDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL 1829  
QY 1851 MKHLEESNKEAEAELEAELEMKLTSQPHSPGLSPFLPGVGVNSTDSKPKGAPH 1910  
Db 1830 MKHLEESNKEAEAELEAELEMKLTSQPHSPGLSPFLPGVGVNSTDSKPKGAPH 1889  
QY 1911 TTAHIGAAAGSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1970  
Db 1890 TTAHIGAAAGSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1949  
QY 1971 ERSGLHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPP 2030  
Db 1950 ERSGLHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPP 2009  
QY 2031 GRSPLAQRPLRQAAIRTDSDLVQGLGSRDLDLSEVSGPSCPLTRSSSFWGSSIQVQOR 2090  
Db 2010 GRSPLAQRPLRQAAIRTDSDLVQGLGSRDLDLSEVSGPSCPLTRSSSFWGSSIQVQOR 2069  
QY 2091 SGIQSKVSKHIRLPAPCPGLEPSWAKDPETRSSLLELDTLSWISGDLPLPSSQEEPLPR 2150  
Db 2070 SGIQSKVSKHIRLPAPCPGLEPSWAKDPETRSSLLELDTLSWISGDLPLPSSQEEPLPR 2129  
QY 2151 DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSR 2210  
Db 2130 DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSR 2189  
QY 2211 PKKLSPPSISIDPPESQSRPPCPGVCLERRRAPASDSKPSVSSPLDSTAASPSPKD 2270  
Db 2190 PKKLSPPSISIDPPESQSRPPCPGVCLERRRAPASDSKPSVSSPLDSTAASPSPKD 2249  
QY 2271 TSLSLGLSSDPTMDP 2286  
Db 2250 TSLSLGLSSDPTMDP 2265

RESULT 5  
AAAY14593  
ID AAAY14593 standard; protein; 2247 AA.  
XX  
AAAY14593;

DEC-1999 (first entry)

XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavTld).  
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
KW Rattus sp.  
KW W09929847-A1.  
OS 17-JUN-1999.  
XX 30-OCT-1998; 98WO-US023161.  
XX 05-DEC-1997; 97US-00985809.  
PR (LOYO ) UNIV LOYOLA CHICAGO.  
XX Perez-Reyes E, Cribbs LL;  
XX WPI; 1999-394972/33.  
DR N-PSDB; AAX83488.  
XX New T-type voltage-gated calcium channels.  
XX Disclosure; Page 94-103; 138pp; English.  
PS This sequence represents a rat T-type voltage-gated calcium (Ca) channel  
XX alpha-1-G designated rCavTld. Voltage gated channels are membrane bound  
CC glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX SQ Sequence 2247 AA;

Query Match 96.5%; Score 11606.5; DB 2; Length 2247;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 2211; Conservative 1; Mismatches 6; Indels 7; Gaps 1;  
QY 62 GAAGAGSTEKDPGSDADSEAGLPYPALAPVFFYLSQDSRPSRSCWLCRTVCNPFERSVSM 121  
Db 30 GRQPGSTEKDPGSDADSEAGLPYPALAPVFFYLSQDSRPSRSCWLCRTVCNPFERSVSM 89  
QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181  
Db 90 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149  
QY 182 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLLDTLP 241  
Db 150 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLLDTLP 209  
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLNRNRCFLPENFSLPLSVLEPPYQTENEDESPF 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLNRNRCFLPENFSLPLSVLEPPYQTENEDESPF 269  
QY 302 ICSQPRENGMRSRCSVPTRLRGEAGGGPPCSLDYETYNSSNTTTCVWNQYTYNCSAGEHN 361  
Db 270 ICSQPRENGMRSRCSVPTRLRGEAGGGPPCSLDYETYNSSNTTTCVWNQYTYNCSAGEHN 329  
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFMDAHSFYNFIFILLIIVGSSFFMINL 421

Db 330 PFKGAINFDNIGYAWIAIFQVITTEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 481  
Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 449  
QY 482 RLAQVSRAIGVRAGLLSPPVARSQEPQPSGSCSTRSHRRLSVHVLVHHHHHHHHYHLGN 541  
Db 450 RLAQVSRAIGVRAGLLSPPVARSQEPQPSGSCSTRSHRRLSVHVLVHHHHHHHHYHLGN 509  
QY 542 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTPSGPPRGAEVSHSFYHADCHLEPVRCQ 601  
Db 510 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTPSGPPRGAEVSHSFYHADCHLEPVRCQ 569  
QY 602 APPRCPSEASGRITVSGKVYPTVHTSPPPPEILKOKALVEVAPSPGPPTLTSTFNIPPGPF 661  
Db 570 APPRCPSEASGRITVSGKVYPTVHTSPPPPEILKOKALVEVAPSPGPPTLTSTFNIPPGPF 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHVMPSDSD 721  
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHVMPSDSD 689  
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIIVDSKYFGRG 749  
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMILLKLVYGPFGYIKNPYN 841  
Db 750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMILLKLVYGPFGYIKNPYN 809  
QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 901  
Db 810 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 869  
QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGDTLDPDRKNFDSLWAIIVTVFQILTQEDWNKV 961  
Db 870 CMLLMFIFIFISILGMHLFGCKFASERDGDTLDPDRKNFDSLWAIIVTVFQILTQEDWNKV 929  
QY 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVD 1021  
Db 930 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVD 989  
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSPHKSSTGVGEALGSGSRRTSS 1081  
Db 990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSPHKSSTGVGEALGSGSRRTSS 1049  
QY 1082 SGSAEPGAHHEMKCPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141  
Db 1050 SGSAEPGAHHEMKCPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1109  
QY 1142 LLSGEGQESQDEESESSEEDRASPGSDHRRGSLEREAKSSFDLPDTLQVPLHRTASGR 1201  
Db 1110 LLSGEGQESQDEESESSEEDRASPGSDHRRGSLEREAKSSFDLPDTLQVPLHRTASGR 1169  
QY 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSLRPACCRE 1261  
Db 1170 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSLRPACCRE 1229  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIIITHKMFHVVLVLIIFLNCITIAMERPKIDPHSAERIFL 1321  
Db 1230 RDSWSAYIFPPQSRFRLLCHRIIITHKMFHVVLVLIIFLNCITIAMERPKIDPHSAERIFL 1289  
QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1381  
Db 1290 TLSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1349  
QY 1382 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVEILMSSLKPIGNIWVICCAFFIIFGILG 1441  
Db 1350 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVEILMSSLKPIGNIWVICCAFFIIFGILG 1409  
QY 1442 VOLFKGKFFVCOGEDTRNITNKSDCAEASRWRVRHKYNFDNLGQALMSLFLVLASKDGWVD 1501  
Db 1410 VOLFKGKFFVCOGEDTRNITNKSDCAEASRWRVRHKYNFDNLGQALMSLFLVLASKDGWVD 1469

QY 1502 IMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE 1561  
Db 1470 IMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE 1529  
QY 1562 EARRREKRLRLEKRRSKEKQMAEACQKPYSDYSRFRLLVHHLCTSHYLDLFTGVI 1621  
Db 1530 EARRREKRLRLEKRRSKEKQMAEACQKPYSDYSRFRLLVHHLCTSHYLDLFTGVI 1582  
QY 1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVEKLVAFAPRRFFQDRWNQDLA 1681  
Db 1583 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVEKLVAFAPRRFFQDRWNQDLA 1642  
QY 1682 IVLLSIMGITLEEIEVNLSPINPTIIRIMRVLIARVLLKLMKAVGMRALLHTVMQALP 1741  
Db 1643 IVLLSIMGITLEEIEVNLSPINPTIIRIMRVLIARVLLKLMKAVGMRALLHTVMQALP 1702  
QY 1742 QVGNLGLLFFLFFIFAALGVLEFGLDECEDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1801  
Db 1703 QVGNLGLLFFLFFIFAALGVLEFGLDECEDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1762  
QY 1802 DNWNGIMKOPSRDCQESTCYNTVISPFIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1861  
Db 1763 DNWNGIMKOPSRDCQESTCYNTVISPFIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1822  
QY 1862 KEAEAELEAELEEMKTLSPQPHSPGLSPFLWPGVEGVNSTSPKPGAPHTTAHIGAASGF 1921  
Db 1823 KEAEAELEAELEEMKTLSPQPHSPGLSPFLWPGVEGVNSTSPKPGAPHTTAHIGAASGF 1882  
QY 1922 SLEHPTWVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHARGWL 1981  
Db 1883 SLEHPTWVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHARGWL 1942  
QY 1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPGSRPLAQRPLR 2041  
Db 1943 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPGSRPLAQRPLR 2002  
QY 2042 RQAARTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHI 2101  
Db 2003 RQAARTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHI 2062  
QY 2102 RLPAPCPGLEPSWAKDPPETRRSSLELDTLSWISGDLPLSPSQEEPLFPRLDKKCYSVETQ 2161  
Db 2063 RLPAPCPGLEPSWAKDPPETRRSSLELDTLSWISGDLPLSPSQEEPLFPRLDKKCYSVETQ 2122  
QY 2162 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRICPSPSSLGQPLGGPGSRPKKLSPPSIS 2221  
Db 2123 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRICPSPSSLGQPLGGPGSRPKKLSPPSIS 2182  
QY 2222 IDPPESQSRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPKKDTLSLGLSSDP 2281  
Db 2183 IDPPESQSRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPKKDTLSLGLSSDP 2242  
QY 2282 TDMDP 2286  
Db 2243 TDMDP 2247  
RESULT 6  
AA70720  
ID AA70720 standard; protein: 2428 AA.  
XX AA70720;  
AC  
XX 18-JUL-2000 (first entry)  
DT  
XX Rat pancreatic T-type calcium channel.  
DE  
XX Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;  
KW pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;  
KW antidiabetic; calcium influx; L type calcium channel; NIDDM;  
KW type II diabetes; non-insulin dependent diabetes mellitus.  
XX



QY 1051 IHTAATPMHPKSSSTGVGEALGSGRRRTSSGSAEPGAHHEMKPPSARSSPHSPWSA 1110  
Db 1094 IHTAATPMSLPKSSSTGVGEALGSGRRRTSSGSAEPGAHHEMKPPSARSSPHSPWSA 1153  
QY 1111 ASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPGSDHR 1170  
Db 1154 ASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPGSDHR 1213  
QY 1171 HRGSLEREAKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKKSASGRILARTLRRTDDPOL 1230  
Db 1214 HRGSLEREAKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKKSASGRILARTLRRTDDPOL 1273  
QY 1231 DGDNDNDEGNLSKGERIQAWVRSLPACCRERDSWSAYIFPQSRFRLLCHRIITHKMF 1290  
Db 1274 DGDNDNDEGNLSKGERIQAWVRSLPACCRERDSWSAYIFPQSRFRLLCHRIITHKMF 1333  
QY 1291 HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLNYSYIFTAVFLAEMTVKVVALGWCFCGEQ 1350  
Db 1334 HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLNYSYIFTAVFLAEMTVKVVALGWCFCGEQ 1393  
QY 1351 AYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRLPLRVISRAQGLK 1410  
Db 1394 AYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRLPLRVISRAQGLK 1453  
QY 1411 LVVETLMSSLPKIGNIVVICAPFIIFGILGVQLFKGFFVCQGEDTRNITNKSDCAEAS 1470  
Db 1454 LVVETLMSSLPKIGNIVVICAPFIIFGILGVQLFKGFFVCQGEDTRNITNKSDCAEAS 1513  
QY 1471 YRWVRHKYNFNDLQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPMNHNPMWMLLYFIS 1530  
Db 1514 YRWVRHKYNFNDLQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPMNHNPMWMLLYFIS 1573  
QY 1531 FLLIVAFFVLNMFVGVVVENFHKROHQBEEARRRREKRLRLEKKRR----- 1579  
Db 1574 FLLIVAFFVLNMFVGVVVENFHKROHQBEEARRRREKRLRLEKKRRMLDDVIAAG 1633  
QY 1580 SKERQMAEAQCKPYYSYSRFRLLVHLLCTSHYLDLDFITGVIGLVNVTWAMEHYQQPQIL 1639  
Db 1634 SSASAASEAQCKPYYSYSRFRLLVHLLCTSHYLDLDFITGVIGLVNVTWAMEHYQQPQIL 1693  
QY 1640 DEALKICNYIFTVIFVFESVFKLVAFARFFQDRWNQDLAIVLLSIMGITLEEIEVNL 1699  
Db 1694 DEALKICNYIFTVIFVFESVFKLVAFARFFQDRWNQDLAIVLLSIMGITLEEIEVNA 1753  
QY 1700 SLPINPTIIRIMRVLRIRVLRKLLKMAVGMRLHTVMQALPQVGNLGLLFFLFFIFAA 1759  
Db 1754 SLPINPTIIRIMRVLRIRVLRKLLKMAVGMRLHTVMQALPQVGNLGLLFFLFFIFAA 1813  
QY 1760 LGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSCDCQES 1819  
Db 1814 LGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCQES 1873  
QY 1820 TCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHEESNKEAELEAELELEMKTLS 1879  
Db 1874 TCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHEESNKEAELEAELELEMKTLS 1933  
QY 1880 PQHSPPLGSPFLWPGEVGNSTDSKPGAPHTTAHIGASGFSLEHPTMVPHPEEVPVPL 1939  
Db 1934 PQHSPPLGSPFLWPGEVGNSTDSKPGAPHTTAHIGASGFSLEHPTMVPHPEEVPVPL 1993  
QY 1940 GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLHGRGWGLPKAQSGSILSVHSQPADT 1999  
Db 1994 GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLHGRGWGLPKAQSGSILSVHSQPADT 2053  
QY 2000 SCILQLPKDVHYLLQPHGAPTGAIPKLPGRSPPLAQRLRQAARTDSDLVQGLGSR 2059  
Db 2054 SCILQLPKDVHYLLQPHGAPTGAIPKLPGRSPPLAQRLRQAARTDSDLVQGLGSR 2113  
QY 2060 EDLLSEVSGSPCLTRSSSFWGSSIOVQQRSGIQSKVKHRLPAPCPGLEPSWAKDPP 2119  
Db 2114 EDLLSEVSGSPCLTRSSSFWGSSIOVQQRSGIQSKVKHRLPAPCPGLEPSWAKDPP 2173  
QY 2120 ETRSSLELDTLSWISGDLPLSPSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSI 2179

Db 2174 ETRSSLELDTLSWISGDLPLSPSQEEPLSPRDLKKCYSVETQSCRRRPGFWLDEQRRHSI 2233  
QY 2180 AVSCLDSGSQPRLCPSPPSSSLGGQPLGGPSRPPKKLSPPSISIDPPESQGSRRPPCSPGVC 2239  
Db 2234 AVSCLDSGSQPRLCPSPPSSSLGGQPLGGPSRPPKKLSPPSISIDPPESQGSRRPPCSPGVC 2293  
QY 2240 LRRRAPASDSKDPVSVPSSPLDSTAASPPKDTLSLSGLSSDPTMDP 2286  
Db 2294 LRRRAPASDSKDPVSVPSSPLDSTAASPPKDTLSLSGLSSDPTMDP 2340  
RESULT 7  
ID AAY14586 standard; protein; 2250 AA.  
XX AAY14586;  
AC AAY14586;  
XX 07-DEC-1999 (first entry)  
DT  
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a).  
DE  
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX Homo sapiens.  
OS  
XX WO9929847-A1.  
FN  
XX 17-JUN-1999.  
PD  
XX 30-OCT-1998; 98WO-US023161.  
PF  
XX 05-DEC-1997; 97US-00985809.  
PR  
XX (LOYO ) UNIV LOYOLA CHICAGO.  
PA  
XX Perez-Reyes E, Cribbs LL;  
PI  
XX WPI; 1999-394972/33.  
DR  
XX N-PSDB; AAX83481.  
DR  
XX New T-type voltage-gated calcium channels.  
PT  
XX  
XX Disclosure; Page 31-40; 138pp; English.  
PS  
XX This sequence represents a human T-type voltage-gated calcium (Ca)  
CC channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane  
CC bound glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2250 AA;

Query Match 90.3%; Score 10857; DB 2; Length 2250;  
Best Local Similarity 93.6%; Pred. No. 0;  
Matches 2084; Conservative 32; Mismatches 104; Indels 6; Gaps 4;  
QY 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSRWCLRTVCNPFERVSML 121  
Db 30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSRWCLRTVCNPFERISML 89



QY 122 VILLNCVTLMFRPCEDACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG 181  
Db 90 VILLNCVTLMFRPCEDACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG 149  
QY 182 DTWNRLDFFIIVAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 241  
Db 150 DTWNRLDFFIIVAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 209  
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVLEPPYQ TENEDESP 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVLEPPYQ TENEDESP 269  
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNQYYTNC SAGEHN 361  
Db 270 ICSQPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNWNQYYTNC SAGEHN 329  
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 421  
Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYBELLKYLVIYILRKAAR 481  
Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYBELLKYLVIYILRKAAR 449  
QY 482 RLAQVSRAIGVRAGLLSSPVARSQEQPPSGSCTSRSHRRLSVHLLVHHHHHHYHLGN 541  
Db 450 RLAQVSRAAGVRVGLLSSPAPLGQETQPSSSCSRSHRRLSVHLLVHHHHHHYHLGN 509  
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSPPTPPSGPPRGAESVHSFYHADCHLEPVRCQ 601  
Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPSPPTPPSGPPRGAESVHSFYHADCHLEPVRCQ 569  
QY 602 APPPRCPSEASGRVCSGKVYPTVHTSPPEILKOKALVEVAPSPGPTLTTSFNIPPGPF 661  
Db 570 APPPRSPSEASGRVCSGKVYPTVHTSPPETLKEKALVEVAASSGPTLTSLNIPPGPY 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721  
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689  
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSDLRDPHS - RRQRSGLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 748  
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMMLKLLVYGPFGYIKNPYN 841  
Db 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMMLKLLVYGPFGYIKNPYN 808  
QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRMLMRVCLKVRFPLAQQLVLMKTMNDVATF 901  
Db 809 IFDGVIVVISVWEIVGQGGGLSVLRTFRMLMRVCLKVRFPLAQQLVLMKTMNDVATF 868  
QY 902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAI VTFQILTQEDWNKV 961  
Db 869 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAI VTFQILTQEDWNKV 928  
QY 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGBATKSESEPDFFSPSYD 1021  
Db 929 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGBATKSESEPDFFSPSYD 988  
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIITHAATPM SHPKSSSTGVGEALGSGSRRTSS 1081  
Db 989 GDGDRKKCLALVSLGEHPELRKSLLPPLIITHAATPM SLPKSTSTGLGEALGPASRRTSS 1048  
QY 1082 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSSRRSRNSLGRAPSLKRSPSGERS 1141  
Db 1049 SGSAEPGAA - HEMKSPSARSSPHSPWSAASSWTSSRRSRNSLGRAPSLKRSPSGERS 1107  
QY 1142 LLSGEGQESQDEEESSEEDRASPA GSDHRRHGSGLERAKSSFDPD TLQVPLHRTASGR 1201  
Db 1108 LLSGEGQESQDEEESSEERASPA GSDHRRHGSGLERAKSSFDPD TLQVPLHRTASGR 1167

QY 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACC RE 1261  
Db 1168 GSASEHQDCNGKSASGRRLARALRPDDPPLDGGDDADDEGNLSKGERVRAWIRARLPAC CLE 1227  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1321  
Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFL 1287  
QY 1322 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1381  
Db 1288 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1347  
QY 1382 TKILGMLRVLRLLRTLRLRPLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILG 1441  
Db 1348 TKILGMLRVLRLLRTLRLRPLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILG 1407  
QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFNDLGOALMSLFLVASKOGWVD 1501  
Db 1408 VQLFKGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFNDLGOALMSLFLVASKOGWVD 1467  
QY 1502 IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQEER 1561  
Db 1468 IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQEER 1527  
QY 1562 EARRREEKRLRLEKKRSKEKQMAEAOCKPYYSYDSYRFRLLVHHLCTSHYLDL FITGVI 1621  
Db 1528 EARRREEKRLRLEKKRSKEKQMAEAOCKPYYSYDSYRFRLLVHHLCTSHYLDL FITGVI 1587  
QY 1622 GLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVFESVFKLVAFAFRFFQDRWNQDLA 1681  
Db 1588 GLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVLESVFKLVAFAFRFFQDRWNQDLA 1647  
QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALHTVMQALP 1741  
Db 1648 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALHTVMQALP 1707  
QY 1742 QVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPC EGLGRHATFRNFGMAFLT LFRVSTG 1801  
Db 1708 QVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPC EGLGRHATFRNFGMAFLT LFRVSTG 1767  
QY 1802 DNWNGIMKDPDRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1861  
Db 1768 DNWNGIMKDTLRDQDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1827  
QY 1862 KEEAELEAELEEMKTLSPQPHSPPLGSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921  
Db 1828 KEEAELEAELEEMKTLSPQPHSPPLGSPFLWPVGVEGVNSTDSPKPGALHPAAHARSASHF 1887  
QY 1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHARGWL 1981  
Db 1888 SLEHPTMQPHPTLP - - GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEGPLGHRGWGL 1944  
QY 1982 PKAQSGSILSVHSQPADTSCILQPKDVHVL LQPHGAPTWGAI PKLPPGRSPLAQRPLR 2041  
Db 1945 PKAQSGSVLSVHSQPADTSYILQPKDAPHL LQPHSAPTWTGTIPKLPPGRSPLAQRPLR 2004  
QY 2042 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101  
Db 2005 RQAAIRTDSDLVQGLGSRREDLLAEVSGPSPPLARAYSFWGQSSSTAQQQHSRSHSKIKHM 2064  
QY 2102 RLPAPCPGLEPSWAKDPPETRSSLDELDTELS WISGDLL - PSSQEPLFPRDLKCCYSVET 2160  
Db 2065 TTPAPCPGPEPNWKGPPETRSSLDELDTELS WISGDLLPPGGQEBEPPSPRDLKCCYSVEA 2124  
QY 2161 QSCRRRPGFWLDEQRRHSIAVSCLDGSPRLCPSPSSLGQPLGPGSGRPPKKLSPPSI 2220  
Db 2125 QSCQRRPTSWLDEQRRHSIAVSCLDGSPHLGTDPSNLGGQPLGPGSGRPPKKLSPPSI 2184  
QY 2221 SIDPPESQGSRRPPCSPGVCLRRRAPASDSKDP SVSSPLDSTAASPSPKDTLSLSGLSSD 2280  
Db 2185 TIDPPESQGRPTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLVSLSGLSSD 2244  
QY 2281 PTMDMP 2286

Db 2245 PADLDP 2250

RESULT 8  
AAY14588  
ID AAY14588 standard; protein; 2268 AA.  
XX  
AC AAY14588;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human T-type voltage-gated Ca channel alpha-1-G (hCav1.1c).  
XX  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX  
OS Homo sapiens.  
XX  
PN WO9929847-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
DR N-PSDB; AAX83483.  
XX  
PT New T-type voltage-gated calcium channels.  
XX  
PS Disclosure; Page 49-58; 138pp; English.  
XX  
CC This sequence represents a human T-type voltage-gated calcium (Ca)  
CC channel alpha-1-G designated hCav1.1c. Voltage gated channels are membrane  
CC bound glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2268 AA;

Query Match 90.1%; Score 10833; DB 2; Length 2268;  
Best Local Similarity 92.8%; Pred. No. 0;  
Matches 2083; Conservative 32; Mismatches 105; Indels 24; Gaps 5;

QY 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVFFYLSQDSRPSWCLRTVCNPNWFERVSM 121  
Db 30 GRPGPSAEKDPGSADSEAGLPYPALAPVFFYLSQDSRPSWCLRTVCNPNWFERISML 89  
QY 122 VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVMVKWVALGIFGKKCYLG 181  
Db 90 VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVMVKWVALGIFGKKCYLG 149  
QY 182 DTWNRLDFFIIVAGMLEYSLDLQNVSFSAVRTVRILPLRAINRVPSMRILVTLTLLDTLP 241  
Db 150 DTWNRLDFFIIVAGMLEYSLDLQNVSFSAVRTVRILPLRAINRVPSMRILVTLTLLDTLP 209

QY 242 MLGNVLLLCFFVFFIFGIVGVQWAGLLRNRCFLPENFSLPSVDLEPYQYOTENEDESPF 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQWAGLLRNRCFLPENFSLPSVDLEPYQYOTENEDESPF 269  
QY 302 ICSQPRENGMRSRCSVPVTLRGEGGGPPCPSLDYETVNSSNTTCVNMNQYVYTNCSAGEHN 361  
Db 270 ICSQPRENGMRSRCSVPVTLRGEGGGPPCGLDYEAYNSSNTTCVNMNQYVYTNCSAGEHN 329  
QY 362 PFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421  
Db 330 PFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQRLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 481  
Db 390 CLVVIATQFSETKQRESQRLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 449  
QY 482 RLAQVSRAGVRAGLLSPPVARSGQEPQPSGCTSRSHRRLSVHHLVHHHHHHHHVHLGN 541  
Db 450 RLAQVSRAGVRAGLLSPPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHVHLGN 509  
QY 542 GTLRVPRAPEIQDRDANGSRRLMLPPPSTPTSGGPPRGAESVHSFYHADCHLEPVRQ 601  
Db 510 GTLRVPRAPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRQ 569  
QY 602 APPPRCPSEASGRVTGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPTLTLSFNIPPGPF 661  
Db 570 APPPRCPSEASGRVTGSGKVYPTVHTSPPPETLKEKALVEVAASSGPTLTSLNIPPGPY 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSPCYCARTGAGEPESADHVMPDSD 721  
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSPCYCARAGAGEVELADREMPDSD 689  
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSDLRDPHS-RRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 748  
QY 782 IMIALVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFYIKNPYN 841  
Db 749 IMIALVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFYIKNPYN 808  
QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF 901  
Db 809 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF 868  
QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGTDLDRKNFDSLLWAIIVTFQILTQEDWNV 961  
Db 869 CMLLMFIFIFISILGMHLFGCKFASERDGTDLDRKNFDSLLWAIIVTFQILTQEDWNV 928  
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPSVD 1021  
Db 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPSLD 988  
QY 1022 GDGRKKRLALVALGEHAELRKSLLPPLIHTAATPMHPKSSSTGVGEALGSGSRRTSS 1081  
Db 989 GDGRKKCLALVSLGEHPELRKSLPPLIHTAATPMSLPKSTSTGLGEALGPASRTSS 1048  
QY 1082 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRS 1141  
Db 1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRS 1107  
QY 1142 LLSGEGQESQDEEESSEDRASPGSDHRHRSGLEREAKSSFDLPDTLQVPLHRTASGR 1201  
Db 1108 LLSGEGQESQDEEESSEERASPPGSDHRHRSGLEREAKSSFDLPDTLQVPLHRTASGR 1167  
QY 1202 SSASEHQDCNGKKSASGLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261  
Db 1168 GSASEHQDCNGKKSASGLARALRPPDPLDGGDDADDEGNLSKGERVRAWIRARLPACCLE 1227  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFL 1321  
Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFL 1287



Db 30 GRPGGSAEKDPSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNWPFERISML 89  
Qy 122 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVMVMAIGIFGKKCYLG 181  
Db 90 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVMVMAIGIFGKKCYLG 149  
Qy 182 DTWNRDLFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP 241  
Db 150 DTWNRDLFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP 209  
Qy 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLNRNRCFLPENFSLPLSDLEPYQIENEDESP 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLNRNRCFLPENFSLPLSDLEPYQIENEDESP 269  
Qy 302 ICSPRENGMRSCRSVPTLRGEGGGPPCSDIYETYNSSNTTCVNNQYNTNCSAGEHN 361  
Db 270 ICSPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNNQYNTNCSAGEHN 329  
Qy 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 421  
Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 389  
Qy 422 CLVVIATQSETKQRESQOLMRQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 481  
Db 390 CLVVIATQSETKQRESQOLMRQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 449  
Qy 482 RLAQVSRAGVRAGLSSPVARSGQEPQPSGCTRSRRLSVHLLVHHHHHHHHYHLGN 541  
Db 450 RLAQVSRAGVRAGLSSPAPLGQETQPSSSCSRSRRLSVHLLVHHHHHHHHYHLGN 509  
Qy 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601  
Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRQ 569  
Qy 602 APPPRCPSEASGRVSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF 661  
Db 570 APPPRCPSEASGRVSGKVPTVHTSPPETLKEKALVEVAASSGPTLTSTFNIPPGPY 629  
Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESEADHVPDSD 721  
Db 630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689  
Qy 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGDAEPSSVLAFWRLICDTRKIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSDLRDPHS -RRQSLGDAEPSSVLAFWRLICDTRKIVDSKYFGRG 748  
Qy 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 841  
Db 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 808  
Qy 842 IFDGVIVVSWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDNVATF 901  
Db 809 IFDGVIVVSWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDNVATF 868  
Qy 902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 961  
Db 869 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 928  
Qy 962 LYNGMASTSSWAALYFIALMTFNGYVLFNLLVAILVEGFAE----- 1003  
Db 929 LYNGMASTSSWAALYFIALMTFNGYVLFNLLVAILVEGFAEISKREDAAGQSLCQLP 988  
Qy 1004 -----GDATKSESEPDFFSPSVDGDRKKRLALVALGEHAELRKSLLPLIHTAATPM 1058  
Db 989 VDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPLIHTAATPM 1048  
Qy 1059 SHPKSSSTGVGEALGSGRRRTSSSGAEPGAHHEMKCPSPARSPPSWSAASSWTSRR 1118  
Db 1049 SLPKSTSTGLGEALGPASRRRTSSSGAEPGAA -HEMKSPARSPPSWSAASSWTSRR 1107  
Qy 1119 SSRNLSGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEDRASPAGSDHRRHGRSLERE 1178  
Db 1108 SSRNLSGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEERASPAGSDHRRHGRSLERE 1167

Qy 1179 AKSSFDPDPTLQVPLHRTASGRSSASEHQCNGKSASGRRLARTLRTDDPQLDGDNDDE 1238  
Db 1168 AKSSFDPDPTLQVPLHRTASGRSSASEHQCNGKSASGRRLARLPDDPPLDGDNDDE 1227  
Qy 1239 GNLSKGERIQAWRSRLPACCRERDSWASYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1298  
Db 1228 GNLSKGERVRAWIRARLPACCLERDSWASYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1287  
Qy 1299 LNCITIAMERPKIDPHSAERIFLTLISNYIFTAFLAEMTVKVVALGWCFCGEQAYLRSSWN 1358  
Db 1288 LNCITIAMERPKIDPHSAERIFLTLISNYIFTAFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347  
Qy 1359 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMS 1418  
Db 1348 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMS 1407  
Qy 1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRYWRVHKY 1478  
Db 1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRYWRVHKY 1467  
Qy 1479 NFDNLGQALMSLVASKDGVIMYDGLDVAVGDDQOPIMNHNPMWMLLYFISFLIVAFF 1538  
Db 1468 NFDNLGQALMSLVASKDGVIMYDGLDVAVGDDQOPIMNHNPMWMLLYFISFLIVAFF 1527  
Qy 1539 VLNMFGVAVENFHKCRHQHEEEARREERKRLRLEKRRSKEKQMAEAOCKPYYSYS 1598  
Db 1528 VLNMFGVAVENFHKCRHQHEEEARREERKRLRLEKRRSKEKQMAEAOCKPYYSYS 1587  
Qy 1599 RFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQLDEALKICNYIFTVIFVLES 1658  
Db 1588 RFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQLDEALKICNYIFTVIFVLES 1647  
Qy 1659 VFKLVAFAFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRAR 1718  
Db 1648 VFKLVAFAFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRAR 1707  
Qy 1719 VLKLLKMAVGMRAALLHTVMQALPQVGNLGLLMLLFFIFAAALGVELFGDLECEHPCEG 1778  
Db 1708 VLKLLKMAVGMRAALLHTVMQALPQVGNLGLLMLLFFIFAAALGVELFGDLECEHPCEG 1767  
Qy 1779 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPDRDCDQESTCVNTVISPFIYFVSFLTA 1838  
Db 1768 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPDRDCDQESTCVNTVISPFIYFVSFLTA 1827  
Qy 1839 QFVLNVVVIAMKHLSEENKEAKEAEAELEAELEEMKTLSPQSPHPLGSPFLWPGEV 1898  
Db 1828 QFVLNVVVIAMKHLSEENKEAKEAEAELEAELEEMKTLSPQSPHPLGSPFLWPGEV 1887  
Qy 1899 NSTDSPKPGAPHTTAHGAASGFSLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLP 1958  
Db 1888 DSPDSPKPGALPHAHARSASHFSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLP 1944  
Qy 1959 NDSYMCNRNGSTAESLGRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHLLQPHGA 2018  
Db 1945 NDSYMCNRHGSTAEGLHGRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAHLLQPHSA 2004  
Qy 2019 PTWGAIPKLPPGSRPLAQRPLRRQAARTDSDVQGLSREDLLSEVSGSPCLTRSSS 2078  
Db 2005 PTWGTIPKLPPGSRPLAQRPLRRQAARTDSDVQGLSREDLLAEVSGSPPLARAYS 2064  
Qy 2079 FWGSSIQVQQRSGTQSKVSKHIRLPAPCGLEPSWAKDPPETRSSLELDTLSWISGDL 2138  
Db 2065 FWGSSITQAQOHSRSHSKISKHMTPPAPCGPEPNWKGPPETRSSLELDTLSWISGDL 2124  
Qy 2139 L-PSQEEPLFRDLKKCYSVETQSCRRRRPGFWLDEQRRHSIAVSCLDGSGQPLCPSPS 2197  
Db 2125 LPPGGQEEPPSPRDLKKCYVEAQSCQRRRTSWLDEQRRHSIAVSCLDGSGQPLGTDPS 2184  
Qy 2198 SLGGQPLGPGSRPKKLLSPPSISIDPPESQGRPPCPSPGVCLRRRAPASDKDPSVSP 2257  
Db 2185 NLGGQPLGPGSRPKKLLSPPSITIDPPESQGRPTPPSPGICLRRRAPSSDKDPLASGP 2244





QY 1322 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1381  
Db 1288 TLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1347  
QY 1382 TKILGMLRVLRRLRLRPLRVRISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1441  
Db 1348 TKILGMLRVLRRLRLRPLRVRISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1407  
QY 1442 VOLFKGKFFVCQGEDTRNITNKSDCAEASVYRVRHKYNFQNLGQALMSLVFLASKDQWVD 1501  
Db 1408 VOLFKGKFFVCQGEDTRNITNKSDCAEASVYRVRHKYNFQNLGQALMSLVFLASKDQWVD 1467  
QY 1502 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFILLIVAFVFLNMPVGVVVENFHKCRQHOREE 1561  
Db 1468 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFILLIVAFVFLNMPVGVVVENFHKCRQHOREE 1527  
QY 1562 EARRREKRLRRLEKKRR-----SKEKQMAEAQCKPYSDYSRFRLLVHHLCTS 1610  
Db 1528 EARRREKRLRRLEKKRRNMLDDVIAAGSSASAASEAQCKPYSDYSRFRLLVHHLCTS 1587  
QY 1611 HYLDLFTIGVIGLNVVTMAMEHYQQOILDEALKICNYIFTVIFVESVFKLVAFAPRRF 1670  
Db 1588 HYLDLFTIGVIGLNVVTMAMEHYQQOILDEALKICNYIFTVIFVESVFKLVAFAPRRF 1647  
QY 1671 FQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMR 1730  
Db 1648 FQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMR 1707  
QY 1731 ALLHTVMQALPOVGNLGLLFFMLFFFAAGVLEFGDLECDETHPCCEGLGRHATFRNFGM 1790  
Db 1708 ALLHTVMQALPOVGNLGLLFFMLFFFAAGVLEFGDLECDETHPCCEGLGRHATFRNFGM 1767  
QY 1791 AFLTLFRVSTGDNWNGIMKDPDRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL 1850  
Db 1768 AFLTLFRVSTGDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL 1827  
QY 1851 MKHLEESNKEAEAEAELEAELEMTKLSPOPHSPGLSPFLWPGVEGVNSTDSPKPGAPH 1910  
Db 1828 MKHLEESNKEAEAEAELEAELEMTKLSPOPHSPGLSPFLWPGVEGVNSTDSPKPGALH 1887  
QY 1911 TTAHIGAASGFSLEHTMVPHPPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1970  
Db 1888 PAAHARSASHFSLEHTMQPHPTLPP-----GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTA 1944  
QY 1971 ERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHVLLOPHGAPTWGAIPKLPPP 2030  
Db 1945 EGPLGHRGWGLPKAQSGSVLSVHSQPADTSCYILQPKDAPHLLOPHSAPTWTGTPKLPPP 2004  
QY 2031 GRSPLAQRPLRRQAARTDSDVQGLSREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQR 2090  
Db 2005 GRSPLAQRPLRRQAARTDSDVQGLSREDLLAEVSGPSPPLARAYSFWGSSSTQAQOH 2064  
QY 2091 SGIQSKYSKHIRLPAPCPGLEPSPWAKOPPETRSSLELDTLSWISGDLI-PSSQEEPLFP 2149  
Db 2065 SRSHSKISKHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLIPLPGQEEPPSP 2124  
QY 2150 RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRCLPSPSSLGQPLGGPGS 2209  
Db 2125 RDLKKCYSVAEQSCQRRPTSNLDEQRRHSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPGS 2184  
QY 2210 RPKKLSPPSISIDPPESQSGRPPCSPGVCLRRRAPASDSKOPSVSSPLDSTAASPSPKK 2269  
Db 2185 RPKKLSPPSITIDPPESQGRPTTSPGICLRRRAPSSDSKOPLASGPPDSMAASPSPKK 2244  
QY 2270 DTLSLSGLSSDPTDMDP 2286  
Db 2245 DVLSLSGLSSDPAADLP 2261

RESULT 11  
AA14589  
ID AAY14589 standard; protein; 2243 AA.

XX AAY14589;  
AC  
XX  
XX 07-DEC-1999 (first entry)  
DT  
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavTid).  
DE  
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX Homo sapiens.  
OS  
XX WO9929847-A1.  
PN  
XX 17-JUN-1999.  
PD  
XX 30-OCT-1998; 98WO-US023161.  
PF  
XX 05-DEC-1997; 97US-00985809.  
PR  
XX (LOYO ) UNIV LOYOLA CHICAGO.  
PA  
XX Perez-Reyes E, Cribbs Lb;  
PI  
XX WPI; 1999-394972/33.  
XX N-PSDB; AAX83484.  
DR  
XX New T-type voltage-gated calcium channels.  
PT  
XX Disclosure; Page 58-67; 138pp; English.  
PS  
XX This sequence represents a human T-type voltage-gated calcium (Ca)  
CC channel alpha-1-G designated hCavTid. Voltage gated channels are membrane  
CC bound glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2243 AA;  
Query Match 89.8%; Score 10806.5; DB 2; Length 2243;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;  
QY 62 GAAGAGSTKDPGSADSEAGLPPALAPVWFFYLSQDSRPRSWCLRTVCNPFERVSM 121  
Db 30 GRPGGSAEKDPGSADSEAGLPPALAPVWFFYLSQDSRPRSWCLRTVCNPFERVSM 89  
QY 122 VILLNCVTLMGFRPCEDIACDQSQRILQAFDDFIFAFFAVEMVVMVALGIFGKCYLG 181  
Db 90 VILLNCVTLMGFRPCEDIACDQSQRILQAFDDFIFAFFAVEMVVMVALGIFGKCYLG 149  
QY 182 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVLLDLP 241  
Db 150 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVLLDLP 209  
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVLDLPEYQOTENEDESPF 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVLDLPEYQOTENEDESPF 269  
QY 302 ICQPRENGMRSCRSVPTLRGEGGGGPPCSDLYETYNSSNTTCVNMNQYTCNSAGEHN 361  
|||||

Db 270 ICSQPRENGMRSCRSVPTLRGDDGGGPPCGLDYEAYNSSNTTCVWNQYTYNCSAGEHN 329

Qy 362 PFKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421

Db 330 PFKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 389

Qy 422 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEEELKYLVIYILRKAAR 481

Db 390 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEEELKYLVIYILRKAAR 449

Qy 482 RLAQVSRAIGVRAGLLSPVARSQEQPQSGSCSTRSHRRLSVHLLVHHHHHHHHYHLGN 541

Db 450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVHLLVHHHHHHHHYHLGN 509

Qy 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 601

Db 510 GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQ 569

Qy 602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF 661

Db 570 APPPRSPSEASGRTVSGKVYPTVHTSPPETLKEKALVEVAASSGPTLTSLNIPPGPY 629

Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721

Db 630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Qy 722 SEAVYEFTQDAQHSDLRDPHSRRRQORSLGPDAPFSSVLAFWRLICDTRKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHS-RRQORSLGPDAPFSSVLAFWRLICDTRKIVDSKYFGRG 748

Qy 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYN 841

Db 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYN 808

Qy 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDVATF 901

Db 809 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDVATF 868

Qy 902 CMLMLFIFIFISILGMLHFGCKFASERDGTLDPRKNFDSLWAIIVTFQILTQEDWNKV 961

Db 869 CMLMLFIFIFISILGMLHFGCKFASERDGTLDPRKNFDSLWAIIVTFQILTQEDWNKV 928

Qy 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLVAILVEGFQAEADATKSESEPDFFSPSVD 1021

Db 929 LYNMGASTSSWAALYFIALMTFGNYVLFNLVAILVEGFQAEADANKSESEPDFFSPSLD 988

Qy 1022 GDGDRKKRLALVALGEHAEIRKSLPLLIHTAATPMHSPKSSSTGVEALGSGSRRTSS 1081

Db 989 GDGDRKKCLALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSS 1048

Qy 1082 SGSAEPGAHHKCPSPARSSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSGERRS 1141

Db 1049 SGSAEPGAA-HEMKSPSPARSSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSGERRS 1107

Qy 1142 LLSGEGQESQDEEESSEEDRASPAAGSDHRRHRSGLEREAKSSFOLDPTLQVPLHRTASGR 1201

Db 1108 LLSGEGQESQDEEESSEERASPAAGSDHRRHRSGLEREAKSSFOLDPTLQVPLHRTASGR 1167

Qy 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGDNDDEGNLSKGERIQAWVRSLPACCRE 1261

Db 1168 GSASEHQDCNGKSASGRRLARALRPDDPPLDGDADDEGNLSKGERVRAWRARLPACCLE 1227

Qy 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERKIDPHSAERIFL 1321

Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERKIDPHSAERIFL 1287

Qy 1322 TLSNYIFTAVFLAEMTKVVALGWCFCGEQAYLRSSWNVLDGLLVLSIDILVSMVSDSG 1381

Db 1288 TLSNYIFTAVFLAEMTKVVALGWCFCGEQAYLRSSWNVLDGLLVLSIDILVSMVSDSG 1347

Qy 1382 TKILGMLRVLLRLRLRLPLRPLVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1441

1348 TKILGMLRVLLRLRLRLPLRPLVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1407

Qy 1442 VQLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGVVD 1501

Db 1408 VQLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGVVD 1467

Qy 1502 IMYDGLDAVVDQOPIMNHNPMMLLYFISFLLIVAFVFLNMFVGVVVENFHKCRHQESEE 1561

Db 1468 IMYDGLDAVVDQOPIMNHNPMMLLYFISFLLIVAFVFLNMFVGVVVENFHKCRHQESEE 1527

Qy 1562 EARRREKRLRRLEKKRRSKEKQMAEAQCKPYSDYSRFRLLVHLCCTSHYLDLFTITGVI 1621

Db 1528 EARRREKRLRRLEKKRR-:-----KAQCKPYSDYSRFRLLVHLCCTSHYLDLFTITGVI 1580

Qy 1622 GLNVVTMAMEHYQQOILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQLDLA 1681

Db 1581 GLNVVTMAMEHYQQOILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLDLA 1640

Qy 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGRALLHTVMQALP 1741

Db 1641 IVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGRALLDTVMQALP 1700

Qy 1742 QVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1801

Db 1701 QVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1760

Qy 1802 DNWNGIMKOPSRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1861

Db 1761 DNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1820

Qy 1862 KEEAELEAELELEMKTLSPQPHSPGLSPFVPGVEGVNSTDSPKPGAPHHTTAHIGAASGF 1921

Db 1821 KEEAELEAELELEMKTLSPQPHSPGLSPFVPGVEGVNSTDSPKPGALHPAAHARSASHF 1880

Qy 1922 SLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRHWGL 1981

Db 1881 SLEHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGRHWGL 1937

Qy 1982 PKAQSGLSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPGRSPLAQRPRLR 2041

Db 1938 PKAQSGLSVHSQPADTSYILQLPKADAPHLLOPHSAPTWTGTIPKLPPGRSPLAQRPRLR 1997

Qy 2042 RQAAIRTDSDLVQGLGSRREDLLSEVSGSPCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHI 2101

Db 1998 RQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQQHRSRSHSKISKHM 2057

Qy 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLL-PSSQEEPLPRDLKCCYSVET 2160

Db 2058 TTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLLPPGGQEEPPSPRDLKCCYSVEA 2117

Qy 2161 QSCRRRPGFWLDEQRHRSIAVSCLDGSPQRLCPSPSSLGGQPLGGPSRPKKLSPPSI 2220

Db 2118 QSCORRPTSWLDEQRHRSIAVSCLDGSPQLHGTDPNLSGQPLGGPSRPKKLSPPSI 2177

Qy 2221 SIDPPESQSRPPCSPGVCLRRRAPASDSKDPVSVPSSPLDSTAASPSPKDITLSLGLSSD 2280

Db 2178 TIDPPESQGPRTPPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVLSLGLSSD 2237

Qy 2281 PTDMDP 2286

Db 2238 PADLDP 2243

RESULT 12

ADJ68819

ID ADJ68819 standard; protein; 2243 AA.

XX

AC ADJ68819;

XX

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID625.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX Homo sapiens.  
OS WO2003087768-A2.  
PN 23-OCT-2003.  
XX 04-APR-2003; 2003WO-US010870.  
XX 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0389987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
PI WPI; 2003-845369/78.  
DR Identifying a mitochondrial target for drug screening assays and for  
XX treating diseases associated with altered mitochondrial function,  
XX comprises detecting a modified polypeptide in a sample and correlating  
XX with the disease.  
XX Claim 1; SEQ ID NO 625; 180pp; English.  
PS This invention relates to novel mitochondrial targets that can be used  
XX for therapeutic intervention in treating a disease associated with  
XX altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nontropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX Sequence 2243 AA;  
SQ Query Match 89.8%; Score 10806.5; DB 7; Length 2243;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;  
QY 62 GAAGAGSTKDPGSDSEAGLPALAPVVFYLSQDSRPRSWCLRTVCNPFVSM 121  
DB 30 GRPGGSAEKDPGSDSEAGLPALAPVVFYLSQDSRPRSWCLRTVCNPFERISML 89  
QY 122 VILLNCVTLMGFRPCEDACDSQRCRILQAFDDFIFAFVAVEMVVKMVALGIFGKKCYLG 181  
DB 90 VILLNCVTLMGFRPCEDACDSQRCRILQAFDDFIFAFVAVEMVVKMVALGIFGKKCYLG 149  
QY 182 DTWNRDLFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLLDTLP 241  
DB 150 DTWNRDLFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLLDTLP 209  
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLPLSVLDLEPYQTENEDES PF 301  
DB 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLPLSVLDLEPYQTENEDES PF 269  
QY 302 ICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNYTNCAGEHN 361

DB 270 ICSPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNWNYTNCAGEHN 329  
QY 362 PFKGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSFYNYFIYILLIIVGSFFMINL 421  
DB 330 PFKGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSFYNYFIYILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 481  
DB 390 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 449  
QY 482 RLAQVSRAGVRAGLLSPPVARSQEQPQPSGCTSRHRLSVHHLVHHHHHHHHYHLGN 541  
DB 450 RLAQVSRAGVRAGLLSPPVARSQEQPQPSGCTSRHRLSVHHLVHHHHHHHHYHLGN 509  
QY 542 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 601  
DB 510 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCQ 569  
QY 602 APPRCPSSEASGRTVSGKVYPTVHTSPPPEILKDALVEVAPSPGPTLTSTFNIPPGPF 661  
DB 570 APPRCPSSEASGRTVSGKVYPTVHTSPPPEILKDALVEVAPSPGPTLTSTFNIPPGPY 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPEPSADHVPDSD 721  
DB 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPEPSADHVPDSD 689  
QY 722 SEAVVEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
DB 690 SEAVVEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 748  
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 841  
DB 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 808  
QY 842 IFDGVIVVISVWEIVGOQGGSLVLRTRFLMRVLKLVRFPAQRLQVLVLMKTMNDVATF 901  
DB 809 IFDGVIVVISVWEIVGOQGGSLVLRTRFLMRVLKLVRFPAQRLQVLVLMKTMNDVATF 868  
QY 902 CMLLMFLFIFSIILGMLHFGCKFASERDGTLPDRKNFDSLWAIWTVFQILTQEDWNKV 961  
DB 869 CMLLMFLFIFSIILGMLHFGCKFASERDGTLPDRKNFDSLWAIWTVFQILTQEDWNKV 928  
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAEGDATKSESEDFSPSVD 1021  
DB 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAEGDATKSESEDFSPSVD 988  
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMSPKSSSTGVGEALGSGSRRTSS 1081  
DB 989 GDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMSPKSSSTGVGEALGSGSRRTSS 1048  
QY 1082 SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSRNRSLGRAPSLKRRSPSGERRS 1141  
DB 1049 SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSRNRSLGRAPSLKRRSPSGERRS 1107  
QY 1142 LLSGEGQESQDEESSEEDRASPGSDHHRGSLEREAKSSFDLPTLTQVPLHRTASGR 1201  
DB 1108 LLSGEGQESQDEESSEEDRASPGSDHHRGSLEREAKSSFDLPTLTQVPLHRTASGR 1167  
QY 1202 SSASEHQDCNGKSGASRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRILPACC 1261  
DB 1168 GSASEHQDCNGKSGASRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRILPACC 1227  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFL 1321  
DB 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFL 1287  
QY 1322 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDG 1381  
DB 1288 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDG 1347  
QY 1382 TKILGMLRVLRLRLTRPLRPLRVISRAQGLKLVVETLMSSLKPIGNIIVICCAFFIIFGILG 1441





QY 302 ICSQPRENGMRSRCSVPPTLRGEGGGPPCSDYETYNSSNTTCVNMNOYVNCSSAGEHN 361  
Db 270 ICSQPRENGMRSRCSVPPTLRGEGGGPPCGLDYEAYNSSNTTCVNMNOYVNCSSAGEHN 329  
QY 362 PFKGAINFDNIGYAWTAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421  
Db 330 PFKGAINFDNIGYAWTAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 481  
Db 390 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 449  
QY 482 RLAQVSRAGVRAGLLSSPVARSQOEPPQSGSCTRSRRLSVHHLVHHHHHHHHYHLGN 541  
Db 450 RLAQVSRAGVRAGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGN 509  
QY 542 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601  
Db 510 GTLRVPASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQ 569  
QY 602 APPPRCSEASGRTVSGKVPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 661  
Db 570 APPPRSPSEASGRTVSGKVPTVHTSPPETLKEKALVEVAASSGPTLTSLNIPPGPY 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGDPSCPYCARTGAGEPESADHVMPDSD 721  
Db 630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGDPSCPYCARAGAGEVELADREMPDSD 689  
QY 722 SEAVYEFTQDAQHSDDLDRPHSRRRQSLGPDAPSSVLAFWRLICDTPFKIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSDDLDRPHS - RRQRS LGPDAPSSVLAFWRLICDTPFKIVDSKYFGRG 748  
QY 782 IMIAILVNTLSMGLEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVGPFYIKNPYN 841  
Db 749 IMIAILVNTLSMGLEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVGPFYIKNPYN 808  
QY 842 IPDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATF 901  
Db 809 IPDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATF 868  
QY 902 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQIILTQEDWNKV 961  
Db 869 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQIILTQEDWNKV 928  
QY 962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAE----- 1003  
Db 929 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEISKREDASGQLSCIQLP 988  
QY 1004 -----GDATKSESEPDPFFSPSLDGDGRKKCLALVSLGEHPELRSLLPPLIIHTAATPM 1058  
Db 989 VDSQGGDANKSESEPDPFFSPSLDGDGRKKCLALVSLGEHPELRSLLPPLIIHTAATPM 1048  
QY 1059 SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAHHEMKCPPSARSPHSPWSAASSTSR 1118  
Db 1049 SLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA - HEMKSPPSARSPHSPWSAASSTSR 1107  
QY 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEESESSEEDRASAGSDHRRHRSLE 1178  
Db 1108 SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEESESSEERASAPAGSDHRRHRSLE 1167  
QY 1179 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGRLARTLRTDPLDGDNDDE 1238  
Db 1168 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGRLARALRPDPLDGDNDDE 1227  
QY 1239 GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1298  
Db 1228 GNLSKGERVRAMTARLPACCLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1287  
QY 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEQAYLRSSWN 1358  
Db 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEQAYLRSSWN 1347

QY 1359 VLDGLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRLPLRVISRAOGLKLVVETLMS 1418  
Db 1348 VLDGLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRLPLRVISRAOGLKLVVETLMS 1407  
QY 1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVQCGEDTRNITNKSDCAEASRVRHKY 1478  
Db 1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVQCGEDTRNITNKSDCAEASRVRHKY 1467  
QY 1479 NFDNLGOALMSLFLVASKDGVWDIMYDGLDVGVDQOQPIMNHNPMWLLYFISFLLIVAFF 1538  
Db 1468 NFDNLGOALMSLFLVASKDGVWDIMYDGLDVGVDQOQPIMNHNPMWLLYFISFLLIVAFF 1527  
QY 1539 VLMFVGVVVENFHKCRHQHEEEARRRERKRRLRLEKKRR-----SKEKQMAE 1587  
Db 1528 VLMFVGVVVENFHKCRHQHEEEARRRERKRRLRLEKKRRNMLDDVVIASGSSASAASE 1587  
QY 1588 AQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTMAMEHYQQPQILDEALKICN 1647  
Db 1588 AQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTMAMEHYQQPQILDEALKICN 1647  
QY 1648 YIFTVIFVFESVFKLVAFARFRFQDRWNQDLAIVLISIMGITLEEIEVNLSUPINPTI 1707  
Db 1648 YIFTVIFVLESVFKLVAFGFRFQDRWNQDLAIVLISIMGITLEEIEVNLSUPINPTI 1707  
QY 1708 IRIMRVLRIARVLKLMVAGMRALLHTVMQALPQVGNLGLLMLFFIFAALGVLEFGD 1767  
Db 1708 IRIMRVLRIARVLKLMVAGMRALLHTVMQALPQVGNLGLLMLFFIFAALGVLEFGD 1767  
QY 1768 LECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDPSSRDCQESTCVNTVIS 1827  
Db 1768 LECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDTLRDCQESTCVNTVIS 1827  
QY 1828 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEEAELEAELMKTLSPOPHSPLG 1887  
Db 1828 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEEAELEAELMKTLSPOPHSPLG 1887  
QY 1888 SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPT----- 1927  
Db 1888 SPFLWPGVEGVNSTDSPKPGALHPAAHARSASHFSLEHPTDRQLFDTISLLIQGSLEWEL 1947  
QY 1928 ----- 1927  
Db 1948 KLMDLAGPGGQPSAFPAPSILGSGSDPQIPLAEMEALSLTSEIVSEPSCSLALTDSDLPD 2007  
QY 1928 -----MVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNCRNGSTAERSL 1974  
Db 2008 DMHTLLLSALESNMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCNCRHGSTAEGPL 2064  
QY 1975 GHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHVLLOPHGAPTWGAIPKLPPGRSP 2034  
Db 2065 GHRGWGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLQPHSAPTWTGTIPKLPPGRSP 2124  
QY 2035 LAQRPLRRQAAIRTDSDLVQGLGSRDILLSEVSGPSCPLTRSSSFVGGSSIOVQQRSGIQ 2094  
Db 2125 LAQRPLRRQAAIRTDSDLVQGLGSRDILLAEVSGPSPPLARAYSFWGQSSTQAQHSRSH 2184  
QY 2095 SKVSKHIRLPAPCPGLEPSPWAKOPPETRSSLELDTLSWISGDL- PSSQEEPLFPRDLK 2153  
Db 2185 SKISKHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLK 2244  
QY 2154 KCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSSSLGGQPLGGPSRPPK 2213  
Db 2245 KCYSVQAQSCQRRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDFSNLGGQPLGGPSRPPK 2304  
QY 2214 KLSPPSISIDPPESQSGSRPPCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKDTLS 2273  
Db 2305 KLSPPSITIDPPESQSGRTPPSPGICLRRRAPSSDSKDPLASGPDMSAASPSPKDVLS 2364  
QY 2274 LSGLSSDPTDMDP 2286  
Db 2365 LSGLSSDPAADLP 2377

RESULT 14  
AAB66481  
ID AAB66481 standard; protein; 2266 AA.  
XX  
AC AAB66481;  
XX  
DT 09-APR-2001 (first entry)  
XX  
DE Human alpha-IG T-type calcium channel protein.  
XX  
KW Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;  
KW T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;  
KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.  
XX  
OS Homo sapiens.  
XX  
PN WO200102561-A2.  
XX  
PD 11-JAN-2001.  
XX  
PF 04-JUL-2000; 2000WO-CA000794.  
XX  
PR 02-JUL-1999; 99US-00346794.  
XX  
PA (NEUR-) NEUROMED TECHNOLOGIES INC.  
XX  
PI Snutch TP, Baillie DL;  
XX  
DR WPI; 2001-123111/13.  
DR N-PSDB; AAF31684.  
XX  
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating  
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
PT epilepsy.  
XX  
PS Example 3; Fig 6; 103pp; English.  
XX  
CC The present sequence is given in a specification providing sequences and  
CC partial sequences for three types of mammalian (human and rat) T-type  
CC calcium channel subunits. An expression cassette has been generated which  
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha\_1  
CC subunit operably linked to control sequences to effect its expression.  
CC The novel calcium channel nucleic acids and proteins are useful for  
CC treating conditions characterised by undesirable levels of T-type calcium  
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
CC hypertension, sleep disorder and epilepsy  
XX  
SQ Sequence 2266 AA;  
  
Query Match 87.6%; Score 10533; DB 4; Length 2266;  
Best Local Similarity 91.2%; Pred. No. 0;  
Matches 2050; Conservative 38; Mismatches 125; Indels 36; Gaps 6;  
  
QY 62 GAAGAGSTKDPGSADSEAEGLYPALAPVFFYLSQDSRPSWCLRTVCNPFERVSM 121  
DB 30 GRPGSABKDPGSADSEAEGLYPALAPVFFYLSQDSRPSWCLRTVCNPFERISML 89  
  
QY 122 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIFAFVAVMVVXNVALGIFGKCYLG 181  
DB 90 VILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIFAFVAVMVVXNVALGIFGKCYLG 149  
  
QY 182 DTWNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVLLDTP 241  
DB 150 DTNNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVLLDTP 209  
  
QY 242 MLGNVLLLCFFVFFIFIGVGVQLWAGLLRNRCFLPENFSLPLSVDLPEYYQTENEDES 301  
DB 210 MLGNVLLLCFFVFFIFIGVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYTENEDES 269  
  
QY 302 ICSPRENGMRSRCSRVPTLRGGGGPPCSLDYETYNSSNTTCVWNQYTTNCSAGEHN 361  
DB 270 ICSPRENGMRSRCSRVPTLRGGGGPPCGLDYEAYNSSSKTTCVWNQYTTNCSAGEHN 329

QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421  
DB 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 389  
  
QY 422 CLVVIATQFSETKQRESQLMREQRVRFSLSNASTLASFSEPGSCYEELLYLVYLKKAAR 481  
DB 390 CLVVIATQFSETKQRESQLMREQRVRFSLSNASTLASFSEPGSCYEELLYLVYLKKAAR 449  
  
QY 482 RLAQVSRAGVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541  
DB 450 RLAQVSRAGVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 509  
  
QY 542 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTPSGGPRGAESVHSFYHADCHLEPVCQ 601  
DB 510 GTLRVPASPEIQDRDANGSRRLMLPPPSTPTPSGGPRGAESVHSFYHADCHLEPVCQ 569  
  
QY 602 APPRCPSEASGRTVSGSKYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTNIPPPFF 661  
DB 570 APPRCPSEASGRTVSGSKYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTNIPPPFF 629  
  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGDPSCPCYARTGAGEPEADHVPDSD 721  
DB 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGDPSCPCYARTGAGEPEADHVPDSD 689  
  
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
DB 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 748  
  
QY 782 IMIALVNTLSMGIEYHEQEPELTNALEISNIVFTSLFALEMLLKLIVYGFYKPNYN 841  
DB 749 IMIALVNTLSMGIEYHEQEPELTNALEISNIVFTSLFALEMLLKLIVYGFYKPNYN 808  
  
QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKMDNVATF 901  
DB 809 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKMDNVATF 868  
  
QY 902 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 961  
DB 869 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 928  
  
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFPQAE----- 1003  
DB 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFPQAEISKREDASQLSQILP 988  
  
QY 1004 -----GDATKSESEPDFFSPSDGDRKKRLALVALGEHAELKSLPLLIHTAATPM 1058  
DB 989 VDSQGGDANKSESEPDFFSPSDGDRKKRLALVALGEHAELKSLPLLIHTAATPM 1048  
  
QY 1059 SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAHHEMKPPSARSSPHSPWSAASSWTSRR 1118  
DB 1049 SLPKSTSTGLGEALGPASRTSSSGSAEPGAA-HEMKSPSARSSPHSPWSAASSWTSRR 1107  
  
QY 1119 SSRNSILGRAPSLKRRSPSGRRSLLSGEGQESQDEESSEEDRASPGSDHRHRSGLERE 1178  
DB 1108 SSRNSILGRAPSLKRRSPSGRRSLLSGEGQESQDEESSEEDRASPGSDHRHRSGLERE 1167  
  
QY 1179 AKSSFDPDPTLQVPLHRTASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGDNDDE 1238  
DB 1168 AKSSFDPDPTLQVPLHRTASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGDNDDE 1227  
  
QY 1239 GNLSKGERIQAVRSRLPACCRERDSWSAYIFPPQSRFLCHRIITHKMFHDHVVLIIF 1298  
DB 1228 GNLSKGERIQAVRSRLPACCRERDSWSAYIFPPQSRFLCHRIITHKMFHDHVVLIIF 1287  
  
QY 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWN 1358  
DB 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWN 1347  
  
QY 1359 VLDGLLVLSVIDILVMSVDSGKILGMLRLVRLRLRLRLRLRLRLRLRLRLRLRLRLRL 1418  
DB 1348 VLDGLLVLSVIDILVMSVDSGKILGMLRLVRLRLRLRLRLRLRLRLRLRLRLRLRLRL 1407  
  
QY 1419 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRVRHKY 1478

Db 1408 SLKPIGNIWVICCAFFIIIFGILGVQLFKGKFFVCQGEDTNIITKSDCAEASRWRMKY 1467  
Qy 1479 NFDNLGOALMSLFVLASKDGVDMYDGLDVGVDQOQPMNHNPNMMLLYFISFLIVAFF 1538  
Db 1468 NFDNLGOALMSLFVLASKDGVDMYDGLDVGVDQOQPMNHNPNMMLLYFISFLIVAFF 1527  
Qy 1539 VLNMFGVVVENFHKCRQHQEHEEARRREKRLRLEKKRSKEKQMAEAOCKPYSDYS 1598  
Db 1528 VLNMFGVVVENFHKCRQHQEHEEARRREKRLRLEKKRR-----KAOCKPYSDYS 1580  
Qy 1599 RFRLLVHLLCTSHYLDLFTITGVIGLNVVTMAMEHYQOQILDEALKICNYIFTVIFVES 1658  
Db 1581 RFRLLVHLLCTSHYLDLFTITGVIGLNVVTMAMEHYQOQILDEALKICNYIFTVIFVLES 1640  
Qy 1659 VFKLVAFAFRFFQDRWNQDLAIVLLSIMGITLEEIVNLSLPINPTIIRMRVLRIAR 1718  
Db 1641 VFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIVNASLPINPTIIRMRVLRIAR 1700  
Qy 1719 VLKLLKMAVGMRAILLHTVMQALPQVGNLGLLFFMLFFIFAALGVLEFGDLECDTHPCEG 1778  
Db 1701 VLKLLKMAVGMRAILLHTVMQALPQVGNLGLLFFMLFFIFAALGVLEFGDLECDTHPCEG 1760  
Qy 1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSPRDCDQESTCYNTVISPIYFVSFVLTA 1838  
Db 1761 LGRHATFRNFGMAFLTLFRVSTGDNWEGIMKDTLDCDQESTCYFTVISPIYFVSFVLTA 1820  
Qy 1839 QFVLNVVVIIVLMMKHLEESNKEAKEAELEAELEMKTLSPQPHSPLGSPFLNPGVEGV 1898  
Db 1821 QFVLNVVVIIVLMMKHLEESNKEAKEAELEAELEMKTLSPQPHSPLGSPFLNPGVEGP 1880  
Qy 1899 NSTDPKPGAPHTTAHIGASGFSLEHPTTMVPHPEVVPVPLGPDLLTVRKSGVSRTHSLP 1958  
Db 1881 DSPDPKPGALMPAAHARSASHFSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLP 1937  
Qy 1959 NDSYMCNRNGSTAERSLGRHGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGA 2018  
Db 1938 NDSYMCNRNGSTAEGPLGRHGWGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLQPMISA 1997  
Qy 2019 PTWGAIPKLPPLPGSRPLAQRLRRQAAIRTDSDVOGLGSRDLDLSEVSGPSCPLTRSSS 2078  
Db 1998 PTWGTIPKLPPLPGSRPLAQRLRRQAAIRTDSDVOGLGSRDLDLAEVSGPSPPLARAYS 2057  
Qy 2079 FWGSSIQVQORSIGQSVKSHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL 2138  
Db 2058 FWGQSSTQAQOQHSRSHSKISKHHTPPAPCAGPEPNMGKPPETRSSLELDTLSNISGDL 2117  
Qy 2139 L-PSSQEEPLFRDLKKCYSVETQSCRRRPGFWLDBQRRHSIAVSCLDGSGQPRCLPSPS 2197  
Db 2118 LPPGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDBQRRHSIAVSCLDGSGQPHLGTDP 2177  
Qy 2198 SLGGQPLGGPSRPPKLLSPSISIDPPESQGSRRPPSPGVCLRRRAPASDKDPSVSSP 2257  
Db 2178 NLGGQPLGGPSRPPKLLSPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGP 2237  
Qy 2258 LDSTAASPPKKTOTLSLGLSSDPTMDP 2286  
Db 2238 PDSMAASPPKDVLSLGLSSDPAADLP 2266

RESULT 15  
AAB66476  
ID AAB66476 standard; protein; 2359 AA.  
XX  
AC AAB66476;  
XX  
DT 09-APR-2001 (first entry)  
XX  
DE Rat alpha-IH calcium channel protein.  
XX  
KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;  
KW hypotensive; cardiant; nootropic; T-type calcium channel subunit;  
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;

KW epilepsy; alpha-IH calcium channel.  
XX Rattus sp.  
OS  
XX WO200102561-A2.  
PN  
XX 11-JAN-2001.  
PD  
XX 04-JUL-2000; 2000WO-CA000794.  
PF  
XX 02-JUL-1999; 99US-00346794.  
PR  
XX (NEUR-) NEUROMED TECHNOLOGIES INC.  
PA  
XX Snutch TP, Baillie DL;  
PI  
XX WPI; 2001-123111/13.  
DR  
DR N-PSDB; AAF31678.  
XX  
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating  
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
PT epilepsy.  
XX  
PS Disclosure; Page 75-85; 103pp; English.  
XX  
CC The present sequence is given in a specification providing sequences and  
CC partial sequences for three types of mammalian (human and rat) T-type  
CC calcium channel subunits. An expression cassette has been generated which  
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha\_1  
CC subunit operably linked to control sequences to effect its expression.  
CC The novel calcium channel nucleic acids and proteins are useful for  
CC treating conditions characterised by undesirable levels of T-type calcium  
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
CC hypertension, sleep disorder and epilepsy  
XX  
SQ Sequence 2359 AA;

Query Match 51.8%; Score 6226.5; DB 4; Length 2359;  
Best Local Similarity 56.1%; Pred. No. 0;  
Matches 1357; Conservative 246; Mismatches 506; Indels 311; Gaps 59;  
Qy 30 LARGWTRRRMERAPRSRDSVP-ASRSSTTCPG---PGAAGAG-STEKDPGS---AD---S 78  
Db 6 LADEVVRVPLGASPPAPAPVRASPASPAGPREEQGGSGVLAPESPGTECGADLGAD 65  
Qy 79 EAEGLPYPALAPVVFYLSQDSRPSRCLRTVCNPFWRVSMVLVILNCVTGLGMRPCED 138  
Db 66 EBQVPYPALAAATVFCGLGQTRPRSWCLRLVCNPFWEHVSMVLVILNCVTGLGMRPCED 125  
Qy 139 IACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVAGMLE 198  
Db 126 VECRSERCSILEAFDDFIFAFFAVEMVIMVALGLFGQKCYLGDTWNRLDFFIVAGMME 185  
Qy 199 YSILDQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFG 258  
Db 186 YSILDGHKVSLSAIRTVRVRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFG 245  
Qy 259 IVGVQLWAGLLRNRCFLPENFSLPLSVD-LPEVYQTENEDESPFICSPRENGMRSCRSV 317  
Db 246 IVGVQLWAGLLRNRCFLDSAFVRNNNLTFLFPYQYQTEEGEENPFICSSRRDNGMQKCSHI 305  
Qy 318 PT---LRGEGGGGPPCSDLYETY-----NSSNTTCVWNQYNTCSAGEHNPFGKAI 367  
Db 306 PSRRELRVQ-----CTLGWEAYGQPOAEDGAGRNACINWNQYNVCRSGEFNPHNGAI 359  
Qy 368 NFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYFIYFILLIIVGSFFMINCLLVIA 427  
Db 360 NFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYFIYFILLIIVGSFFMINCLLVIA 419  
Qy 428 TQFSETKQRESQLMRQORVRFSLNASTLASFSPEPGSCYEELLYLVILRKAARRLAQVS 487  
Db 420 TQFSETKQRENQLMRQARARYLSNDSTLASFSPEPGSCYEELLYVGVGHIFRKVKRRSLRLY 479



QY 488 RAIGVRAGLSSPVAR-----SGQEPQPSGSTRSHRRLSVHHLV-HHHHHHHHHYHLGN 541  
Db 480 ARWQSRWRKVDPSSTVHGQPGRRPRAG-----RRTASVHLLVYHHHHHHHHYHFSH 534  
QY 542 GTLRVPRAPEIQDRDANGRRRLM-LPPSTPTSPGGPRGAESVHSFYHADCHLEPVR 599  
Db 535 GGPR--RPSPE---PGAGDNRLVRACAPPPSPSGHGP-DSESVHSIYHADCHVEGPQ 587  
QY 600 COAPPPRCFSEASGRVTGSG---KVYPTV-----HTSPPEILKDKALVEVAPSP 646  
Db 588 ERARVAHSIATAASLKLASGLGTMYPTILPSGTVNSKGTSSRPKGLRG-----AGAP 641  
QY 647 GPPTLTSENI-PPGPFSSMHKLLTQSTGACHSSCK-ISSPC-----SKADSGACGPDSCP 700  
Db 642 GAAVHSPSLGSPRPRYEKIQDVVGEQGLGRASSHLSGLSVCPPLPSPQAGTLTCELKSCP 701  
QY 701 YCARTGAGEP--ESADHVMPDSEAVYEFTQDAQHSDLRDP-----HSRRRQR 747  
Db 702 YCA-SALEDPFEFSGSESGSDAHGVYEFTQDVRHGDCRDPVQOPHEVGTGPHSNERR 760  
QY 748 S-LGPDAPSSVLAFWRLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHQBPEELTN 806  
Db 761 TPLRKASQPGGIGHLWASFSGKLRIIVDSKYFNRGIMAILVNTLSMGVEYHQBPEELTN 820  
QY 807 ALEISNIVTSLFALEMLLKLIVYGPFGYIKPNYNIFDGVIVVISWEIVGQGGGLSVL 866  
Db 821 ALEISNIVTSMFALEMLLKLACGLGYIRPNYNIFDGVIVVISWEIVGQADGGQSVL 880  
QY 867 RTFRLMRVLKVRFLPALQRLVVLMTMDNVATFCMLLMFIFIFISILGMHLFGCKFAS 926  
Db 881 RTFRLRLVLKVRFLPALRRQLVVLMTMDNVATFCMLLMFIFIFISILGMHLFGCKFSL 940  
QY 927 ERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGN 985  
Db 941 KTDSGDTPVDRKNFDSLLWAIVTVFQILTQEDWNVVLNGMASTSSWAALYFVALMTFGN 1000  
QY 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVGDGDRKKRL-----ALVALG 1036  
Db 1001 YVLFNLLVAILVEGFOAEGDATSDTDEDKTSTQLEGDFDKLRDLRATEMKMYSLAVTPN 1060  
QY 1037 EHAELRKSLLPPLIHTAATPMShPKSS-STGVGEALGSGSRRTSSSGSAEPGAHHEMK 1095  
Db 1061 GHLEGRLPPLIHTAATPMPTPKSSPNLDVAHAL-LDSRR-SSSGSVDPQLG--DQK 1116  
QY 1096 CPPSARSPSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEGESQDEEE 1155  
Db 1117 SLASLRSSPCTPWGPNAGSSRRSSWNSLGRAPSLKRSSQGERESLLSGEGKSTDEE- 1175  
QY 1156 SSEEDRAS-----PAGDHRHRRGSLEREAKSSFDL-----PDTLQVPLHRTAS 1199  
Db 1176 -AEDSRPSTGTHPGASPGPRATPLRRAESLDH--RSTLDLCPRPAPPVAVQV----- 1224  
QY 1200 GRSSASEHQDCKGKSASGLARTLRTDDPOLDGDNDNDEGNLSKGERIQAWRSRLPACC 1259  
Db 1225 -----HDCNGQMVALPSEFFLRIIDSHKEDAAEFDDIEDSCCFRLHKVLEPYAPQC 1276  
QY 1260 RERDSWASYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPKIDPHSAERI 1319  
Db 1277 RSRESWALYIFPPQNRRLRVSCQVIAHKMFDHVVLVIFLNCITIALERPDIDPGSTERA 1336  
QY 1320 FLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLISVIDILVMUSD 1379  
Db 1337 FLSVSNYIFTAVFVEMVMKVVALGLLWGEHAYLQSSWNVDGLLVLVSLVDIIVAMASA 1396  
QY 1380 SGTKILGMLRVLRLLRTLRLPLRVISRAQGLKLVETLMSSLKPIGNIVVICAFFIIFGI 1439  
Db 1397 GGAKILGVLVRVRLRTLRLPLRVISRAPGLKLVETLISLRPIGNIVLICAFFIIFGI 1456  
QY 1440 LGVOLFKGKFPVCQGEDTRNITNKSDCAEASVYRWVRHKYNFNDNLGQALMSFLVLASKDGM 1499  
Db 1457 LGVOLFKGKFPYCEGTDRNITTKAECHAAHYRWVRKYNFNDNLGQALMSFLVLSSKGM 1516  
QY 1500 VDIMYDGLDAVGVDQOQPMHNPNWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHQE 1559

Search completed: April 13, 2005, 19:09:38  
Job time : 267 secs

Db 1517 VNIMYDGLDAVGIDQOPVQNHNPWMLLYFISFLLIIVSFFVLNMFVGVVVENFHKCRQHQE 1576  
QY 1560 EEEARRREKRLRRLEKRRSKBKQMAEAOCKPYYSYDRFRLLVHHLCTSHYLDLFTIG 1619  
Db 1577 AEEARRREKRLRRLEKRRSKBKQMAEAOCKPYYSYDRFRLLVHHLCTSHYLDLFTIF 1629  
QY 1620 VIGLNVVTMAMEHYQQQILDEALKICNYIFTVIFVFSVFKLVAFARFRFFQDRWNQLD 1679  
Db 1630 IICLNVITSMHEYNQPSLDEALKYCNVFTIVFVFEAALKLVAFGFRFFQDRWNQLD 1689  
QY 1680 LAIVLSIMGITLEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMRLHVTMOA 1739  
Db 1690 LAIVLSIMGIALEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMATGMRLHVTMOA 1749  
QY 1740 LPQVGNLGLLFFLFFIIFALGVLFGLDECEDETHPCBGLGRHATFRNFGMAFLTLFRVS 1799  
Db 1750 LPQVGNLGLLFFLFFIIFALGVLFGLRLECESDNPNCEGLSRHATFTNFGMAFLTLFRVS 1809  
QY 1800 TGDWNGIMKDPSPRDC---DOESTCYNVTVISPIYFVSFVLTAQFVLNVVVIAMKHLSE 1856  
Db 1810 TGDWNGIMKDTLRECTREDKHLCLSYLPALSPVYFVTFMVLAQFVLNVVVIAMKHLSE 1869  
QY 1857 SNKEAKEAEAELEAELEMLKTLSPQSPHSPPLWPGVEGVNSTDSPKPGAPHTAHIG 1916  
Db 1870 SNKEAREDAEMDAEIELEM-----AQGSTAQPPPTAQES----- 1903  
QY 1917 AASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1976  
Db 1904 -----QGTQDPTPNLLVVRKVSVRMLSLPNDSYMFRPVAPAAAPHSH 1946  
QY 1977 RGWGLP-----KAQSGSILSVHSQPADTSCILQLP-----KOVHLLQPHGAPTW 2021  
Db 1947 -----PQEVEMETTYTGPVTSAHSPLEPRASFQVPSAASSPARVSDPLCALSPTGP-- 1999  
QY 2022 GAIPKLPPPGRSPLAQRPLRQAARTDSDL--VQGLSREDLLSEVSGSPCLTRSSSF 2079  
Db 2000 -----RSLSLRILCRQEAHSESLGKVDVGG--DSIPDYTEPAENMSTSQAS 2047  
QY 2080 WGG-----SSIQVQRSGIQSKVSKHRLPAPCPGLEPSWAKDPPETRSLELDT 2129  
Db 2048 TGAPRSPSPCPASVTRKHTFGQRCISSR-----PPTLGGDEAEAADP-----ADE 2095  
QY 2130 ELSWISGDLPLSPSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDE 2173  
Db 2096 EVSHITSSAHPWPATEPHSPASPTASPVKGTMGSGRDPRRFCVDAQSFLDKPG-RPDA 2154  
QY 2174 QRRHSIAV---SCLDSGS-----QPRLCPSPLSGGQPLGGPGSRPKKLSPPSIS 2221  
Db 2155 QRWSSVELDNGESHLESGEVGRASELEPAL-----GSRKKKMSPPCIS 2199  
QY 2222 IDPP--ESQGSRRPPCSPG--VCLRRRAPASDS---KDFSVSSPLDSTAASP----- 2265  
Db 2200 IEPPTKDEGSSRPPAAEGGNTLRRRTPSCEAALHRDCPEPTGPGTGGDPVAKGERWQ 2259  
QY 2266 -SPKDTLSLSGLSSDPTDM 2284  
Db 2260 ASCRAEHLTVPNFAFEPLDM 2279

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OM protein - protein search, using sw model

Run on: April 13, 2005, 19:00:09 ; Search time 57 Seconds  
(without alignments)  
2995.130 Million cell updates/sec

Title: US-09-611-257A-24  
Perfect score: 12028  
Sequence: 1 MLPHRVPRCVTPPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10820.5	90.0	2273	3	US-09-426-998-5
2	10512	87.4	2220	4	US-09-949-016-9730
3	6221	51.7	2353	3	US-08-984-709A-50
4	5872	48.8	1207	4	US-09-398-522-52
5	5409	45.0	2175	3	US-09-404-650-2
6	5409	45.0	2175	4	US-09-935-541-2
7	5405.5	44.9	2188	3	US-09-404-650-4
8	5405.5	44.9	2188	4	US-09-935-541-4
9	5345	44.4	1835	3	US-09-404-650-5
10	5345	44.4	1835	4	US-09-935-541-5
11	1678	14.0	2343	3	US-09-268-163-4
12	1677	13.9	2337	3	US-08-713-118-2
13	1677	13.9	2337	3	US-09-452-007-2
14	1676	13.9	2339	1	US-08-455-543A-47
15	1676	13.9	2339	2	US-08-223-305C-47
16	1674	13.9	2339	3	US-09-268-163-6
17	1642.5	13.7	2237	1	US-08-455-543A-48
18	1642.5	13.7	2237	2	US-08-223-305C-48
19	1642.5	13.7	2336	3	US-09-268-163-10
20	1642	13.7	1985	4	US-09-495-714C-6
21	1640.5	13.6	2237	3	US-09-268-163-8
22	1634.5	13.6	1984	3	US-08-836-325-10
23	1634.5	13.6	1984	4	US-09-457-571-10
24	1631	13.6	2181	4	US-09-949-016-5981
25	1631	13.6	2188	4	US-09-949-016-8295
26	1628.5	13.5	1977	4	US-09-495-714C-4
27	1628	13.5	1873	1	US-08-435-675B-4
					Sequence 5, Appli
					Sequence 9730, Ap
					Sequence 50, Appl
					Sequence 52, Appl
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 4, Appli
					Sequence 2, Appli
					Sequence 47, Appl
					Sequence 47, Appl
					Sequence 6, Appli
					Sequence 48, Appl
					Sequence 48, Appl
					Sequence 10, Appl
					Sequence 8, Appli
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 5981, Ap
					Sequence 8295, Ap
					Sequence 4, Appli
					Sequence 4, Appli

28	1625.5	13.5	1989	3	US-08-836-325-12	Sequence 12, Appl
29	1625.5	13.5	1989	4	US-09-457-571-12	Sequence 12, Appl
30	1625	13.5	2161	1	US-08-455-543A-51	Sequence 51, Appl
31	1625	13.5	2161	2	US-08-223-305C-51	Sequence 51, Appl
32	1622	13.5	2161	1	US-07-745-206A-2	Sequence 2, Appli
33	1622	13.5	2161	1	US-08-455-543A-49	Sequence 49, Appl
34	1622	13.5	2161	2	US-08-223-305C-49	Sequence 2, Appli
35	1622	13.5	2161	2	US-08-311-363-2	Sequence 2, Appli
36	1617.5	13.4	1969	3	US-08-836-325-16	Sequence 16, Appl
37	1617.5	13.4	1969	4	US-09-457-571-16	Sequence 16, Appl
38	1616.5	13.4	1668	4	US-09-949-016-11611	Sequence 11611, A
39	1616	13.4	1873	1	US-08-336-257A-7	Sequence 7, Appli
40	1614.5	13.4	1977	4	US-09-976-594-757	Sequence 757, App
41	1614.5	13.4	1977	4	US-09-919-039-367	Sequence 367, App
42	1614	13.4	1872	6	5386025-6	Patent No. 5386025
43	1614	13.4	1872	6	5386025-6	Patent No. 5386025
44	1595.5	13.3	1912	4	US-09-495-714C-2	Sequence 2, Appli
45	1589.5	13.2	2516	3	US-08-374-077C-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-426-998-5  
; Sequence 5, Application US/09426998  
; Patent No. 6358706  
; GENERAL INFORMATION:  
; APPLICANT: DUBIN, ADRIENNE E.  
; APPLICANT: PYATI, JAYASHREE  
; APPLICANT: ZHU, JESSICA Y  
; APPLICANT: ERLANDER, MARK G  
; APPLICANT: GALINDO, JOSE E  
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM  
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)  
; FILE REFERENCE: ORT-1057  
; CURRENT APPLICATION NUMBER: US/09/426,998  
; CURRENT FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PATENTIN VER. 2.0  
; SEQ ID NO 5  
; LENGTH: 2273  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-426-998-5

Query Match	90.0%	Score 10820.5;	DB 3;	Length 2273;
Best Local Similarity	92.5%	Pred. No. 0;		
Matches 2080;	Conservative 35;	Mismatches 105;	Indels 29;	Gaps 5;
QY	62	GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFERSVMSL	121	
Db	30	GRPGGSAEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFERSVMSL	89	
QY	122	VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	181	
Db	90	VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	149	
QY	182	DTWNRDLDFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP	241	
Db	150	DTWNRDLDFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP	209	
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDVLEPYQYOTENEDESPF	301	
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDVLEPYQYOTENEDESPF	269	
QY	302	ICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSSNTTCVWNQYTTNCAGEHN	361	
Db	270	ICSPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSSNTTCVWNQYTTNCAGEHN	329	
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	421	
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	389	

QY 422 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 481  
Db 390 CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 449  
QY 482 RLAQVSRAGVRAVGLSSPAPLGGQETQPPSSCSRSRRLSVHLLVHHHHHHHHYHLGN 541  
Db 450 RLAQVSRAGVRAVGLSSPAPLGGQETQPPSSCSRSRRLSVHLLVHHHHHHHHYHLGN 509  
QY 542 GTLRVPRASPEIQDRDANGSRRMLLPPPTSTPPSGPPRGAESVHSFYHADCHLEPVRQ 601  
Db 510 GTLRVPRASPEIQDRDANGSRRMLLPPPTSTPPSGPPRGAESVHSFYHADCHLEPVRQ 569  
QY 602 APPPRCPSEASGRTVSGKVPTVHTSPPPEILKDXALVEVAPSPGPTLTSTFNIPGPF 661  
Db 570 APPPRCPSEASGRTVSGKVPTVHTSPPPEILKDXALVEVAPSPGPTLTSTFNIPGPF 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYCARAGAGEVELADREMPDSD 721  
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYCARAGAGEVELADREMPDSD 689  
QY 722 SEAVYEFTQDAQHSRLDRPHSRRRQSLGPDAPSSVLAFWRLLICDTERKIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSRLDRPHSRRRQSLGPDAPSSVLAFWRLLICDTERKIVDSKYFGRG 748  
QY 782 IMTAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLIVYGFYIKNPYN 841  
Db 749 IMTAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLIVYGFYIKNPYN 808  
QY 842 IFDGVIVVISVWEIVGQGGSLVLRTRFRLMRVLKVRFLPALQRLVLMKTMNDVATF 901  
Db 809 IFDGVIVVISVWEIVGQGGSLVLRTRFRLMRVLKVRFLPALQRLVLMKTMNDVATF 868  
QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQIILTQEDWNV 961  
Db 869 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQIILTQEDWNV 928  
QY 962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAE----- 1003  
Db 929 LYNMGMASTSSWAALYFIALMTFGNYVLFNLVAILVEGFOAEISKREDASGQSLCIQLP 988  
QY 1004 -----GDATESESEPDFSPSDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1058  
Db 989 VDSQGGDANKSESEPDFSPSDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1048  
QY 1059 SHPKSSSTGVGEALGSGRRRTSSGSAEPGAHHMKPCPPSARSSPHSPWSAASSWTSRR 1118  
Db 1049 SLPKSTSTGLGEALGPASRRRTSSGSAEPGAH-HMKSPPSARSSPHSPWSAASSWTSRR 1107  
QY 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPGSDHRRHRSGLERE 1178  
Db 1108 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPGSDHRRHRSGLERE 1167  
QY 1179 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGRRLARTLRDTPDQDGDNDDE 1238  
Db 1168 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGRRLARTLRDTPDQDGDNDDE 1227  
QY 1239 GNLKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFLLCHRIITHKMFHDHVLVIIF 1298  
Db 1228 GNLKGERVRAWIRARLPACCLERDSWSAYIFPPQSRFLLCHRIITHKMFHDHVLVIIF 1287  
QY 1299 LNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1358  
Db 1288 LNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347  
QY 1359 VLDGLLVLSVIDILVSMVSDSGTKILGMLRLVRLRLTLRPLRVISRAQGLKLVVETLMS 1418  
Db 1348 VLDGLLVLSVIDILVSMVSDSGTKILGMLRLVRLRLTLRPLRVISRAQGLKLVVETLMS 1407  
QY 1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKY 1478  
Db 1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKY 1467

QY 1479 NFDNLGQALMSLVASKDGVWDIMYDGLDAVGVDQOPIMNHNPMWLLYFISFLLIVAFF 1538  
Db 1468 NFDNLGQALMSLVASKDGVWDIMYDGLDAVGVDQOPIMNHNPMWLLYFISFLLIVAFF 1527  
QY 1539 VLNMFVGVVVENFHKCRHQHEEEARRRERKRRLRLEKRRSKEKQMAEAOCKPYSDYS 1598  
Db 1528 VLNMFVGVVVENFHKCRHQHEEEARRRERKRRLRLEKRRSKEKQMAEAOCKPYSDYS 1587  
QY 1599 RFRLLVHLLCTSHYLDLFTITGVIGLVNVTMAMEHYQOQIILDEALKICNYIFTVIFVES 1658  
Db 1588 RFRLLVHLLCTSHYLDLFTITGVIGLVNVTMAMEHYQOQIILDEALKICNYIFTVIFVES 1647  
QY 1659 VFKLVAFAFRFRFQDRWNQDLAIIVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIAR 1718  
Db 1648 VFKLVAFAFRFRFQDRWNQDLAIIVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIAR 1707  
QY 1719 VLKLLKMAVGMRAVLLHTVMOALPOVGNLGLLMLLFFIFAALGVLEFGLDECDETHPCEG 1778  
Db 1708 VLKLLKMAVGMRAVLLHTVMOALPOVGNLGLLMLLFFIFAALGVLEFGLDECDETHPCEG 1767  
QY 1779 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDCDOESTCYNTVISPIYFVSFVLTA 1838  
Db 1768 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDCDOESTCYNTVISPIYFVSFVLTA 1827  
QY 1839 QFVLNVVIVIAVLMKHEESNKEAEEAELEAELEEMKTLSPHSPPLGSPFLWPVEGV 1898  
Db 1828 QFVLNVVIVIAVLMKHEESNKEAEEAELEAELEEMKTLSPHSPPLGSPFLWPVEGV 1887  
QY 1899 NSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP 1958  
Db 1888 DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHTLP---GPDLLTVRKSGVSRTHSLP 1944  
QY 1959 NDSYMCNRNGSTAERSLGHGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHLLQPHGA 2018  
Db 1945 NDSYMCNRHGSTAEGPLGHGWGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLQPHSA 2004  
QY 2019 PTWGAI PKLPPGRSPLAQRPLRQAARTDSDLVQGLSREDLLSEVSGSPCLTRSSS 2078  
Db 2005 PTWGAI PKLPPGRSPLAQRPLRQAARTDSDLVQGLSREDLLAEVSGSPPLARAYS 2064  
QY 2079 FWGSSIQVQQRSGIQSKVSKHTRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL 2138  
Db 2065 FWGSSSTQAQHSRSHSKISKHMTFPAPCPGPEPNWKGKPPETRSSLELDTLSWISGDL 2124  
QY 2139 L-PSSQEEPLFPRDLKKCYSVETQSCRRRRPGFWLDEQRHRSIAVCLDSGSPRLCPSPS 2197  
Db 2125 LPPGQEEPPSPRDLKKCYSVAEQSCORRPTSWLDEQRHRSIAVCLDSGSPHLGTDPS 2184  
QY 2198 SLGGQPLGGPSRPPKLLSPPSISIDPPESQSGRPPCSPGVCLRRRAPASDKDPSVSSP 2257  
Db 2185 NLGGQPLGGPSRPPKLLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPPLASGP 2244  
QY 2258 LDSTAASPPKOTLSLGLSSDPTMDP 2286  
Db 2245 PDSMAASPPKXOVLSLGLSSDPADLDP 2273

RESULT 2

US-09-949-016-9730  
; Sequence 9730, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498



; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows  
 ; SEQ ID NO 9730

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; LENGTH: 2220
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9730

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Query Match 87.4%; Score 10512; DB 4; Length 2220;  
Best Local Similarity 89.6%; Pred. No. 0;  
Matches 2041; Conservative 32; Mismatches 112; Indels 94;

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QY	69	TEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNP-WFERVSMVLVILNC	127
Db	85	AEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPTWFERISMLVILNC	144
QY	128	VTILGMRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGD TNRL	187
Db	145	VTILGMRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGD TNRL	204
QY	188	DFFI VIAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLD TPLMGNVL	247
Db	205	DFFI VIAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLD TPLMGNVL	264
QY	248	LLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPLSVDLEPYQTENEDESPFCSQPR	307
Db	265	LLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPLSVDLEPYQTENEDESPFCSQPR	324
QY	308	ENGMRSCRSVPTLRGEGGGPPCSDLDYETYNSSNTTCVNWNQYYTNC SAGEHNPFKGAI	367
Db	325	ENGMRSCRSVPTLRGDGGGGPPCGLDYEAYNSSNTTCVNWNQYYTNC SAGEHNPFKGAI	384
QY	368	NFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVIA	427
Db	385	NFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVIA	444
QY	428	TQSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAARRLAQVS	487
Db	445	TQSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAARRLAQVS	504
QY	488	RAIGVRAGLLSSPVARSGQEPQPSGSCSTRSHRRRLSVHHLVHHHHHHHHYHLNGT LRVP	547
Db	505	RAAGVRVGLLSSPAPLGQEQETQPSSSCSRSHRRRLSVHHLVHHHHHHHHYHLNGT LRAP	564
QY	548	RASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVR CQAPP PRC	607
Db	565	RASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAEVHSFYHADCHLEPVR CQAPP PPRS	624
QY	608	PSEASGRVTGSGKVYPTVHTSPPEILKOKALVEAPSGPPTLT SFNIPPGPFSSMHKL	667
Db	625	PSEASGRVTGSGKVYPTVHTSPPETLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKL	684
QY	668	LETQSTGACHSSCKI SSPCKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYE	727
Db	685	LETQSTGACQSSCKI SSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYE	744
QY	728	FTQDAQHSDLRDPHSRRRRQSLGDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAIL	787
Db	745	FTQDAQHSDLRDPHS--RRQPSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAIL	803
QY	788	VNTLSMGI EYHQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFD GVI	847
Db	804	VNTLSMGI EYHQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFD GVI	863
QY	848	VVISVWEIVGQGGGLSVLRTFRLMRVLKLVRF PALQRQLVLMKTMNDNVATFCMLLM L	907
Db	864	VVISVWEIVGQGGGLSVLRTFRLMRVLKLVRF PALQRQLVLMKTMNDNVATFCMLLM L	923

Db 2000 SVLSVHSQPADTSYILQLPKDAPHLLOPHSAPTWTGTPKLPPEGSRPLAQRLRQAAIR 2059  
Qy 2048 TDSLDDVQGLSREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQRSGIQSKVSKHRLPAPC 2107  
Db 2060 TDSLDDVQGLSREDLLAE----- 2077  
Qy 2108 PGLEPSWAKDPPETRRSSLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQSCRRRP 2167  
Db 2078 -----EPPSPRDLKKCYVEAQSCORRP 2101  
Qy 2168 GFWLDEQRHRSIAVSCLDGSGQRLCPSPSSLGQGLGGPGSRPKKLSPPSISIDPPES 2227  
Db 2102 TSWLDEQRHRSIAVSCLDGSGQHLGTDPSNLGGQPLGGPGSRPKKLSPPSITIDPPES 2161  
Qy 2228 QGSRPPCSPGVCLRRRAPASDSKDPSSVSPDLSTAASPPKDTLSLSGLSSDPTMDP 2286  
Db 2162 QGPRTPSPGICLRRRAPSSDSKDPLASGPPDSMAASPPKDVLSLSGLSSDPADLDP 2220

RESULT 3

US-08-984-709A-50  
; Sequence 50, Application US/08984709A  
; Patent No. 6320032  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Stauderman, Kenneth A.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McAuliffe  
; STREET: 4250 Executive Square, Suite 700  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/984,709A  
; FILING DATE: 02-DEC-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 450-8400  
; TELEFAX: (619) 587-5360  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2353 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-984-709A-50

Query Match 51.7%; Score 6221; DB 3; Length 2353;  
Best Local Similarity 56.6%; Pred. No. 0;  
Matches 1368; Conservative 209; Mismatches 530; Indels 310; Gaps 62;  
Qy 25 PPGPRLARGWTRRRMERAPRRSDSP--VASRSSTTCGPGGAGAGSTKDPGSADSEAG 82

Db 19 PPGPAALVG-----ASPESPGAPGREARSELGVSPSPSPAERGAELGA--DEEQR 69  
Qy 83 LPYPALAPVWFYLSQDSRPRSWCLRTVCNPFERVSMLVILLNCVTLMFPCEDIACD 142  
Db 70 VYPALAAATVFFCLGQTTRPRSWCLRLVCNPFHVSMLVIMLNCVTLMFPCEDVECG 129  
Qy 143 SQRCLLQAFDDFIFAFVAVEMVVMVALGIFGKKCYLGDWTNRLDFFIVIAGMLEYSLD 202  
Db 130 SERCNILEAFDAFIFAFVAVEMVIKVALGFLGQKCYLGDWTNRLDFFIVVAGMEYSLD 189  
Qy 203 LQNVESAVRTRVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGV 262  
Db 190 GHNVSLSAIRTRVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGV 249  
Qy 263 QLWAGLLRNCFLENFSLPSVD-LEPYQOTENEDESPFICSQPRENGWRSCRVPVTLR 321  
Db 250 QLWAGLLRNCFLDLSAFVRNNNLTLFLRPYYQTEEGEENPFICSSRRDNGMKCCHIP--- 306  
Qy 322 GEGGGGPPCSDIYETYN-----SSNTTTCVNNNOYTNCSAGEHNPKGAINFDNIGY 374  
Db 307 GRRELMPCTLGWEAYTQPAEGVGAARNACINMNQYVNCVCRSGDSNPHNGAINFDNIGY 366  
Qy 375 AWIAIFQVITLEGWVDIMYFVMDAHSFYFIYFILLIIVGSFFMINCLVVIATQFSETK 434  
Db 367 AWIAIFQVITLEGWVDIMYVMDAHSFYFIYFILLIIVGSFFMINCLVVIATQFSETK 426  
Qy 435 QRESQLMREQVRFLSNASTLASFPSEPGSCYEELKLVILKAAARLAQVSRRAIGVRA 494  
Db 427 QRESQLMREQARHLSNDSTLASFPSEPGSCYEELKLVYGHIFRKVRSLRLYARQSRW 486  
Qy 495 GLLSSPVARSQOEPPQPSGSCSTRSHR-----LSVHVLV-HHHHHHHHHVHLGNGTLRV 546  
Db 487 RKKVDPASVQGGP-----GHRQRRAGRHTASVHLVYHHHHHHHHHHFHSHPRR 538  
Qy 547 PRASPEIQDRDANGSRRLML--PPSTPTPSGGPRGAESVHSFYHADCHLE--PVRQA 602  
Db 539 PGPEPGACD-----TRLVRAGAPPSPSPGRGPP-DAESVHSIYHADCHIEGPOERARV 591  
Qy 603 PPRPCPSEASGR-TVGSGKV-YPTV-----HTSPPEILKDKALVEVAPSP--- 646  
Db 592 AHAATAAASLRLATGLTGMNYPTILPSGVSGKSGTSPGPK-----GKWAGGPPGTG 644  
Qy 647 --GPPTLTSTFNIPPGPFSSMHKLLTQSTGAC--HSS-----CKISSPCSKADSGACGPD 697  
Db 645 GHGPLSLNS---PDPYEKIPHVVGHLGQAPGHLGSLGSLVPCPLPSP--PAGTLTCELK 698  
Qy 698 SCPVCART-GAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDP----- 740  
Db 699 SCPYCTRALEDPEGELSGSESGLSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGS 758  
Qy 741 HSRRRQSLGPDAPESVLAFLWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQ 800  
Db 759 PQRRAQORAAP-GEPGWMGRLVVTFSGLKRLRIIVDSKYFSRGIMMAILVNTLSMGVEYHEQ 817  
Qy 801 PEELTNALNISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGIIVVISWEIVGQOG 860  
Db 818 PEELTNALNISNIVFTSMFALEMLLKLACACPLGVIIRNPYNIFDGIIVVISWEIVGQAD 877  
Qy 861 GGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFISILGMHLF 920  
Db 878 GGLSVLRTFRLLRVLKLVRLPALRRQLVVLVKTMDNVATFCTLLMLFIFISILGMHLF 937  
Qy 921 GCKFASERD-GDTLPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIA 979  
Db 938 GCKFSLKTDGTVDPDRKNFDSLLWAIIVTFQILTQEDWNVLYNGMASTSSWAALYFVA 997  
Qy 980 LMTFGNYVLENLLVAILEVQAEQDATKSESEPDFFSPSVGDGDRKKRLALVAL--- 1035  
Db 998 LMTFGNYVLENLLVAILEVQAEQDANRSDTDEKTSVHFEEDFKLRELQTELKMC 1057  
Qy 1036 -----GEHAELRKSLLPPLIIHTAATPMSHPKSSS-TGVGEALGSGSRRTSSSGSAEPGA 1089  
Db 1058 LAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRRGSSSGSDPPLG- 1116



542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGPPRGAESVHSFYHADCHLEPVRCQ 601  
510 GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ 569  
602 APPRCPSEASGRTVSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPILTTSFNIPPGPF 661  
570 APPRSPSEASGRTVSGKVYPTVHTSPPPETLKEKALVEVAASSGPPILTSLNIPPGPY 629  
662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPPSCPCYARTGAGEPESADHVMPDSD 721  
630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPPDSCPCYCARAGAGEVELADREMPDSD 689  
722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIIVDSKYFGRG 781  
690 SEAVYEFTQDAQHSDLRDPHS-RRQSLGPDAPSSVLAFWRLICDTFRKIIVDSKYFGRG 748  
782 IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFYIKNPYN 841  
749 IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFYIKNPYN 808  
842 IFDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATE 901  
809 IFDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATE 868  
902 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTOEDWNKV 961  
869 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTOEDWNKV 928  
962 LYNGMASTSSWAALFYIALMTFGNYVFNLLVAILVEGFAEGDATKSESEPDFFSPSVD 1021  
929 LYNGMASTSSWAALFYIALMTFGNYVFNLLVAILVEGFAEGDANKSESEPDFFSPSLD 988  
1022 GDGDRKKRLALVALGHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRRRTSS 1081  
989 GDGDRKKLALVSLGHEPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSS 1048  
1082 SGSAEPGAAHEMKCPSPARSSPHSPWASAASSWTSSRRSRNSLGRAPSLKRRSPSGERRS 1141  
1049 SGSAEPGAA-HEMKSPSPARSSPHSPWASAASSWTSSRRSRNSLGRAPSLKRRSPSGERRS 1107  
1142 LLSGEGESQDEEESSEEDRASPAAGSDHRRHRSLEAKSSFDLPDTLOVPLHRTASGR 1201  
1108 LLSGEGESQDEEESSEERASPAAGSDHRRHRSLEAKSSFDLPDTLOVPLHRTASGR 1167  
1202 SSASEHQCNGKSASGRLARTLRTDDPQLDGDNDDEGNL 1241  
1168 GSASEHQCNGKSASGRLARALRPDDPPLDGDADDDEGNL 1207

RESULT 5  
US-09-404-650-2  
; Sequence 2, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2175  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-09-404-650-2

Query Match 45.0%; Score 5409; DB 3; Length 2175;  
Best Local Similarity 50.5%; Pred. No. 0;  
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

51 ASRSTTCPGPGAAGAGSTEDPG--SADSEAEGL-----PYPALAPVWFFYLS 97  
5 ASPSSSAAAP-AAEPGVITTEQGPGRSPSPSPGEEPLDGADPHVHPDLAPIAFFCLR 63  
98 QDSRPRSWCLRTVCNPFERVSMVLVILLNCVTLGMRPCEDIAQDSQRCRILQAFFDDFIF 157  
64 OTTSRPNWIKMVCNPFECVSMVLVILLNCVTLGMYQPCDDMDCLSDRCKILQVDFDFIF 123  
158 AFFAVEMVVMKVALGIFGKCKVLGDTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVL 217  
124 IFFAMEMVLMKVALGIFGKCKVLGDTWNRLDFFIVWAGWEYSLDLQNLINLSAIRTVRVL 183  
218 RPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLPE 277  
184 RPLKAINRVPSMRILVNLTLTLLDTPMLGNVLLLCFFVFFIFGIIQVQLWAGLLNRCLFEE 243  
278 NFSPLSLVDLEPYQYQTENEDESPFICSQPRENGMRSCSVPTLRGEGGGGPPCSL----- 332  
244 NFTIQGDVALPPYQPEEDDEMPFICSLSGDNGIMGCHIEPPLKEQ---GRECLSKDDV 300  
333 -DYETYNSSNTT--CVWNQYVYTCNSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWV 389  
301 YDFGAGRQDLNASGLCVWNRYVYVCRGTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV 360  
390 DIMYFVMDAHSFYNYFILLIIVGSPFMINCLVVIATQSETKQRESQLMREQVRFL 449  
361 EIMYVMDAHSFYNYFILLIIVGSPFMINCLVVIATQSETKQREHRLMEOQRYL 420  
450 SNASTLASFSEPCGYEELLKYLVIYLRKAARRLAQVSRALGVRAGLLSSPVARSQGEPPQ 509  
421 S-SSTVASAEPGDCYEEIFQYVCHILKAKR-----RALGLYQALQS----- 462  
510 PSGSCTRSHRRLSVHLLVHHHHHHHVLHNGTLRVPRASPEIQDRDANGSRRLMLPPP 569  
463 -----RRQAL-----GPE-----APAP 474  
570 STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVSGKVYPTVHTSP 629  
475 AKPGD-----HAK---EPRHYQLCPQHSPLDA-----TPHT-- 502  
630 PPEILKDKALVEVAPSPGPPILTTSFNIPPGFSSMHKLLETQSTGAC-HSSCKISSPCSK 688  
503 -----LVQ-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGS 534  
689 ADGAGCPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS 748  
535 TDSGQEGSGS---GSSAGGEDEA-----DGDGA---RSSEDEGASSELGKEEEEEQ-- 579  
749 LGPDAPSSVLA--FWRLICDTFRKIIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTN 806  
580 ----ADGAVWLCGDVWRETTRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN 635  
807 ALEISNIVFTSLFALEMLLKLIVYGPFYIKNPYNIFDGVIVISVWEIVGQGGGLSVL 866  
636 ILEICNVVFTSMFALEMILKLAAPGLFDYLRNPYNIFDSIIIIISWEIVGQADGGLSVL 695  
867 RTFRLMRVLKVRFLPALQRLVLMKTMNDNVATFCMLLMLFIFIFISILGMHLFGCKFAS 926  
696 RTFRLRLVLKVRFPALRRQLVLMKTMNDNVATFCMLLMLFIFIFISILGMHLFGCKFSL 755  
927 ERD-GDTLPDRKNFDSLWAIIVTFQILTOEDWNKVLNGMASTSSWAALFYIALMTFGN 985  
756 RTDGTDTVPDRKNFDSLWAIIVTFQILTOEDWNVLYNGMASTSPWASLYFVALMTFGN 815  
986 YVLFNLLVAILVEGFAEGDATKSESEPDFFSPSV-----DGDGDRKKRLALVAL 1035  
816 YVLFNLLVAILVEGFAEGDANRSYDDEQSSSNIIEEDFKLQEGLDSSGDPK--LCP1PM 873  
1036 GEHAELRKSLLPPLIIHT- ---AATPMShPKSSSTGVGEALGSGRRTSSSGSAEPGAAH 1091  
874 TPNGHLDPSL--PLGGHLGPAGAGPA--PRLSLQDPMLVALGSRKSSVMSL---GRMS 926







; TITLE OF INVENTION: AND USES									
; FILE REFERENCE: R0043B-REG sequence listing									
; CURRENT APPLICATION NUMBER: US/09/404,650									
; CURRENT FILING DATE: 1999-09-23									
; NUMBER OF SEQ ID NOS: 12									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 4									
; LENGTH: 2188									
; TYPE: prt									
; ORGANISM: Homo sapiens									
US-09-404-650-4									
Query Match 44.9%; Score 5405.5; DB 3; Length 2188;									
Best Local Similarity 50.3%; Pred. No. 0;									
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;									
QY	51	ASRSSTTC	PGGAAGAGSTEKDPG--SADSEAEGL-----PYPALAPVVFYLS	97					
Db	5	ASPPSSAAAP-AAEPGVTT	EQPGRSPSPGLEPLDGDAPHVPHPDIAPIAFFCLR	63					
QY	98	QDSRPRSW	CLRTVCNPFERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDPIF	157					
Db	64	QTTSPRNWC	IKMVCNPFECVSMVLILLNCVTLGMYPQCDMDCLSDRCKILQVDFDPIF	123					
QY	158	AFFAVEMVVM	VALGIFGKCYLGDWTNRLDFFIVIAGLEYSLDLQNVSFSAVRTVRVL	217					
Db	124	IFFAMEMVLM	VALGIFGKCYLGDWTNRLDFFIVMAGMVEYSLDLQINLSAIRTVRVL	183					
QY	218	RPLRAINRV	PSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLPE	277					
Db	184	RPLKAINRV	PSMRILVNLLDTPMLGNVLLLCFFVFFIFGIIGVQLWAGLLNRNCFLEE	243					
QY	278	NFSLPLSV	DLBPPYQ TENEDESPFCSPRENGMRSCRSVPTLRGEGGGPPCSL-----	332					
Db	244	NFTIQGDV	ALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV	300					
QY	333	-DYETYNSS	NNT--CVNWNQY YTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWV	389					
Db	301	YDFGAGRQ	DLNASGLCVNWNRYNVNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWV	360					
QY	390	DIMYFVMD	AHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFL	449					
Db	361	EIMYYVMD	AHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQREHRLMLEQRQRYL	420					
QY	450	SNASTLAS	FSEPGSCYEBELLKYLVIILRKAARLQAQVSRRAIGVRAGLLSSPVARSGQEPQ	509					
Db	421	S-SSTVAS	YAEFGDCYEEIFQYVCHILRKAKR-----RALGLYQALQS-----	462					
QY	510	PSGSCTR	SHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP	569					
Db	463	-----RRQAL-----	-----GPE-----APAP	474					
QY	570	STPTSPG	PPRGAESVHSFYHADCHLEPVRCQAPPPRCPSSEASGRTVSGKVYPTVHTSP	629					
Db	475	AKGP	-----HAK-----EPRHYQLCPQHSPLDA-----TPHT--	502					
QY	630	PPEILK	KALVEVAPSPGPPTLTFSNIPPGPFSSMHKLTETQSTGAC-HSSCKTSSPCSK	688					
Db	503	-----LVQ-----	PIPATLAS-----DPASCPCQHEGDRPPSLGS	534					
QY	689	ADSGAC	PDPCPYCARTGAGEPESADHVPDSDSEAVVEFTQDAQHSDLRDPHSRRQRS	748					
Db	535	TDSGQEG	SGS-----GSSAGGEDEA-----DGDGA-----RSSEDGASSELGKEEEEEQ--	579					
QY	749	LGPDAEP	SSVLA--FWRLICDTFRKIVDSKYFGRGIMTAILVNTLSMGIYHEQPEELTN	806					
Db	580	-----ADG	AVMLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHQPEELTN	635					
QY	807	ALEISN	IVTSLFALEMLLKLVYGPFGYIKPNYNIFDGVIVVVISVWEIVGQQGGLSVL	866					
Db	636	ILEICNV	VFTSMFALEMLKLAAGFLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVL	695					
QY	867	RTFRLMR	VLKLVRFLPALQRLVVLMTMDNVATFCMLLMLFIFIFSILGMHLFGCKFAS	926					

Db	696	RTFRLLR	VLKLVRFMPALRRQLVVLMTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSL	755					
QY	927	ERD-GDT	LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN	985					
Db	756	RTDTG	TVPDRKNFDSLLWAIVTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGN	815					
QY	986	YVLFNLL	VAILVEGFAEGDATKSEBPDFFSV-----DGDGRKRLALVAL	1035					
Db	816	YVLFNLL	VAILVEGFAEGDANRSYDDEQSSSNIEEFDKLBGLDSSGDPK--LCPIPM	873					
QY	1036	GEHAELR	KSLPLPIIHT---AATPMShPKSSSTGVGEALGSGSRRRTSSSGSAEPGAH	1091					
Db	874	TPNGHL	DPSL--PLGGHLGPAGAAGPA--PRLSLQDPDMLVALGSRKSSVMSL---GRMS	926					
QY	1092	HEMKCPP	SARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE-QGBS	1150					
Db	927	YDQRLS	SSRSYYGPGWGRSAAMASRRSWN-----SLKHKPPSAEHESLLSAERGGGA	980					
QY	1151	QDEESES	EE--DRASPAGSDH-----RHGSLEREAKSSFDLPDTLQVPG	1193					
Db	981	RVCEVA	ADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRTLSLDNRDSVDLAELVPAVG	1040					
QY	1194	LHRTAS	GRSS--ASEHQDCNGKSASGRLARLTRD-DPQLDGDGDDNDEGNLSKGERIQAW	1250					
Db	1041	AHPRAA	WRAAGPAPGHEDCNGRMP--IAKDVFTKMGDRGRGEDEEIDYTLCFVRVKM	1098					
QY	1251	VRSLPAC	CRERDSWSAYIFPPQSRFRLCHRIITHKMPDHVVLVIFLNCITIAMERP	1310					
Db	1099	IDVYKPD	WCEVREDWSVYLFSPENRFRVLCQTIIAHKLFVYVLAFLFNCITIALERP	1158					
QY	1311	IDPHSA	ERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVI	1370					
Db	1159	IEAGST	ERIFLTVSNYIFTAIFGEMTLKVSLGLYFGEQAYLRSSWNVDGLFVFSII	1218					
QY	1371	DILVSM	SDSGTKILMLRVLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC	1430					
Db	1219	DIVVSL	ASAGGAKILGVLRLTLRPLRVISRAPGLKLVVETLISSLKPIGNIVLIC	1278					
QY	1431	CAFFIIF	GILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYSRWVRHKYNFDNLQALMSL	1490					
Db	1279	CAFFIIF	GILGVQLFKGKFYHCLGVDTRNITNRSDCVAANYRWVHKYNFDNLQALMSL	1338					
QY	1491	FVLASK	DGWVDIMYDGLDAVGVDQPIIMHNPMLLYFISFLLIIVAFFVLNMFVGVVYEN	1550					
Db	1339	FVLASK	DGWVNIYNGLDVAVDQQPVTNHPMLLYFISFLLIIVSFFVLNMFVGVVYEN	1398					
QY	1551	FHKCRQ	HQEEEEARRREEKRLRLEKKRSKEKQMAEAQCKPYSDYSRFRLLVHHLCTS	1610					
Db	1399	FHKCRQ	HQEAEEARRREEKRLRLEKKR-----KAQRLPYATYCTHRLLIHSMCTS	1451					
QY	1611	HYLDL	ITGVIGLVNVTMAMHYQQPQILDEALKICNVITFVIFVFESVFKLVAFARRF	1670					
Db	1452	HYLDL	IFITFIICLVNVTMSLEHYNQPTSLETALKYCYNMFTTVFVLEAVLKLVAFLURRF	1511					
QY	1671	FQDRWN	QLDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMR	1730					
Db	1512	FKDRWN	QLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIRARVLKLLKMATGMR	1571					
QY	1731	ALLHTV	MQALPQVGNLGLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGM	1790					
Db	1572	ALLD	TVQALPQVGNLGLLFFIYAALGVELFGKLVNDENPCCEGMSRHATFENFGM	1631					
QY	1791	AFLTLF	RVSTGDNWNGIMKDPSSDC-DQESTCYNTV--ISPIYFVSFVLTQFVLNVVVI	1847					
Db	1632	AFLTLF	QVSTGDNWNGIMKDLTRDCTHDSRCLSSLQFVSPLYFVSFVLTQFVLNVVVI	1691					
QY	1848	AVLMKH	LEESNKEAKEEAELAELELEM-KTLSPOQHSPLGSP-----1889						
Db	1692	AVLMKH	LDSDSNKEAQEDAEMDAELELEMAHGLGPGPRDPTGSPGAPGRPGGAGGGDTE	1751					
QY	1890	-----FLW-----	PGVEG-VNSTDSPKPGAPHTTAAHIGASG-----1920						

Db 1752 GGLRRCYSPAQENLWLDVSLIKDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHH 1808

Qy 1921 -----FSLEHPTMVP-----HPEEVPV-PLG 1940

Db 1809 DKQEVQLAETAFSLNSDRSSILLGDDLSLEDFTACPPGRKDSKGELDPPEPMRVGDLG 1868

Qy 1941 PDLLTVRKSGVSRTHSLPN-DSYMCNRNGSTAERSLGHGWLGLPKAQSGSILSVHSQPADT 1999

Db 1869 ECFPLSSTAVS-----PDPENFLCEMEEIPFPNV--RSW--LKHDSSQAPSPFSPDAS 1919

Qy 2000 SCILQLPKDVHY-----LLQPHGAPTGAIPKLPPEG-----RSLAQRLRRQAART 2048

Db 1920 SPLPMPAEFFHFAVASQKGPCKGTGCTLPKIALQGSWASLRSRPNVNCITLLRQATGSD 1979

Qy 2049 DSLDVQGLSREDLLSEVSGSPCLTRSSSFWGGSSIQVQORSGIOQSVSKHIRLPAPCP 2108

Db 1980 TSLDAS-----PSSAGSLQTTLEDSTLSDSPRRALGPPAPAP 2018

Qy 2109 GLEPSWAKDPPETRSSLELDELTELWISGDLPLSSQEEPLFPRLDKKCYSVETQSCRRRPG 2168

Db 2019 G-----PRAGLSPAARRL-----SLRGRGL 2039

Qy 2169 FWLDEQRHRSIAVCLDSGSPRLCPSPSSL-----GGQPLGGPGRPKKLSPPSI 2220

Db 2040 FSLRGLRAHQSHS--SGGSTSPGCTHHDSMDPSDEGRGAGGAGGAGSEHSETLSSLSL 2097

Qy 2221 S---IDPPESQSRPPCSPGVCLRR-----RAP---ASDSK 2250

Db 2098 TSLFCPPP-----PPAPGLTPARKFSSSTSLAAPGRPHAAALAHGLARSPSWAADRSK 2151

Qy 2251 DPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2286

Db 2152 DPPGRAPLPMGLGLAPPPQPL-----PGELEP 2179

RESULT 8

US-09-935-541-4

; Sequence 4, Application US/09935541

; Patent No. 6589787

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 2188

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-935-541-4

Query Match 44.9%; Score 5405.5; DB 4; Length 2188;

Best local Similarity 50.3%; Pred. No. 0;

Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

Qy 51 ASRSSTTCFPGAAGAGSTEKDPG--SADSEAEGL-----PYPALAPVVFYFYS 97

Db 5 ASPPSSAAAP-AAEPGVTTTEQPGPRSPSPPPGLEEPLDGDADPHVPHDPIAFACLR 63

Qy 98 QDSRPRSWCLRTVCNPFERVSMLVILNCVTLMFRPCEDIACDQSQRILQAFDDFIF 157

Db 64 QTTSPRNWCIKMVCNPFECVSMVLVILNCVTLMGYQPCDDMDCLSDRCKILQVDFDDFIF 123

Qy 158 AFFAVEMVKNVALGIFGKKCYLGTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVL 217

Db 124 IFFAMEMVKNVALGIFGKKCYLGTWNRLDFFIVMAGMVBYSLDLQNLNSAIRTVRVL 183

Qy 218 RPLRAINRVPSMRILVTLILLDTPLMGLNVLILLCFVFFIFGIVGVQLWAGLLRNRCFLPE 277

Db 184 RPLKAINRVPSMRILVNLILLDTPLMGLNVLILLCFVFFIFGIIIGVQLWAGLLRNRCFLEE 243

Qy 278 NFSPLSLVDLEPYQYQTENEDESPFICSQPRENMRSCRSVPTLRGEGGGGPPCSL----- 332

Db 244 NFIQGDVALPPYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300

Qy 333 -DYETYNSSNTT--CVNMNQYNTNCSAGEHNPFGAINFDNIGYAWIAFQVITLEGWV 389

Db 301 YDFGAGRDNLNASGLCVNMNRYNVCRTGSANPHKGAINFDNIGYAWIAFQVITLEGWV 360

Qy 390 DIMYFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQOLMREQVRFL 449

Db 361 EIMYVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYL 420

Qy 450 SNASTLASFSEPGSCYBELLYLKYILRKAARRLAQVSRRAIGVRAGLLSSPVARSQEPQ 509

Db 421 S-SSTVASYAEPGDCYEIFOYVCHILRAKR-----RALGLYQALQS----- 462

Qy 510 PSGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPP 569

Db 463 -----RRQAL-----GPE-----APAP 474

Qy 570 STPTPSGGPPRGAESVHSFYHADCHLEPVRCOAPPPRCPSEASGRTVSGKVYPTVHTSP 629

Db 475 AKPGP-----HAK---EPRHYQLCPQHSPLDA-----TPHT-- 502

Qy 630 PPEILKDKALVEAPSPGPPTLTSTFNIPPGPFSSMHKLLTETQSTGAC-HSSCKISSPCSK 688

Db 503 -----LVQ-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGS 534

Qy 689 ADGACGPDSCPYCARTGAGEPESADHVMPSDSSEAVVEFTQDAQHSDLRDPHSRRRQRS 748

Db 535 TDSQEGSGS---GSSAGGEDEA-----DGDGA---RSSEDGASSELGKEEEEEEQ-- 579

Qy 749 LGPDAPSPSVLA--FWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTN 806

Db 580 ----ADGAVWLCGDVWRETRAKLRGIVDSKYFRGIMMAILVNTVSMGIEHHEQPEELTN 635

Qy 807 ALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVIVISWEIVCQGGGLSVL 866

Db 636 ILEICNVFTSMFALEMILKLAAGFLDYLRNPYNIFDSIIIVISWEIVCQADGGLSVL 695

Qy 867 RTFRLMRVLKLVRLPALQRLVLMKTMNDVATFCMLLMLFIFIFSLGMHLFGCKFAS 926

Db 696 RTFRLRLVLKLVRFMPALRRQLVLMKTMNDVATFCMLLMLFIFIFSLGMHIFGCKFSL 755

Qy 927 ERD-GDTLPDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGN 985

Db 756 RTDGTGTVPDRKNFDSLWAIWTVFQILTQEDWNVVLNGMASTSPWASLYFVALMTFGN 815

Qy 986 YVLENLVAILVEGFAEGDATKSESEPDFFSPSV-----DGDGRKKRLALVAL 1035

Db 816 YVLENLVAILVEGFAEGDANRSYDEDDQSSSNIEBEFDKLQEGLDSSGDPK--LCPIPM 873

Qy 1036 GEHAELRKSLLPPLIHT----AATPMShPKSSSTGVEALGSGSRRTSSSGSAEPGAH 1091

Db 874 TPNGHLDPSL--PLGGHLGPAGAAGPA--PRLSLQDPMLVALGSRKSSVMSL---GRMS 926

Qy 1092 HEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES 1150

Db 927 YDQSLSSSRSSSYGPGWGRSAAWASRRSSWN-----SLXHKPPSAEHESLISAERGGA 980

Qy 1151 QDEESSEE--DRASPAGSDH-----RHRGSLEREAKSSFDLPTLQVPG 1193

Db 981 RVCEVAADGPPRAAPLHTPHAHHHHGHPLAHRHRHRRRTLSLDRSDVDLAELVPAVG 1040

Qy 1194 LHRTAGRSS--ASEHQDCNKGKSASGLARTLRTD-DPQLDGGDDNDEGNLSKGERIQAW 1250

Db 1041 AHPRAAWRAAGPAPGHEDCNGRMP--IAKDVFTKMGDRGDEDEEIDYTLCFVRVKM 1098

Qy 1251 VRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERP 1310



Db	1099	IDVYKPDWC	EVREDWSYLFSPENRFRVLCQTI	AHKLFDYVVLAFIFLNCIT	IALERPQ	1159	
QY	1311	IDPHSAER	IFLTLSNYIFTAVFLAEMTVKVVAL	GCWCFGEQAYLRSSWNVDGLLV	LISVI	1370	
Db	1159	IEAGSTER	IFLTVSNYIFTAIFVGEMTLKVVS	LGIFYGEOAYLRSSWNVDGLFV	FVSII	1218	
QY	1371	DILVSMVSD	GTKILGMLRVLRLTLRPLRVISRA	QGLKLVVETLMSLLKPIGNIVVIC		1430	
Db	1219	DIVVSLAS	AGGAKILGVLRVLRLLTLRPLRVIS	RAPGLKLVVETLISSLKPIGNIVLIC		1278	
QY	1431	CAFFIIFGIL	VQLFKGFVVCQGEDTRNITNKS	DCAEASRVRWHKYNFDFNLGQALMSL		1490	
Db	1279	CAFFIIFGIL	VQLFKGFYHCLGVDTRNITRSD	CMANRVRWHKYNFDFNLGQALMSL		1338	
QY	1491	FVLASKD	GWVDIMYDGLDAVGVDQOPI	MHNPNWMLLYFISFLLIVAFV	LNMFVGVVVEN	1550	
Db	1339	FVLASKD	GWVNMVINGLDAAVADQO	PVTNHNPNWMLLYFISFLLIVS	FFVLNMFVGVVVEN	1398	
QY	1551	FHKCRQH	QHEEEARRREKRLRLEKRRS	KEKQMAEACQKPYSDYSRFRLLV	VHHLCTS	1610	
Db	1399	FHKCRQH	QHEEEARRREKRLRLEKRR	-----KAQRLPYATYCH	TRLLIHSMCTS	1451	
QY	1611	HYLDLFI	TGIVGLNVVTMAEHYQQPQIL	DEALKICNYIFTVIFVFESVFKL	VAFARFRF	1670	
Db	1452	HYLDIFI	TIIICLVNVTMSLEHYNQPT	SETALCYNYMFTTVFLEAVL	KLVAFGLRRF	1511	
QY	1671	FQDRWNQ	LDLAILVLLSIMGITLEEIE	VNLSLPINPTIIRIMRVLRI	ARVLKLLKMAVGMR	1730	
Db	1512	FKDRWNQ	LDLAILVLLSVMGITLEEIE	INAALPINPTIIRIMRVLRI	ARVLKLLKMATGMR	1571	
QY	1731	ALLHTVM	QALPQVGNLGLLFLMLFFI	FAALGVELFGDLECDETHPC	EGLGRHATFRNFGM	1790	
Db	1572	ALLDTVQ	ALPQVGNLGLLFLMLFFI	YAALGVELFGKLVNDENP	CEGMSRHATFENFGM	1631	
QY	1791	AFLTFRV	STGDNWNGIMKDP	SRDC-DQESTCYNTV--ISPIYFV	SFVLTAQFVLNVVI	1847	
Db	1632	AFLTFLQ	VSTGDNWNGIMKDTLRD	CTHDERSCLSLQFVSPLYFV	SFVLTAQFVLINVV	1691	
QY	1848	AVLMKH	LEESNKEAKEAELEAELE	LEM-KTLSPOPHSP	PLGSP-----	1889	
Db	1692	AVLMKHL	DDSNKEAQDAEMDAE	LELEMAHGLGPGPRLPTG	SPGAPGRPGGAGGGGDTE	1751	
QY	1890	-----	FLW-----	PGVEG-VNSTDSPKGP	APHTTAHGAASG-----	1920	
Db	1752	GGLCRR	CYSPAQENLWLD	SVSLIIKOSLEGELTI	DNLSGSIFH---HYSSPAG	CKKCHH	1808
QY	1921	-----	-----	FSLEHPTMVP-----	-----HPEEVPV-PLG	1940	
Db	1809	DKQEVQ	LAETEAFSINSDRSS	ILLGDDLSLEDPTACPP	GRKDSKGELDPPEPMRV	GDGLG	1868
QY	1941	PDLLTVR	KSGVSRTHSLPN-DSY	MCNRNGSTAERSLGH	RGWGLPKAQSGSILSVHS	QPADT	1999
Db	1869	ECFFPL	SSTAVS-----	PDPENFLCEMEEI	PFNPV--RSW--LKHDSS	QAAPPSPFPDAS	1919
QY	2000	SCILQ	LPKDVHY-----	LLQPHGAPTWGAIP	KLPPPG-----RSPLAQ	RPLRQAAIRT	2048
Db	1920	SPLLMP	AEFFHPAVSASQ	GPEKGTGTGTLPKIAL	QGSWASLRSPRVNCT	LLRQATGSD	1979
QY	2049	DSL	DVQGLSREDLLSEVSG	PCPLTRSSSFWGSSIQV	QQRSGIQSKVKHIRL	PAPCP	2108
Db	1980	TSLDAS	-----	-----PSSSAGSL	QTTLED	SLTSDSPRALGPPAP	2018
QY	2109	GLEPSW	AKDPPTFRSSLEL	DTLSWISGDLPLPSS	QEEPLFPRDLKCCY	SVETQSCRRPG	2168
Db	2019	G-----	-----	-----PRAGLS	PAARRL-----	SLRGRGL	2039
QY	2169	FWLDEQ	RRHSIAVSCLD	SGSQPRLCPSSSL-----	GGQPLGGP	GRPKKLSPPSI	2220
Db	2040	FSLRGL	RAHQRSH--SGGST	SPGCTTHDSMDP	SDDEGRGGAGGGAG	SEHSETLSSLSL	2097
QY	2221	S----	IDPPESQ	GRPPCSPGVCLRR-----	-----RAP----	ASDSK	2250

Db	2098	TSLFCPPP-----PPPAPGLTPARKFSSSTSSLAAPGRPHAAALAHGLARSPSWAADRSK	2151
QY	2251	DPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP	2286
Db	2152	DPPGRAPLMGLPLAPPPQPL-----PGELEP	2179
RESULT 9			
US-09-404-650-5			
; Sequence 5, Application US/09404650			
; Patent No. 6309858			
; GENERAL INFORMATION:			
; APPLICANT: Dietrich, Paul S.			
; APPLICANT: McGivern, Joseph G.			
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;			
; TITLE OF INVENTION: AND USES			
; FILE REFERENCE: R0043B-REG sequence listing			
; CURRENT APPLICATION NUMBER: US/09/404,650			
; CURRENT FILING DATE: 1999-09-23			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 5			
; LENGTH: 1835			
; TYPE: PRT			
; ORGANISM: Rattus sp.			
US-09-404-650-5			
Query Match 44.4%; Score 5345; DB 3; Length 1835;			
Best Local Similarity 55.4%; Pred. No. 0;			
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;			
QY	43	PRSRDSPVASRSTTCPPGGAAGAGSTEKOPGSADSEAG-----LPYPALAPVVPFYLQ	98
Db	8	PSSAAAPAPEGITEQGP-----RSPPPSPGLEEPLGTPDVPHPDLAPVAFCLRQ	62
QY	99	DSRPRSWCLRTVCNPWFERSVLMVILLNCVTLMGFRPCEDIAQDSQRCRILQAFDDFIFA	158
Db	63	TTSPRNWCIMKVCNPWFECVSMVILLNCVTLMGYQPCDDMECLSDRCKILQVDFDIFI	122
QY	159	FFAEMVVMKVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLR	218
Db	123	FFAEMVVMKVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNLINLSAIRTVRVL	182
QY	219	PLRAINRVPSMRILVTLTLLDTPMLGNVLLCFFVFFIGVIGVQVWAGLLRNRCELPE	278
Db	183	PLKAINRVPSMRILVNLNLLDTPMLGNVLLCFFVFFIGVIGVQVWAGLLRNRCELPE	242
QY	279	FSLPLSDLEPYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL-----	332
Db	243	FTIQGDVALPPYQPEEDDENPFICSLTGDNGIMGCHIEPPLKEQ---GRECCLSKDDVY	299
QY	333	DYETYNSSNTT--CVWNQYVYTNCSAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVD	390
Db	300	DFGAGRQDLNASGLCVWNRYVNCRTGNANPHKGAINFNDNIGYAWIAIFQVITLEGWVE	359
QY	391	IMYFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRVFLS	450
Db	360	IMYVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQYLS	419
QY	451	NASTLASFSEPGSCYEELLYVILRKAARLAQVSRRAIGVRAGLLSSPVARSQEPQP	510
Db	420	SSIVASVYAEFGDCYEEIFQYVCHILRKAKR-----RALGLYQAL-----	458
QY	511	SGSCTFHRRLSVHLLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPPS	570
Db	459	QNRQA-----MGPGT-----PAPA	473
QY	571	TPTSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPEASGRVTGSGKYVPTVHTSPP	630
Db	474	KPGP-----HAK---EPHCKLCPRHSPLD-----PTPHT---	500
QY	631	PEILKDKALVEAPSPGPPTLTSTFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSKAD	690

Db 501 -----LVQ-----PISAIL----- 509

QY 691 SGACGDPSCPYC-----ARTGAGEPESADHVPDSDSEAVIEFTQDAQH 734

Db 510 --ASDPSSCPHCQHEAGRRRPSGLGSTDSQGSGSGSAE---AEANGDGL-QSSEGDVGS 563

QY 735 SLD RPHSRRRQ RSLGPDAPSSVLA-----FWRLICDTRFKIVDSKYFGRGIMAILVN 789

Db 564 SD-----LGKEEQEDGAARLCGDVWRETRKRLRGIVDSKYFNRGIMMAILVN 611

QY 790 T L S M G I E Y H E Q P E E L T N A L E I S N I V F T S L F A L E M L K L L V Y G P F G Y I K N P Y N I F D G V I V 849

Db 612 T V S M G I E H E Q P E E L T N I L E I C N V V F T S M F A L E M I L K L A A F G L F D Y L R N P Y N I F D S I I V I 671

QY 850 I S V W E I V G Q O G G L S V L R T F R L M R V L K L V R F L P A L Q R O L V V L M K T M D N V A T F C M L L M L F I 909

Db 672 I S I W E I V G Q A D G L S V L R T F R L R L V L K L V R F M P A L R Q L V V L M K T M D N V A T F C M L L M L F I 731

QY 910 F I F S I L G M H L F G C K F A S E R D - G D T L P D R K N F D S L L W A I V T V F Q I L T Q E D W N K V L Y N G M A S 968

Db 732 F I F S I L G M H I F G C K F S L R T D T G D T V P D R K N F D S L L W A I V T V F Q I L T Q E D W N V V L Y N G M A S 791

QY 969 T S S W A A L Y F I A L M T F G N Y V L F N L L V A I L V E G F Q A E G A T K S E S E P D F F S P S V D G ----- 1022

Db 792 T T P W A S L Y F V A L M T F G N Y V L F N L L V A I L V E G F Q A E G D A N R S C S D E D Q S S N L E E F D K L P E 851

QY 1023 --DGDRKKRLALVALGEHAELRKSLLPLLIH--TAATPM SHPKSSSTGVGEALGSGSRR 1078

Db 852 GLD NSRDLKLCPIPMTPNGHLDPSL--PLGAHLGPAGTGMGTAPRLSLQPDVPLVALDSRK 909

QY 1079 T S S G S A E P G A A H E M K C P P S A R S S P H S P W S A A S S W T S R R S S N S L G R A P S I L K R R S P S G E 1138

Db 910 S S V M S L ---GRMSYDQ RSLSSRSYYPGWGRSGTWASRRSSWN-----SLKHKPPSAE 960

QY 1139 R R S L L S G E Q E S --QDEEESSEE--DRASPAGSDH-----RHRGSLEREA 1179

Db 961 H E S L L S G E G G S C V R A C E G A R E A P T R A P L A P H A H A H G P H L A H R H R H R T L S L D T 1020

QY 1180 K S S F D L P D T L Q V P G L H R T A S --GRSSASEHQDCNGKASGRRLARTLRTD-DPQLDGD D D D N 1236

Db 1021 R D S V D L G E L V P V V G A H S R A A W R G A G O A P G H E D C N G R M P N --IAKDVFTKMDRRDRGEDE 1078

QY 1237 D E G N L S K G E R I Q A W R S R L P A C C R E R D S W A Y I F P P Q S R F R L L C H R I I T H K M F D H V V L V I 1296

Db 1079 E E I D Y T L C F R V R K M I D V Y K P D W C E V R E D W S V Y L F S P E N K F R I L C Q T I I A H K L F D Y V V L A F 1138

QY 1297 I F L N C I T I A M E R P K I D P H S A E R I F L T S N Y I F T A V F L A E M T V K V A L G W C F G E Q A Y L R S S 1356

Db 1139 I F L N C I T I A L E R P Q I E A G S T E R I F L T V S N Y I F T A I F V G E M T L K W S L G L Y F G E Q A Y L R S S 1198

QY 1357 W N V L D G L L V I S V I D I L V M V S D S G T K I L G M L R V L R L T R L P L R V I S R A Q G L K L V V E T L 1416

Db 1199 W N V L D G L V F V S I I D I V V S V A S A G A K I L G V L R V L R L T R L P L R V I S R A P G L K L V V E T L 1258

QY 1417 M S S L K P I G N I V V I C C A F F I I F G I L G V Q L F K G K F F V C Q E D T R N I T N K S D C A E A S Y R W V R H 1476

Db 1259 I S S L K P I G N I V L I C C A F F I I F G I L G V Q L F K G K F Y H C L G V D T R N I T N R S D C V A A N Y R W V H H 1318

QY 1477 K Y N F D N L G Q A L M S L F V L A S K D G W D I M Y D G L D A V G D Q O P I M N H N P W M L L Y F I S F L L I V A 1536

Db 1319 K Y N F D N L G Q A L M S L F V L A S K D G W N I M Y N G L D A V A D Q O P V T N H N P W M L L Y F I S F L L I V S 1378

QY 1537 F F V L N M F V G V V V E N F H K C R Q H Q E E E A R R E E K R L R L E K R R S K E Q M A E A Q C K P Y Y S D 1596

Db 1379 F F V L N M F V G V V V E N F H K C R Q H Q E A E A R R E E K R L R L E K R R -----KAQRLPYAT 1431

QY 1597 Y S R F R L L V H L C T S H Y L D L F I T G V I G L N V V T M A M E H Y Q O P I L D E A L K I C N Y I F T V I F V F 1656

Db 1432 Y C P T R L L I T H S M C T S H Y L D I F I T F I C L N V V T M S L E H Y N Q P T S L E T A L K Y C N Y M F T V F V L 1491

QY 1657 E S V F K L V A F A F R R F F Q D R W N Q L D L A I V L L S I M G I T L E E I E V N L S L P I N P T I I R I M R V L R I 1716

Db 1492 E A V L K L V A F G L R R F F K D R W N Q L D L A I V L L S V M G I T L E E I E I N A A L P I N P T I I R I M R V L R I 1551

QY 1717 A R V L K L L K M A V G M R A L L H T V M Q A L P Q V G N L G L L F M L L F F I F A A L G V E L F G D L E C D E T H P C 1776

Db 1552 A R V L K L L K M A T G M R A L L D T V V Q A L P Q V G N L G L L F M L L F F I Y A A L G V E L F G K L V C N D E N P C 1611

QY 1777 E G L G R H A T F R N F G M A F L T L F R V S T G D N W N G I M K D P S R D C - D Q E S T C Y N T V -- I S P I Y F V S 1833

Db 1612 E G M S R H A T F E N F G M A F L T L F Q V S T G D N W N G I M K D T L R D C T H D E R T C L S S I Q F V S P L Y F V S 1671

QY 1834 F V L T A Q F V L V N V V I A V L M K H L E E S N K E A E E A E L E M K T L S P Q H S P L G S P F L W P 1893

Db 1672 F V L T A Q F V L I N V V A V L M K H L D D S N K E A Q E A D E M D A E I E L M ----- 1713

QY 1894 G V E G V N S T D S P K P G A P H T T A H I G A A S G F S L E H P T W V P H P E E V P P - L G P D L L T V ----- 1946

Db 1714 -A H G L G P C P G P C G -----P C P C P C P C A G P R L P T S S P G A P G 1750

QY 1947 R K S G V S R T H S L P N D S Y M C R N - G S T A E R S L G H R G W G L P K A Q S G S I L S V H S Q P A D T S C I L Q L 2005

Db 1751 R G S G G A G A G G - D T E S H L C R H C Y S P A Q E T L -----W-----L D S V S L I I K D S L E G E L T I D N L 1801

QY 2006 P K D V - H Y L L Q P H G 2017

Db 1802 S G S V F H H Y A S P D G 1814

RESULT 10

US-09-935-541-5

; Sequence 5, Application US/09935541

; Patent No. 6589787

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-935-541-5

Query Match 44.4%; Score 5345; DB 4; Length 1835;

Best Local Similarity 55.4%; Pred. No. 0;

Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

QY 43 PRSRDSPVASRSTTCPGGAAGAGAGSTEKDPGSADSEAE-----LPYPALAPVVFYLSQ 98

Db 8 PSSAAAPAPEPGITEQGP-----RSPPPSPPGLEPLEGTNPDPVHPDLAPVAFCLRQ 62

QY 99 DSRPRSWCLRTVCNPWFERYSMVLILLNCVTILGMFRPCEDIACDQSQRILQAFDDFIFA 158

Db 63 TTSPRNWCIKMVCNPFECVSMVLILLNCVTILGMVQPCDDMECLSDRCKILQVDFDFIFI 122

QY 159 FFAVEMVVMVALGIFGKKCYLGDTWNRLDFFVIAGMLEYSLDLQNVSAFVTVRLR 218

Db 123 FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVNAGMVEYSLDLQNLNSAIRTVRLR 182

QY 219 PLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPEN 278

Db 183 PLKAINRVPSMRILVNLTLTLLDTPMLGNVLLLCFFVFFIFGIIIGVQLWAGLLNRNRCFLEEN 242

QY 279 FSLPLSVDLPEYYQTENEDESPFFICSQPRENGMRSCRSVPTLRGEGGGPPCSL----- 332

Db 243 FTIQGDVALPPYYQPEEDDEMPFFICSLTGDNGINGMCHEIPLPKEQ---GRECCLSKDDVY 299

QY 333 DYETYNSSSNTT--CVNNWQYYTNCSEAGHNPFKGAINFNDNIGYAWIAIFQVITLEGWVD 390

Db 300 DFGAGRODLNASGLCVNWNRYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVE 359  
Qy 391 IMYFVMDAHSFYNFIYFILLIIVGFFMINCLVVIATOFSETKQRESQLMREORVRFLS 450  
Db 360 IMYVMDAHSFYNFIYFILLIIVGFFMINCLVVIATOFSETKQREHRLMLEQRQYLS 419  
Qy 451 NASTLASFSEPGSCYEELLYLVYLKKAARRLAQVSRALGVRAGLLSPPVARSQEPQP 510  
Db 420 -SSTVASYAEPGDCYEEIFQYVCHILRAKAR-----RALGLYQAL----- 458  
Qy 511 SGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPPS 570  
Db 459 -----QNRROA-----MGPGT-----PAPA 473  
Qy 571 TPTPSGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSBASGRTVGSKVYPTVHTSPP 630  
Db 474 KGP-----HAK-----EPHCKLCPRHSPLD-----PTPHT--- 500  
Qy 631 PEILKDKALVEVAPSPGPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISSPCSKAD 690  
Db 501 -----LVQ-----PISAIL----- 509  
Qy 691 SGACGPDPCYC-----ARTGAGEPESEDHVMPPDSSEAVYEFQDAQH 734  
Db 510 --ASDPSSCPHCQHEAGRRPSGLGTDGSGEGSGGSAE---AEANGDGL-QSSEDEGVS 563  
Qy 735 SLDLDPHRRRRQRSGLPDAEPSSVLA-----FWRLICDTFRKIVDSKYFGRGIMAILVN 789  
Db 564 SD-----LGKEEEQEDGAARLCGDVWRETRKRLRGIVDSKYFNRGIMMAILVN 611  
Qy 790 TLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPEGYIKNPYNIFDGVIVV 849  
Db 612 TVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAPGLFDYLRNPYNIFDSIIVI 671  
Qy 850 ISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLMTKMDNVATFCMLLMFI 909  
Db 672 ISIWEIVGADGGLSVLRTFRLRLVLKLVRFMPALRRQLVVLMTKMDNVATFCMLLMFI 731  
Qy 910 FIFSILGMHLFGCKPFASERD-GDTLPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMAS 968  
Db 732 FIFSILGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIIVTFQILTQEDWNVVLNGMAS 791  
Qy 969 TSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFSPSVDG----- 1022  
Db 792 TTPWASLYFVALMTFGNYVLFNLLVAILVEGFAEGDANKRSCDEQSSSNLEEFDKLPE 851  
Qy 1023 --DGRKXRLALVALGEHAELRKSLLPLLIH--TAATPMWHPKSSSTGVGEALGSGSRR 1078  
Db 852 GLDNRSLDKLCPIPMTPNGHLDPSL--PLGAHLGPAGTMTAPRLSLQDPVVALDSRK 909  
Qy 1079 TSSSGSAEPGAHAHEMKCPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGE 1138  
Db 910 SSVMSL---GRMSYDQORLSRSSRYGPGWGRSGTWSRRSWN-----SLKHKPPSAE 960  
Qy 1139 RRSLLSGEQES--QDEEESSE--DRASPAGSDH-----RHRSGLEREA 1179  
Db 961 HESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAAHGHGPHLAHRHRHRTLSLDT 1020  
Qy 1180 KSSFDLPDTLQVGLHRTAS--GRSSASEHQDCNGKSASGLARTLRTD-DPQLDGDGDDN 1236  
Db 1021 RDSVDLGEVVPVGAHRAAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDDRDRGEDE 1078  
Qy 1237 DEGNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFLLCHRIITHKMFHVVULVI 1296  
Db 1079 EBIDYTLCFVRKMWIDVYKPDWCEVEDWSVYLFSPENKFRILCQTIIAHKLFYVVLAF 1138  
Qy 1297 IFLNCITIAMERPKIDPHSAERIFLTLNSYIIFTAVFLAEMTVKVVALGWCFCGEQAYLRSS 1356  
Db 1139 IFLNCITIALERPOIEAGSTERIFLTVSNYIIFTAIFVGEMTLKVVSGLGYFGEQAYLRSS 1198  
Qy 1357 WNVLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLRLRPLRVISRAQGLKLVVETL 1416

Db 1199 WNVLDGFLVFSVSIIDIVSVASAGGAKILGVLRVLRLLRLRPLRVISRAPGLKLVVETL 1258  
Qy 1417 MSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASVWRVRH 1476  
Db 1259 ISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFFHCLGVDRNITNRSDCVAANYRWVHH 1318  
Qy 1477 KYNFDNLGOALMSLVASKDGVVDIMYDGLDVGVDQDQPIMNHNPMWMLLYFISFLIIVA 1536  
Db 1319 KYNFDNLGOALMSLVASKDGVNIMYNGLDVAVDQDQPTNHNPMWMLLYFISFLIIVS 1378  
Qy 1537 FFVLNMFVGVVVVENFHKCRHQHEEARRRREKRLRLLEKKRSKEKQMAEAQCKPYSD 1596  
Db 1379 FFVLNMFVGVVVVENFHKCRHQHQAEEARRRREKRLRLLEKKRR-----KAQRLPYAT 1431  
Qy 1597 YSRFRLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQOQILDEALKICNYIFTVIVF 1656  
Db 1432 YCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQOTSLETALKYCNMFTTVFVL 1491  
Qy 1657 ESVKLVAFAPRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRI 1716  
Db 1492 EAVLKLVAFLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRI 1551  
Qy 1717 ARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFLMLFFIFAALGVLEFGDLECDTHPC 1776  
Db 1552 ARVLKLLKMATGMRALDVTVQALPQVGNLGLLFLMLFFIYAALGVLEFGKLVNDENPC 1611  
Qy 1777 EGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSPRDC-DQESTCYNTV--ISPIYFVS 1833  
Db 1612 EGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCSSLOQFVSPLYFVS 1671  
Qy 1834 FVLTAQFVLNVVIAVLMKHLEESNKEAKEEAELEAELEEMKTLSPQHPSPGSPFLWP 1893  
Db 1672 FVLTAQFVLNVVAVLMKHLDSDNKEAQEDAEMDAEIELEM----- 1713  
Qy 1894 GVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEVPVP-LGPDLLTV----- 1946  
Db 1714 -AHGLGPCPGPCPG-----PCPCPCPCAGPRLPTSSPGAPG 1750  
Qy 1947 RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHARGWGLPKAQSGSILSVHSQPADTSCILQL 2005  
Db 1751 RSGSGAGAGG-DTESHLCHRCYSQAQETL---W-----LDSVSLIIKDSLEGELTIIDNL 1801  
Qy 2006 PKDV-HYLLQPHG 2017  
Db 1802 SGSVFHYASPDG 1814  
RESULT 11  
US-09-268-163-4  
; Sequence 4, Application US/09268163B  
; Patent No. 6353091  
; GENERAL INFORMATION:  
; APPLICANT: Lipscombe, Diane  
; APPLICANT: Schorge, Stephanie  
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF  
; FILE REFERENCE: B1055/7000  
; CURRENT APPLICATION NUMBER: US/09/268,163B  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: US 60/077,901  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 2343  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-268-163-4  
Query Match 14.0%; Score 1678; DB 3; Length 2343;  
Best Local Similarity 23.3%; Pred. No. 4.9e-126;  
Matches 625; Conservative 354; Mismatches 828; Indels 872; Gaps 81;  
Qy 59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----VFFYLSQDSRPRSWCLRT 109

Db 32 PGPGGLPGQORVLYKQSIQARARTMALYNPIPVKQNCFTVNRSLFVSEDNVVRKYAKRI 91  
QY 110 VCNPFERVSMLVILLNCVTLMGMRPCEDIACDSORCILQAFDD---FIFAFFAVEMVV 166  
Db 92 TEWPPFYMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIFGFCFEAGI 147  
QY 167 KMVALG-IFGKKCYLGDWTNRRLDFFIIVIAAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA 222  
Db 148 KIIALGFVPHKGYLRNGMNVMDFVVVLTGILATAGTDFDLR-----TLRAVRVLRPLK 202  
QY 223 INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCLPENFSLP 282  
Db 203 VSGIPSLQVVLKSIKAMVPLLIQIGLLFFAILMFAIGLEFYMKGFKHACF-----P 255  
QY 283 LSVDLPEYQ TENEDESPFCISQPRENGMRSCRSVPTLRGEGGGPPPCSLDYETYNSSN 342  
Db 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280  
QY 343 TTCVNMNQYNTCSAGEHNPFGKAINFDNIGYAWIALFOVITLEGWVDIMYFVMD-AHSF 401  
Db 281 TEC---REYWP-----GPNFGITNFDNIFAILTVFQCITMEGTWTDILYNTNDAAGNT 330  
QY 402 YNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRFLSNASTL 455  
Db 331 WNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENRRAFLKLRROQQIE----- 382  
QY 456 ASFSEPGSCYEBELLKYLVIILRKAARRLAQVSRAGVRAGLLSPPVARSGQPPSGSCT 515  
Db 383 -----RELNGYLEWIFKAEEVMLAED-----RNAEKSPLDLVK 417  
QY 516 RSHRRLSVHVLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS 575  
Db 418 RAATKKSRLDIH-----AEEGEDRFAD----- 440  
QY 576 GPPRGAESVHSFYHADCHLEVPVRCQAPPPRCPSSEASGRITVSGKVYPTVHTSPPPEILK 635  
Db 441 ----- 440  
QY 636 DKALVEAPSPGPPTLTFSNIPPGPSSMHKLLTQSTGACHSSCKISSPCKADSGACG 695  
Db 441 -----LCAVGSPFFARAS----- 452  
QY 696 PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRLSGPDAEP 755  
Db 453 -----LKSCKTESSYF-----RRKEK----- 469  
QY 756 SSVLAFWRLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVP 815  
Db 470 --MFRFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTTLYFAEFVF 521  
QY 816 TSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGLSVLRTFR 870  
Db 522 LGLFLTEMSLKMVGLGPRSYFRSSFNCFDFGIVGVSVFEVWAAIKPGSSFGISVLRALR 581  
QY 871 LMRVLKLVRFPLQRLVLMKTMNDVATFCMLLMLFIFIFISILGMHLFGCKFASERDG 930  
Db 582 LIRIFKVTKYWSSLRNLVSVLLNSMKSIISLLFLFLFVIVFALLGMQLFGGQFNQDET 641  
QY 931 DTLPRKNFDSLWAIIVTFQILTQEDWNKVLNGM-----ASTSSWAALYFIALMTFGN 985  
Db 642 PT-----TNFDTFPAAILTTFQILTGEDWNVAMVYHGIESQGGVSKGMFSSFYFIVLTLPFN 697  
QY 986 YVLFNLLVAILVEGFAEGDATKSESEPDFFSPVDGDRKKRLALVALGEHAELRKS 1045  
Db 698 YTLNVLFLAIVDNLANAQELTKDEEMEBEA-----NQKLALQAKEVAEV--SP 746  
QY 1046 LPPLIIHTAATPMSPKSSSTGVGEA----- 1071  
Db 747 MSAANISIAARQONSARARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTHLR 806  
QY 1072 -----LGSGSRRTSSSGSAEPGAA-----HH-----EMKCP----- 1097

Db 807 PDMKTHLDRPLVVELGRDGARGPVGKGARPEAAEAPEGVDPPRRHRRDKDKTPAAGDQ 866  
QY 1098 -----PSARSS---PHSPWSAASSWTSSRSSNSLGRAPSLKRRSPSGERRSL 1142  
Db 867 DRAEAPKAESGEPGAREERPRPHRSHSKEAA--GPPEARSEGRGP-----GPEGGRHH 919  
QY 1143 LSGEGQESQDEE-----ESSEEDRASPAAGSDHRRHRSLE---REAKSSFDLPDPTL 1189  
Db 920 RRGSPPEAAERERHRAHRHQDPSKECAGAGERRARHRGGPRAGPREAESG----- 972  
QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE 1238  
Db 973 EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032  
QY 1239 GNLSKGERIQAWVRSRLPACCRR-----DSW----- 1265  
Db 1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQRNVTMRMGSPDPDPNTIVHIPVMLTG 1086  
QY 1266 -----SAYIFPPQSRFRLLCHRI 1283  
Db 1087 PLGEATVPSGNVDLESQAEGKEVEADDVNRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146  
QY 1284 ITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVAL 1343  
Db 1147 VTMRYFEVILVVIALLSSIALAEDP-VRTDSPRNNAKYLDYIFTGVFTFEMVIKMDL 1205  
QY 1344 GWCFFEQAYLRSSMNVDGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRPLRV 1402  
Db 1206 GLLLHPGAYFRDLWNILDFIVVSGALVAFAPSSFVGGSGKGDINTIKSLRVLRPLKT 1265  
QY 1403 ISRAQGLKLVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQE-----D 1456  
Db 1266 IKRLPKLKAVFDCVNSLKNVNLIVVLMFMFIFAVIAVQLFKGKFFCYCTDESKELERD 1325  
QY 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLQALMSLFLVASKDGWVDIMYDGLDVGVD 1513  
Db 1326 CRGQYLDYEKEEVEAQPQWKYDFHYDNVLWALITLFTVSTGEGWPMVLKHSVDATYEE 1385  
QY 1514 QOPIMNHNPMWLLYFISFLIIVAFFVLNMFVGVVVENFHKCRHQHEEERREKRLRR 1573  
Db 1386 QGSPGYRMELSIIFYVYVVFVFFPFFVNFVALLIITF-----QEQGDKVMSE---CS 1435  
QY 1574 LEKRRSKEKQMAEAQCKPYSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTMAME 1631  
Db 1436 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKWTWTFVSPFFEFYFIMAMIALNTVLMK 1495  
QY 1632 HYQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLAIVLLSIMGIT 1691  
Db 1496 FYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAAGVLNFRDAWNVDFVTVLGSITDIL 1555  
QY 1692 LEEIE-----VNLSLPINPTIIRIMRVLRIRARVLLKLMVGMRRALLHTVMOALPOVGNL 1746  
Db 1556 VTEIAETNNFINLS-----FLRLFRAARLIKLRQGYTIRILLWTFVQSFKALPYV 1606  
QY 1747 GLLFMLLFFIFAALGVLEFGDLECDETHPCGEGLRHATFRNFGMAFLTFRVSTGDNWNG 1806  
Db 1607 CLLIAMLFFIYAIIGMQVFGNIALDDD--TSINRHNNTFTFLQALMLLFRSATGEAWHE 1663  
QY 1807 IMKD--PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLM----- 1851  
Db 1664 IMLSCLSNQACDEQANATECSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1723  
QY 1852 ----KHLEE----- 1856  
Db 1724 ILGPHHLDDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPPLGLKCKPCARVAYKRLVRMN 1783  
QY 1857 -----SNKEAKEAELEAEL-----ELEMKTLS- 1879  
Db 1784 MPISNEDMTVHTSTLMALIRTALEIKLAPAGTKHQCDALRKEISVVWANLPQKTLDL 1843  
QY 1880 -PQHPSP-----LGSPF-----LWPGVEGVNSTDSPKPGAPHHTTAHIGAAAGFSLEHPTMVP 1930  
Db 1844 LVPPHKPDGMTVGVKYAALMIFDYKQNKTTTRDQMOQAPGGLSQMGPSVSLF---HPLKAT 1900



QY 1931 HPEEVPVL-GPDLITVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRCWGLPKAQSGSI 1989  
Db 1901 LEQTQPAVLRGARVFLRQKST-----SLNGGAIQNESGIKESV---SWGTRQTDAA-- 1951  
QY 1990 LSVHSQPADTSCILQPKDVHYLLQPHGAPTGAIPKLPGRSPLAQRPLRRQAARTD 2049  
Db 1952 -----PHEA-----RPPLERGHSTEIPVGRSGALAVD 1978  
QY 2050 -----SLDVQGLSGREDLLSEVSGPSCPLTRSSFWGGSSIQVQQRSG 2092  
Db 1979 VQMOSITRRGDPGEPPGLESG-----RAASMPRLAAETQPTDASPMKRSISTLAQRPRG 2035  
QY 2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTLSWIS 2135  
Db 2036 -----THLCSTTP-----DRPPSQASSHHHHHRRCHRRDRKQORSLEKGPSLS-AD 2080  
QY 2136 GDLLPSSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDLS 2186  
Db 2081 MDGAPSSAVGCLPPGEGPTGCRERRRQERGRSQERRQPSSSSEKQRF---YSCDRF 2137  
QY 2187 GSQRLCPSPS-----SLGGQPL-----GGPGRPRPKK 2213  
Db 2138 GGREPPKPKPSLSHPTSTAGQEPGHPQGGSVNGSPLLSTSGASTPGRGRRQLPQT 2197  
QY 2214 KLSP-PSISIDPPES-----QGSRPSPG-----VCLRRRAPASD----- 2248  
Db 2198 PLTPRPSITYKTANSSPIHFAGAQTSIPAFSPGRSLRGLSEHNALLQDPLSQPLAPGSR 2257  
QY 2249 -SKDPSVSSPLDSTAASPKKDTLSL-----SGLSS 2279  
Db 2258 IGSDPYLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS 2296

RESULT 12

US-08-713-118-2  
; Sequence 2, Application US/08713118  
; Patent No. 6040436

GENERAL INFORMATION:

; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

; LENGTH: 2337 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-713-118-2

Query Match 13.9%; Score 1677; DB 3; Length 2337;  
Best Local Similarity 23.4%; Pred. No. 5.9e-126;  
Matches 627; Conservative 350; Mismatches 829; Indels 868; Gaps 82;

QY 59 PGPGAAGAGSTEKDPGSADSEAGLPYPALAPV-----VFFYLSQDSRPRSRWCURT 109  
Db 32 PGPGGLQPGQRVLYKQSIQAQARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI 91  
QY 110 VCNPWFERVSMVLILLNCVTLGMRPCEDIACDSQRCRILOAFDD--FIFAFFAVEMVV 166  
Db 92 TEWPPFEYMLATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIFGFCFEAGI 147  
QY 167 KMVALG-IFGKKCYLGDWTNRDLDFIIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA 222  
Db 148 KIIALGFVPHKGSYLRNGWNVMDVVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL 202  
QY 223 INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVLWAGLLNRNCFLPENFSLP 282  
Db 203 VSGIPSLQVVLKSIKAMVPLLIQIGLLLFALLMFAIIGLEFYMGKFHKACF-----P 255  
QY 283 LSVLDLEPYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSN 342  
Db 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280  
QY 343 TTCVNNWNOYNTCSAGEHNPFKAINFDNIGYAWIAIFQVITLEGVVDIMYFVMD-AHSF 401  
Db 281 TEC---REYWP-----GPNFGITNFDNILFAILTQFCITMEGWTDLINTNDAAGNT 330  
QY 402 YNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRVRLSNASTL 455  
Db 331 WNWLYFIPLIIGSFFMLNLVGLVSGEFAKERERVENRRAFLKLRQQOIE----- 382  
QY 456 ASFSEPGSCYEELLYLVYILRKAARRLAQVSRAGVRAGLLSSPVARSQGPQSPGSCT 515  
Db 383 -----RELNGYLEWIFKABEVMLEED-----RNAEKSPLDVLK 417  
QY 516 RSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS 575  
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QY 576 GPPRGAESVHSFYHADCHLEPVRCAQAPPPRCPCSEASGRIVGSGKVYPTVHTSPPEILK 635  
Db 441 ----- 440  
QY 636 DKALVEVAPSPGPTLTSTFNIPGPFSSMHKLLTQSTGACHSSCKISSPCSKADSGACG 695  
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QY 696 PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSHRRRQSLGPDAP 755  
Db 453 -----LKSGKTESSSYF-----RRKEK----- 469  
QY 756 SSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF 815  
Db 470 --MFRFF-----IRRMVKAQSFYVWVLCVWALNTLCVAMVHYNQPRRLTTTLYFAEFV 521  
QY 816 TSLFALEMLKLLVYGPFGYIKNPYNIIFDGVIVVISVWEIVGQ-----QGGGLSVLRTR 870  
Db 522 LGLFLTEMSLKMVGLGPRSYRFSNFCDFGVIVGVFVWAAIKPGSSFGISVLRALR 581  
QY 871 LMRVLKLVRFPLPALQRLVVLMTMDNVATFCMLLMFLIFISILGMHLFGCKFASERDG 930  
Db 582 LLRIFKVTYKWSLRLNVLSLNSMKSIIISLLFLFVIVFALLGMQLFGGQNFQDET 641  
QY 931 DTLPRKKNFDSLLWAIIVTFQILTQEDWNKVLNYGM-----ASTSSWAALYFIALMTFGN 985  
Db 642 PT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSGKGMFSSFYFIVLTJFGN 697  
QY 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGHEAELRKSL 1045

Db 698 YTLNVLAIADNLANAQELTKDEEEMEEAA-----NQKLALQAKEVAEV--SP 746

QY 1046 LPPLIIHTAATPMSPKSSSTGVGEA----- 1071

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Db 807 PDMKTHLDRPLVVELGRDGARGPVGKGARPEAAEPEGVDPPRRHHRHRDKDTPAAGDQ 866

QY 1098 -----PSARSS---PHSPWSAASWTSSRRSRNSLGRAPSLKRRSPSGERRSL 1142

Db 867 DRAEAPKAESGEPGAREPRPHSHSKEAA--GPPEARSERGRP-----GEGGRRH 919

QY 1143 LSGEGQESQDEE-----ESSEEDRASPAGSDHHRHRSLE---REAKSSFDLPDTL 1189

Db 920 RRGSPPEAAERPRRHRAHRHQDPSKECAGAKGERRARRHGGPRAGPREAESG----- 972

QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKKSASGRLA-----RTLRTDDPQLDGGDDNDDE 1238

Db 973 EEPARRHRAHKAQPAHEAVEKETEKATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032

QY 1239 GNLSKGERIAQAVRSRLPACCRER-----DSW----- 1265

Db 1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQNRNVRMGSPQDPNTIVHIPVMLTG 1086

QY 1266 -----SAYIFPPQSRFRLLCHRI 1283

Db 1087 PLGEATVPSGNVDLESQAEKKEVEADDMRSGRPPIVPYSSMFCLSPTNLLRRFCHYI 1146

QY 1284 ITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLNYSIIFTAVFLAEMTVKVVAL 1343

Db 1147 VTMRYFEVILVIALSSIALAEDP-VRTDSPRNNAKLYLDYIFTGVFTFEMVIKIDL 1205

QY 1344 GWCFGQAYLRSSWNVDGLLVLSIDILVSMV-SDSGTKILGMLRVLRLTLRPLRV 1402

Db 1206 GLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRLPLKT 1261

QY 1403 ISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGKFVCOGE-----D 1456

Db 1262 IKRLPKLKAVIDCVVNSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFYCTDESKELERD 1321

QY 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGOALMSLFLVASKOGWVDIMYDGLDAVGVD 1513

Db 1322 CRGQYLDYEKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381

QY 1514 QPIMNHNPMWMLLYFISFLLIIVAFVFLNMFGVVVENFHKCRQHOOEEEEARRREKRLRR 1573

Db 1382 QGSPGPGYRMELSIYVYVYVVFVFFVFNIFVALIITP-----QEQGDKMSE----CS 1431

QY 1574 LEKRRSKEQMAEAQCKPYYSYR--FRLLVHLCCTSHYLDLFTITGVIGLNVVTNAME 1631

Db 1432 LEKNERACIDFAISAKPLTRYMPQNRSQFQYKTTWTFVSPPPFEYFIMAMIALNTVVLMMK 1491

QY 1632 HYQQPQILDALKICNYIFTVIFVFESVFKLVAFARFFQDRWNQDLAIVLLSIMGIT 1691

Db 1492 FYDAPYEYELMKCLNIVFTSMESMECVLKIIAFGVNLNFRDANWVDFVTVLGSITDIL 1551

QY 1692 LEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRAALLHTVMQALPOVGNLGLLFM 1751

Db 1552 VTEIANNF---IN---LSFLRLFAARLIKLLRQGYTIRILLWTFTVQSFKALPYVCLLIA 1605

QY 1752 LFFIFALGVELFGDLECDETHPCGGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD- 1810

Db 1606 MLFFIYAIIGMQVFGNIALDDD--TSINRHNFRFLQALMLLFRSATGEAWHEIMLSC 1662

QY 1811 -PSRDCQOE--STCYNTVISPIYFVSVFLTAQFVLNVVIAVLM-----K 1852

Db 1663 LSNQACDEQANATECGSDFAFYFVFSFIFLCSFLMLNLFVAVIMDNFYLTRDSSILGPH 1722

QY 1853 HLEE----- 1856

Db 1723 HLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPLGLGKPCPARVAYKRLVRMNPISN 1782

QY 1857 -----SNKEAKEEALEAEEL-----ELEMKTLS--PQPH 1883

Db 1783 EDMTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDLLVPPH 1842

QY 1884 SP-----LGSPF---LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEV 1935

Db 1843 KPDEMTVGKYYAALMIFDFYKQNKTTTRDQMQAQPGCLSQMGVPVSLF---HPLKATLEQTQ 1899

QY 1936 FVPL-GPDLITVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRGWGLPKAQSGSILSVHS 1994

Db 1900 PAVLRGARVFLRQKSST-----SLNNGGAIQNESGIKESV---SWGTRQTDQ----- 1945

QY 1995 QPADTSCILQLPKDVHYLLQPHGAPTWGAIKPLPPGRSPLAQRPLRRQAIRTD----- 2049

Db 1946 -----PHEA-----RPPLERGHSTEIFVGRSGALAVDVQMOS 1977

QY 2050 -----SLDVQGLGSREDLLSEVSGPSCPILTRSSSFWGGSSIQVQORSIGISKV 2097

Db 1978 ITRRGPDGEPQGLSQG---RAASMPRLAAETQPVTDASPMKRSISTLAQPRG----- 2029

QY 2098 SKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTLSWISGDLPL 2140

Db 2030 -THLCSTTP-----DRPPPSQASSHHHHHCHRRDRKQSRLEKGPSSL-ADMDGAP 2079

QY 2141 SSQEEPLFP-----RDLKKCYSVETQSCRRPPGFWLDEQRRHSIAVSLDSGSQPR 2191

Db 2080 SSAVGGLPPGEGPTGCRERRRQERSRQERRQPSSSSEKQRF---YSCDRFGGREGP 2136

QY 2192 LCSPS-----SLGGQPL-----GGGSRPCKKLSP- 2217

Db 2137 PKKPSSLSSHPTSPTAGQEPGPHPGQSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPR 2196

QY 2218 PSISIDPPES-----QGSRRPPCSPG-----VCLRRRAPASD-----SKDP 2252

Db 2197 PSITYKTANSSPIHFAGAQTSLPAFSPGRLSRGLSEHNALLQORDPLSQPLAPGSRIGSDP 2256

QY 2253 SVSSPLDSTAASPSPKKDTLSL-----SGLSS 2279

Db 2257 YLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS 2290

RESULT 13

US-09-452-007-2  
; Sequence 2, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/452,007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:

; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-452-007-2

Query Match		13.9%;	Score 1677;	DB 3;	Length 2337;
Best Local Similarity		23.4%;	Pred. No. 5.9e-126;		
Matches 627;		Conservative 350;	Mismatches 829;	Indels 868;	Gaps 82;
QY	59	PGPGAAGAGSTEKDPGSADSEAGLPYPALAPV-----VFFYLSQDSRPRSWCLRT	109		
Db	32	PGPGGLQPGQRLVKQSIQAQRARTWALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI	91		
QY	110	VCNPWFERSMLVILLNCVTLMGFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV	166		
Db	92	TEWPPFEYMLATIIANCIVLAL----EQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI	147		
QY	167	KMVALG-IFGKKCYLGDWTNRDLDFEIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA	222		
Db	148	KIIALGFVFHKGSLRNGWNVMDFFVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL	202		
QY	223	INRVPSMRILVTLILLDTLPMGNVLLLCFFVFFIFGIVGVLWAGLLRNRCFLPENFSLP	282		
Db	203	VSGIPSLQVVVLKSIKAMVPLLQIGLLFFAILMFAIIGLEFYMKGFKACF-----P	255		
QY	283	LSVDLEPYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCLDYETYNSSSN	342		
Db	256	NSTDAEPV-----GDFPCGKEAPARLCEGD	280		
QY	343	TTCVNWNQYNTCSAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF	401		
Db	281	TEC---REYWP-----GPNFGITNFDNILFAILTVFCITMEGWTDLINTNDAAGNT	330		
QY	402	YNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRES-----QLMREQVRFLSNASTL	455		
Db	331	WNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENRRAFLKLRRQQIE-----	382		
QY	456	ASFSEPGSCYEELKLYVILRKAAARLQAQVSRAIGVRAGLLSSPVARSQGPQPSGCT	515		
Db	383	-----RELNGYLEWIFKAEVVMLEED-----RNAEEKSLDVLK	417		
QY	516	RSRRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS	575		
Db	418	RAATKKSRLDIH-----AEEGEDRFAD-----	440		
QY	576	GGPPRGAESVHSFYHADCHLEPVRQAPPPRCPSSEASGRTVSGKVYPTVHTSPPEILK	635		
Db	441	-----	440		
QY	636	DKALVEAPSPGPPTLTSTFNIPPGPFSSMHKLLLETQSTGACHSSCKISSPCKADSGACG	695		
Db	441	-----LCAVGSPPFARAS-----	452		
QY	696	PDSCPYCARTGAGEPESADHVMPSDSEAVYEFTQDAQHSDLRDPHSRRRRQRLGPDAP	755		
Db	453	-----LKSGKTESSSYF-----RRKEK-----	469		
QY	756	SSVLAFWRLICDTERKIVDSKYFGRGIMIAILVNTLSMGIEYHQPEELTNALETINIVF	815		
Db	470	--MREFF-----IRRMVKAQSFYVVLVCWALNTLCVAMVHYNQPRRLTTTLVFAEFVF	521		
QY	816	TSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGLSVLRTFR	870		
Db	522	LGLFLTEMSLKMVGLGPRSYFRSSFNCFDFGIVGVSFVEVFWAAIKPGSSFGISVLRAIR	581		

QY	871	LMRVLKLVRFLPALQRLVVLMTMDNVATFCMLLMFLFIPISILGMHLFGCKFASERDG	930
Db	582	LLRIPKVTYKWSLRLNVLSLSNMKSIISLLFLFLFIVV FALLGMQLFGGQNFQDET	641
QY	931	DTLPDRKNFDSLMLWAIIVTFQILTQEDWNKVLYNGM-----ASTSSWAALYFIALMTFGN	985
Db	642	PT----TNFDTFPAAILTVFQILTGEDWNVAMVYHGIESQGVSKGMFSSFYFIVLTFLGN	697
QY	986	YVLFNLLVAILVEGFOAEGDAYKSESEPDFFSPSPVDGDGRKKRLALVALGEHAELRKSL	1045
Db	698	YTLNVLFLAIVADNLANAQELTKDEEEMEEAA-----NQKLALQKAKEVAEV--SP	746
QY	1046	LPPLIIHTAATPM SHPKSSSTGVGEA-----	1071
Db	747	MSAANISIAARQNSAKARSVMQQRASQLRLQNLRASCEALYSEMDPEERLRFATTHRR	806
QY	1072	-----LGSGRRTSSSGSAEPGAA-----HH-----EMKCP-----	1097
Db	807	PDMKTHLDRPLVVELGRDGARGVGKARPEAAEAPEGVDPPRRHRRHRDKDKTPAAGDQ	866
QY	1098	-----PSARSS---PHSPWSAASSWTSRRSRNSLGRAPSLKRRRSPSGERRSL	1142
Db	867	DRAEAPKAESGEPGAREERPRHRSHSKEAA--GPPEARSERGRGP-----GPEGGRHH	919
QY	1143	LSGEGQESQDEE-----ESSEEDRASPAAGSDHRRHRSLE---REAKSSFDLPDTL	1189
Db	920	RRGSPEEAAEREPRRRHRAHRHQDPKSKCAGAKGERARRHRGGRAGPREAESG-----	972
QY	1190	QVPG-LHRTASGRSSASE--HQDCKGKSASGLA-----RTLRTDDPQLDGDNDDE	1238
Db	973	EEPARRHRAHKAQPAHEAVEKETTEKEATEKEAEIVAEADKEKELRNHQPREPHCDLETS	1032
QY	1239	GNLSKGERIQAWVRSRLPACCRER-----DSW-----	1265
Db	1033	GTVTGVP-----MHTLPSTCLQKVEEQPEDADNQNRNVRMGSQPPDPNTIVHIPVMLTG	1086
QY	1266	-----SAYIFPPQSRFRLLCHRI	1283
Db	1087	PLGEATVVPNGVNDLESQAEGKKEVEADDDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI	1146
QY	1284	ITHKMFHVLVLIIFLNCITTIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL	1343
Db	1147	VTMRVFEVILVWIALSSIALAEDP-VRTDSPRNNAKYLDYIFTGVFTFEMVIKMDL	1205
QY	1344	GWCFGEQAYLRSSWNVDGLLVLSVIDILVSMV-SDSGTKILGMLRLVLRLLRTPLRV	1402
Db	1206	GLLLHPGAYFRDLWNILD---FIVVSGALVAFAFSGSGKDKINTIKSLRVLRLPLKT	1261
QY	1403	ISRAQGLKVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE-----D	1456
Db	1262	IKRLPKLKA VDCVNSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERD	1321
QY	1457	TRN--ITNKSDCAEASYR-WVRHKYNFDNLQALMSLFLVASKDGWVDIMYDGLDAVGVD	1513
Db	1322	CRGQYLDYEKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE	1381
QY	1514	QQPIMNHNPMMLLYFISFLLIVAFVFLNMFVGVVVENFHKRQHQQEERREERREKLRR	1573
Db	1382	QGSPSGYRMELSI FYVVYFVVPFFVFNIFVALIITF-----QEQGDKVMSE----CS	1431
QY	1574	LEKRRSKEKQMAEAQCKPYYSYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTNAME	1631
Db	1432	LEKNERACIDFAISAKPLTRYMPQNRSQFYKWTFTVVSPPFEYFIMAMIALNTVVLMMK	1491
QY	1632	HYQQPQILDALKICNYIFTVIFVESVFKLVAFARRRPFQDRWNQLDAIVLLSIMGIT	1691
Db	1492	FYDAPYEYELMLKCLNIVFTSMESMECVLKIIAFGVNLNFRDAMNVEDFTVLGSDTIL	1551
QY	1692	LEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLHTVMOALPOVGNLGLLFM	1751
Db	1552	VTEIANNF---IN---LSFLRLFAARLIKLLRQGYTIRILLWTFTVQSFKALPYVCLLIA	1605





QY 343 TTCVWNOYNTCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFMD-AHSF 401  
Dd 281 TEC---REYWP-----GPNFGITNFDNILFAILTVFQCITMEGWTDLINTNDAAAGNT 330  
QY 402 YNFIYFILLIIVGSPFMINCLVVIATQFSETKQRES-----QLMREQVRFLSNASTL 455  
Dd 331 WNWLYFIPLIIGSFMLNLVLGVLGSEFAKERERVENRRAFLKLRRQQQIE----- 382  
QY 456 ASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRRAIGVRAGLLSSPVARSQEQPQSGSCT 515  
Dd 383 -----RELNGYLEWIFKAEVMLAEED-----RNAEEKSPLDVLK 417  
QY 516 RSHRRLSVHHLVHHHHHHHHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS 575  
Dd 418 RAATKKSRLDIH-----AEEGEDRFAD----- 440  
QY 576 GPPPRGABSVHSFYHADCHLEPVRCQAPPPRCPPSEASGRTVGSGKVYPTVHTSPPEILK 635  
Dd 441 ----- 440  
QY 636 DKALVEVAPSGPPTLTSTFNIPGPFSSMHKLLTQSTGACHSSCKISSPCSKADSGACG 695  
Dd 441 -----LCAVGSPFARAS----- 452  
QY 696 PDSCPYCARTGAGEPEADHVMPSDSEAVYFTQAOHSDLRDPHSRRRQRSGLGDAEP 755  
Dd 453 -----LKSGKTESSSYF-----RRKEK----- 469  
QY 756 SSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALBISNIVF 815  
Dd 470 --MFRFF-----IRRMVKAQSFYVVLVWALNTLCVAMVHYNQPRRLTTTLYFAEFVF 521  
QY 816 TSLFALEMLKLLVYGPFGYIKNPYNIPDGVIIVISVWEIVGQ-----QGGGLSVLRTFR 870  
Dd 522 LGLFLEMSLKMYGLGPRSYFRSSFCDFGVIIVGSVFVWAAIKPGSSFGISVLRALR 581  
QY 871 LMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFTIFPSILGMHLFGCKFASERDG 930  
Dd 582 LLRIKVTKYWSSLRNLVSSLNSMKSIISLLFLFLFVIVFALLGMQLFGGQFNQDET 641  
QY 931 DTLPRKNFDSLLWAIWTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIALMTFGN 985  
Dd 642 PT----TNFDTFPAAILTVQILTGEDWNAVYHGIESQGVSKGMFSSFYFIVLTLFGN 697  
QY 986 YVLFNLVAILVEGFAEQDATKSESEPDFFSPSVDGDGDKRKLALVALGEHAELRKS 1045  
Dd 698 YTLNVLFLAIVDNLANAQELTXDEEMEEAA-----NQKALQAKEVAEV--SP 746  
QY 1046 LPPLIIHTAATPMSHPKSSSTGVGEA----- 1071  
Dd 747 MSAANISIAARQONSAKARSVWEQBRASQLRLQNLRASCEALYSEMDPEERLREATRHLR 806  
QY 1072 -----LGSGSRRTSSSGSAEPGAA-----HH-----EMKCP----- 1097  
Dd 807 PDMKTHLDRPLVVELGRDGARGPVGCKARPEAAEAPEGVDPPRRHHRHDKDKTPAAGDQ 866  
QY 1098 -----PSARSS---PHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSL 1142  
Dd 867 DRAEAPKABSGEPGAREERPRPHRSHSKEAA--GPPEARSERGRGP-----GPEGRRHH 919  
QY 1143 LSQEGQESQDEE-----ESSEEDRASPAQSDHRRHRSLE---REAKSSFDLPDTL 1189  
Dd 920 RRGSPPEEAAREPRRHRHRHQDPSKECAGAKERRARRHGRGPRAGPREAESG----- 972  
QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE 1238  
Dd 973 BEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032  
QY 1239 GNLSKGERIQAWVRSLRPACCRER-----DSW----- 1265  
Dd 1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQNRNVTRNGSQPPDPNTIVHIPVMLTG 1086

QY 1266 -----SAYIFPPQSRFRLLCHRI 1283  
Dd 1087 PLGEATVVPNGVNDLESQAEGKKEVEADDMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146  
QY 1284 ITHKMPDHVVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVAL 1343  
Dd 1147 VTMRYFEVILVIALSSIALAABDP-VRTDSPRNNAKYLDYIFTGVFTFEMVIKMDL 1205  
QY 1344 GWCFGEOAYLRSSWNVLGDLVLISVIDILVSMV-SDSGTKILGMLRVLRLRLRPLRV 1402  
Dd 1206 GLLHPGAYFRDLWNILD---FIVVSGALVAFAFSGSGKGDINTIKSLRVLRLRPLKT 1261  
QY 1403 ISRAQGLKVVTETLMSSSLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCQGE-----D 1456  
Dd 1262 IKRLPKLKAVIDCVVNSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELEED 1321  
QY 1457 TRN--ITNKSDDCAEASYSR-WVRHKYNFDNLQOALMSLFLVASKDGWVDIMYDGLDAVGVD 1513  
Dd 1322 CRGQYLDYEKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381  
QY 1514 QPIMNHNPMWMLLYFISFLLIIVAFVVLNMFVGVVVENFHKCRQHQQEERREKRLRR 1573  
Dd 1382 QGSPSGYRMELSIFYVVFVVFVFFVFNIFVALIITF-----QEQQDKVMSE---CS 1431  
QY 1574 LEKRRSKEQMAEAQCKPYYSYSR--FRLLVHHLCTSHVLDLFTITGIVGLNVVTMAME 1631  
Dd 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKWTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491  
QY 1632 HYQPOQLDEALKICNYIFTVIVFVSVFKLVAFARFRFQDRWNQDLAIIVLLSIMGIT 1691  
Dd 1492 FYDAPYBELMLKCLNIVFTSMFMECVLKIIAFGLVNLFRDANWVDFVTVLGSITDIL 1551  
QY 1692 LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMALLHTVMQALPQVGNL 1746  
Dd 1552 VTEIAETNNEINLS-----FLRLFRAARLIKLLRQGYTIRILLTWFVQSFKALPYV 1602  
QY 1747 GLLFMLLPFIFAALGVLFGLDECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNG 1806  
Dd 1603 CLLIAMLFFIYAIIGMQVFGNIALDDD--TSINRHNFRFTFLQALMLLFRSATGEAWHE 1659  
QY 1807 IMKD--PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLM----- 1851  
Dd 1660 IMLSCLSNQACDEQANATECGSDPAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1719  
QY 1852 ----KHLLE----- 1856  
Dd 1720 ILGPHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPLGLGKCKPARVAYKRLVRMN 1779  
QY 1857 -----SNKEAKEAELEAEL-----ELEMKTLS- 1879  
Dd 1780 MPISNEDMTVHTSTLMALIRTALEIKLAPAGTKHQHQCDAELRKEISVVWANLPQKTLDL 1839  
QY 1880 -PQHSP-----LGSPF---LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVP 1930  
Dd 1840 LVPPHKPDDEMTVGKYYAALMIFDFYKQNKTTTRDQMQQAPGGLSQMGVPSLF---HPLKAT 1896  
QY 1931 HPEEVVPVL-GPDLTLTVRKSGVSRTHSLPNDSYMCNRNGSTAERSLGHARGWGLPKAQSGSI 1989  
Dd 1897 LEQTQPAVLRGARVFLRQKSSST---SLNNGGAIQNEQSGIKESV---SWGTRTQDA-- 1947  
QY 1990 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTGWGAIKPLPPGRSPLAQORPLRRQAIRTD 2049  
Dd 1948 -----PHEA-----RPPLERGHSTEIPVGRSGALAVD 1974  
QY 2050 -----SLDVQGLGSRREDLLSEVSGPSCPLTRSSSFWGSSIQVQQRSG 2092  
Dd 1975 VQMOSITRRGPDGEPQPGLESQG---RAASMPRLAAEQPVTASPMKRSISSTLAQPRG 2031  
QY 2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTLSWIS 2135  
Dd 2032 -----THLCSTTP-----DRPPPSQASSHHHHHRRRRDRKQSRLEKGPSLS-AD 2076  
QY 2136 GDLLPSSQBEPLFP-----RDLKKCYSVETQSCRRRRPGFWLDEQRRHSIAVSClds 2186

Db 2077 MDGAPSSAVGGLPPGEGPTGCRERRRQERGRSQRRQPSSSSEKQRF---YSCDRF 2133  
QY 2187 GSQRLCPSPS-----SLGGQPL-----GGPGSRPKK 2213  
Db 2134 GGREPPKPKPSLSSHPTSPTAGQEPGPHPOGSGSVNGSLSTSGASTPGRGRRQLPQT 2193  
QY 2214 KLSP-PSISIDPPES-----QSRPPCSPG-----VCLRRRAPASD----- 2248  
Db 2194 PLTPRPSITYKTANSSPIHFAGAQTSLPAPSPGRLSRGLSEHNALLQRPDPLSOLAPGSR 2253  
QY 2249 -SKDPSVSSPLDSTAASPSPKDTLSL-----SGLSS 2279  
Db 2254 IGSDPYLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS 2292

RESULT 15  
US-08-223-305C-47  
; Sequence 47, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062

; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2339 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-223-305C-47  
  
Query Match 13.9%; Score 1676; DB 2; Length 2339;  
Best Local Similarity 23.4%; Pred. No. 7.1e-126;  
Matches 627; Conservative 350; Mismatches 826; Indels 876; Gaps 82;  
  
QY 59 PGGAAGAGSTEKDPGSDSEAEGLPYPALAPV-----VFFYLSQDSRPRSWCLRT 109  
Db 32 PGGGLQPGQORVLYKQSIQAQARTMALYNPIPVKQNCFTVNRSLFVSEDNVVRKYAKRI 91  
  
QY 110 VCNPFERFVSMVLVILNCVTLMFRPCEDIACSQRCRILQAFDD---FIAFAFAVEMVV 166  
Db 92 TEWPPFENMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIFGICFEAGI 147  
  
QY 167 KMVALG-IFGKKCYLGDWNRLDFFIVIAGLEYS---LDLQNVSFSAVTRVRLPLRA 222  
Db 148 KIIALGFVFKGSYLRNGWNVDMFVVVLGTILATAGTDFDLR-----TLRAVRVLRPLKL 202  
  
QY 223 INRVPSMRILVTLTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNCFLPENFSLP 282  
Db 203 VSGIPSLQVLKSIKAMVPLLIQIGLLFFAILMFAIIGLEFYMGKFKHACF-----P 255  
  
QY 283 LSVDLPEYYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSN 342  
Db 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280  
  
QY 343 TTCVNNQYNTNCAGHNPFKGAINFEDNIGYAWIAFOVITLEGWVDIMYFVMD-AHSF 401  
Db 281 TEC---REYWP-----GPNFGITNFDNILEFALTIVFQCITMEGWTDILYNTNDAAGNT 330  
  
QY 402 YNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRFLSNASTL 455  
Db 331 WNWLYFIPLIIIGSFFMLNLVLGVLGSGEFAKERERVENRRAFLKLRQOOIE----- 382  
  
QY 456 ASFSEPGSCYEELKYLVIILKAAARRLAQVSRRAIGVRAGLLSSPVARSQGEPPQSGSCT 515  
Db 383 -----RELNGYLEWIFKAEVLEAED-----RNAEKSPLDVLK 417  
  
QY 516 RSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS 575  
Db 418 RAATKKSRLDLI-----AEGEDRFAD----- 440  
  
QY 576 GGPPRGAESVHSFYHADCHLEPVRCAQPPPCPSEASGRTVSGKVPYVHTSPPEILK 635  
Db 441 ----- 440  
  
QY 636 DKALVEVAPSPGPPTLTSENIPPGPFSSMHKLLTQSTGACHSSCKISSPCSKADSGACG 695  
Db 441 -----LCAVGSPPFARAS----- 452  
  
QY 696 PDSCPYCARTGAGEPESADHVMPSDSEAVVEFTQDAHQHSDLRDPHSRRRQSRSLGPDAP 755  
Db 453 -----LKSGKTESSESYF-----RRKEK----- 469  
  
QY 756 SSVLAFWRLICDTRFKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPELTNALEISNIVF 815  
Db 470 --MERFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTYFAEFVF 521  
  
QY 816 TSLFALEMLLKLIVYGPFGYIKPNYNIFDGVIVVISVWEIVGQ-----QGGGLSVLRTFR 870  
Db 522 LGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGSVFVVWAAIKPGSSFGISVLRALR 581  
  
QY 871 LMRVLKLVRLPALQRLVLMKTMNDNVATPCMLLMLFIFISILGMHLFGCKFASERDG 930  
Db 582 LLRIKVTKYWSSSLRNVLVSLNSMKSIIISLLFLFLFVIVFALLGMQLFGGQNFQDET 641

QY	931	DTLPDRKNFDSLWAIWTVFQILTQEDWNKVLNGM-----ASTSSWAALYFIALMTFGN	985
Db	642	PT---TNFDTFPAAILTVFQILTGEDWNAVYHGLESGQGVSKGMFSSFFYFVLTFLGN	697
QY	986	YVLFNLLVAILVEGFOAEGDATKSESEPFFSPSVDGDRKKRLALVALGEHAELRKSL	1045
Db	698	YTLNVLFLAIVDNLANAQELTKDEEMEEAA-----NQKALQKAKEVAEV--SP	746
QY	1046	LPPLIIHTAATPMSPKSSSTGVGEA-----	1071
Db	747	MSAANISIAARQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATRHRLR	806
QY	1072	-----LGSGSRRTSSSGSAEPGAA-----HH-----EMKCP-----	1097
Db	807	PDMKTHLDRPLVLVELGDGARGPVGGKARPEAAEAPGVDPRRHHRHRDKDKTPAAGDQ	866
QY	1098	-----PSARSS---PHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSL	1142
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QY	1143	LSGEGQESQDEE-----ESSEEDRASPAAGSDHHRHGSLE--REAKSSFDLPDTL	1189
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QY	1190	QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE	1238
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QY	1266	-----	1283
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QY	1344	GWCFGEQAYLRSSWNVLGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRPLRV	1402
Db	1206	GLLLHPGAYFRDLWNILD---FIVVSGALVAFAPFSGSKGKDINTIKSLRVLRVLRPLKT	1261
QY	1403	ISRAQGLKLVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCOGE-----D	1456
Db	1262	IKRLPKLKA VDCV VNSLKNVLNIIIVMLFMFIFAIVIAVQLFKGKFFYCTDESKELERD	1321
QY	1457	TRN--ITNKSDCAEASVR-WVRHKYNFDNLGQALMSLFLVLASKDGWVDIMYDGLDVGVD	1513
Db	1322	CRGQYLDYEKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE	1381
QY	1514	QOPIMNHPWMLLYFISFLLI VAFVVLNMFVGVVVENPHKCRHQHEEEARRRREEKRLRR	1573
Db	1382	QGPSGYRMELSIFYVYVYVVPFFFFVNFVALLIITF-----QEQGDKVMSE-----CS	1431
QY	1574	LEKKRRSKEKOMAEAQCKPYYSYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTNAME	1631
Db	1432	LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTYTFVVSPPFEYFIMAMIALNTVVLMMK	1491
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QY	1692	LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALPQVGNL	1746
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Job time : 102 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 19:11:35 ; Search time 215 Seconds  
(without alignments)  
3535.497 Million cell updates/sec

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Perfect score: 12028  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues  
Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11542.5	96.0	2425	10 US-09-383-894-4	Sequence 4, Appli
2	11532	95.9	2374	10 US-09-383-894-2	Sequence 2, Appli
3	10806.5	89.8	2243	16 US-10-408-765A-625	Sequence 625, App
4	10732.5	89.2	2377	16 US-10-757-262-16	Sequence 16, Appl
5	6222	51.7	2353	16 US-10-408-765A-1128	Sequence 1128, Ap
6	5872	48.8	1207	17 US-10-930-301-52	Sequence 52, Appli
7	5409	45.0	2175	9 US-09-935-541-2	Sequence 2, Appli
8	5409	45.0	2175	14 US-10-425-800-2	Sequence 2, Appli
9	5405.5	44.9	2188	9 US-09-935-541-4	Sequence 4, Appli
10	5405.5	44.9	2188	14 US-10-425-800-4	Sequence 4, Appli
11	5345	44.4	1835	9 US-09-935-541-5	Sequence 5, Appli
12	5345	44.4	1835	14 US-10-425-800-5	Sequence 5, Appli
13	3950	32.8	1853	9 US-09-030-482B-19	Sequence 19, Appl

14	3553	29.5	1657	15	US-10-369-493-6836	Sequence 6836, Ap
15	1680.5	14.0	2264	15	US-10-627-370-2	Sequence 2, Appli
16	1678	14.0	2343	13	US-10-033-026-4	Sequence 4, Appli
17	1676	13.9	2339	15	US-10-375-253-12	Sequence 12, Appl
18	1674	13.9	2339	13	US-10-033-026-6	Sequence 6, Appli
19	1647.5	13.7	2313	16	US-10-322-696-178	Sequence 178, App
20	1642.5	13.7	2237	15	US-10-375-253-14	Sequence 14, Appl
21	1642.5	13.7	2336	13	US-10-033-026-10	Sequence 10, Appl
22	1640.5	13.6	2237	13	US-10-033-026-8	Sequence 8, Appli
23	1638	13.6	2251	15	US-10-375-253-38	Sequence 38, Appl
24	1637.5	13.6	2270	15	US-10-375-253-40	Sequence 40, Appl
25	1636	13.6	2251	16	US-10-322-696-84	Sequence 84, Appl
26	1635.5	13.6	2270	16	US-10-322-696-176	Sequence 176, App
27	1634.5	13.6	1984	10	US-09-457-571-10	Sequence 10, Appl
28	1631	13.6	2181	13	US-10-029-413A-18	Sequence 18, Appl
29	1631	13.6	2181	13	US-10-029-413A-20	Sequence 20, Appl
30	1631	13.6	2181	14	US-10-205-823-50	Sequence 50, Appl
31	1631	13.6	2181	15	US-10-411-010-29	Sequence 29, Appl
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34	1630.5	13.6	2166	13	US-10-029-413A-4	Sequence 4, Appli
35	1628	13.5	1873	13	US-10-029-413A-22	Sequence 22, Appl
36	1625.5	13.5	1989	10	US-09-457-571-12	Sequence 12, Appl
37	1618	13.5	2141	17	US-10-875-892-4	Sequence 4, Appli
38	1617.5	13.4	1969	10	US-09-457-571-16	Sequence 16, Appl
39	1617	13.4	2161	15	US-10-375-253-2	Sequence 2, Appli
40	1614.5	13.4	1977	10	US-09-919-039-367	Sequence 367, App
41	1614	13.4	2161	17	US-10-875-892-6	Sequence 6, Appli
42	1607	13.4	1745	15	US-10-627-370-4	Sequence 4, Appli
43	1599	13.3	1815	17	US-10-856-122-22	Sequence 22, Appl
44	1598.5	13.3	2016	16	US-10-632-342-2	Sequence 2, Appli
45	1598.5	13.3	2016	16	US-10-632-342-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-383-894-4  
; Sequence 4, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004.00191  
; CURRENT APPLICATION NUMBER: US/09/383,894  
; EARLIER FILING DATE: 1999-08-26  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399  
; EARLIER FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 2425  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-383-894-4

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Best Local Similarity		95.4%	Pred. No. 0;		
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QY 1880 PQPHSPLGSPFLWPGEVGNSTDSKPKGAPHTTAHGAASGSFSLHPTMVPHPEVPVPL 1939

Db 1933 PQPHSPLGSPFLWPGEVGNSTDSKPKGAPHTTAHGAASGSFSLHPTMVPHPEVPVPL 1992

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RESULT 2

US-09-383-894-2  
; Sequence 2, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004.00191  
; CURRENT APPLICATION NUMBER: US/09/383,894  
; CURRENT FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: US 60/098,004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399  
; EARLIER FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2374  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-383-894-2

		Query Match	95.9%;	Score 11532;	DB 10;	Length 2374;
		Best Local Similarity	97.7%;	Pred. No. 0;		
		Matches 2206;	Conservative 1;	Mismatches 18;	Indels 34;	Gaps 2;
QY	62	GAAGAGSTKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPNWPERVSM	121			
Db	30	GROQPGSTKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPNWPERVSM	89			
QY	122	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKCYLG	181			
Db	90	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKCYLG	149			
QY	182	DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLD	241			
Db	150	DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLD	209			
QY	242	MLGNVLLCFFVFFIFIGVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQYQENEDES	301			
Db	210	MLGNVLLCFFVFFIFIGVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQYQENEDES	269			
QY	302	ICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNQYTTNCSAGEHN	361			
Db	270	ICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNQYTTNCSAGEHN	329			
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYILLIIVGSFFMIN	421			
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYILLIIVGSFFMIN	389			
QY	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSFPGSCYEELLKYLVIILRKAAR	481			
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSFPGSCYEELLKYLVIILRKAAR	449			
QY	482	RLAQVSRAGVIRAGLLSSPVARSQGPQPSGCTRSRRLSVHHLVHHHHHHHHYHLGN	541			
Db	450	RLAQVSRAGVIRAGLLSSPVARSQGPQPSGCTRSRRLSVHHLVHHHHHHHHYHLGN	509			
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ	601			
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ	569			
QY	602	APPPRCPEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF	661			
Db	570	APPPRCPEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF	629			
QY	662	SSMHKLELTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD	721			
Db	630	SSMHKLELTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD	689			
QY	722	SEAVYEFTQDAQHSDLRDPHSRRRQSRSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRG	781			

Db	690	SEAVYEFTQDAQHSDLRDPHSRRRQSRSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRG	749
QY	782	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFYIKNPYN	841
Db	750	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFYIKNPYN	809
QY	842	IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATF	901
Db	810	IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATF	869
QY	902	CMLMLFIFIPFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV	961
Db	870	CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV	929
QY	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE-----	1003
Db	930	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEIGKREDASGQLSCIQLP	989
QY	1004	-----GDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPM	1058
Db	990	VNSQGGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPM	1049
QY	1059	SHPKSSSTGVGEALGSGRRRTSSSGSAEPGAHHEMKPPSARSSPHSPWSAASWTSRR	1118
Db	1050	SLPKSSSTGVGEALGSGRRRTSSSGSAEPGAHHEMKPPSARSSPHSPWSAASWTSRR	1109
QY	1119	SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRGSLERE	1178
Db	1110	SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRGSLERE	1169
QY	1179	AKSSFDPDLTQVPLGHLRTASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGDNDDE	1238
Db	1170	AKSSFDPDLTQVPLGHLRTASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGDNDDE	1229
QY	1239	GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFLLCHRIITHKMFHDHVVLIIF	1298
Db	1230	GNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFLLCHRIITHKMFHDHVVLIIF	1289
QY	1299	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEAYLRSSWN	1358
Db	1290	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEAYLRSSWN	1349
QY	1359	VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRVISRAOGLKLVVETLMS	1418
Db	1350	VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRVISRAOGLKLVVETLMS	1409
QY	1419	SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITKSDCAEASRWRHKY	1478
Db	1410	SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITKSDCAEASRWRHKY	1469
QY	1479	NFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQOPIMNHNPMMLLYFISFLIVAFF	1538
Db	1470	NFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQOPIMNHNPMMLLYFISFLIVAFF	1529
QY	1539	VLANMFVGVVVENFHKCRQHQEERREARRRLEKRRLEKRR-----SKEQMAE	1587
Db	1530	VLANMFVGVVVENFHKCRQHQEERREARRRLEKRRLEKRRNMLDDVIASSSSASAASE	1589
QY	1588	AQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVVVTWAMEHYQQPQILDEALKICN	1647
Db	1590	AQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVVVTWAMEHYQQPQILDEALKICN	1649
QY	1648	YIFTVIVFVESVFKLVAFARFRFFQDRWNQDLDAIVLLSIMGITLEEIEVNLSLPINPTI	1707
Db	1650	YIFTVIVFVESVFKLVAFARFRFFQDRWNQDLDAIVLLSIMGITLEEIEVNLSLPINPTI	1709
QY	1708	IRIMRVLRIRARVLKLLKMAVGNRALLHTVMQALPQVGNLGLLFFLFFIFIAALGVELFGD	1767
Db	1710	IRIMRVLRIRARVLKLLKMAVGNRALLHTVMQALPQVGNLGLLFFLFFIFIAALGVELFGD	1769
QY	1768	LECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKOPSRDCQESTCYNTVIS	1827
Db	1770	LECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKOTLRDCQESTCYNTVIS	1829

QY 1828 PIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAEAELELENMKTLSPOPHSPLG 1887  
Db 1830 PIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAEAELELENMKTLSPOPHSPLG 1889  
QY 1888 SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAAAGSLEHPTMTVPHEEVPVPLGPDLLTVR 1947  
Db 1890 SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAAAGSLEHPTMTVPHEEVPVPLGPDLLTVR 1949  
QY 1948 KSGVSRTHSLPNDSYMCRNGSTAERSLGHGWLGPKAQSGSILSVHSOPADTSCILQLPK 2007  
Db 1950 KSGVSRTHSLPNDSYMCRNGSTAERSLGHGWLGPKAQSGSILSVHSOPADTSCILQLPK 2009  
QY 2008 DVHYLLOPHGAPTGWAI PKLPPPGRSPLAQRPLRQAAIRTDSLVDQGLGSRREDLLSEVS 2067  
Db 2010 DVHYLLOPHGAPTGWAI PKLPPPGRSPLAQRPLRQAAIRTDSLVDQGLGSRREDLLSEVS 2069  
QY 2068 GPSCPLTRSSSFVGGSSIQVQORSGIOQKVKSHIRLPAPCPGLEPSWAKDPPETRSSLEL 2127  
Db 2070 GPSCPLTRSSSFVGGSSIQVQORSGIOQKVKSHIRLPAPCPGLEPSWAKDPPETRSSLEL 2129  
QY 2128 DTELSWISGDLPLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRHSHIAVSCLD SG 2187  
Db 2130 DTELSWISGDLPLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRHSHIAVSCLD SG 2189  
QY 2188 SQRLCPSPSSLGQPLGGPGSRPKKLSPPSISIDPPESQSGRPPCSPGVCLRRRAPAS 2247  
Db 2190 SQRLCPSPSSLGQPLGGPGSRPKKLSPPSISIDPPESQSGRPPCSPGVCLRRRAPAS 2249  
QY 2248 DSKDPSVSSPLDSTAASPSPKKDTLSLGLSSDPTDMDP 2286  
Db 2250 DSKDPSVSSPLDSTAASPSPKKDTLSLGLSSDPTDMDP 2288

RESULT 3

US-10-408-765A-625  
; Sequence 625, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 625  
; LENGTH: 2243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-625

Query Match 89.8%; Score 10806.5; DB 16; Length 2243;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;  
QY 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSCLRTVCNPPWFERVSML 121  
Db 30 GRPGGSAEKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSCLRTVCNPPWFERISML 89  
QY 122 VILLNCVTILGMRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKCYLG 181  
Db 90 VILLNCVTILGMRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKCYLG 149  
QY 182 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLLDITLP 241

Db 150 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLLDITLP 209  
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVLDLEPYQOTENEDESP 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVLDLEPYQOTENEDESP 269  
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCPSLDYETYNSSNTTCVNNQYYTNC SAGEHN 361  
Db 270 ICSQPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNNQYYTNC SAGEHN 329  
QY 362 PFKGAINFEDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFFMINL 421  
Db 330 PFKGAINFEDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQRLMREQVRFLSNASTLASFSEPGSCYBELLYLVYLKKAAR 481  
Db 390 CLVVIATQFSETKQRESQRLMREQVRFLSNASTLASFSEPGSCYBELLYLVYLKKAAR 449  
QY 482 RLAQVSRAIGVRACLLSSPVARSQEQPQSGSCTSRSHRRLSVHHLVHHHHHHHHYHLGN 541  
Db 450 RLAQVSRAAGVRVGLSSPAPLGGQEQPSSCSRSRRLSVHHLVHHHHHHHHYHLGN 509  
QY 542 GTLRVPRASPEIQORDDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601  
Db 510 GTLRVPRASPEIQORDDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 569  
QY 602 APPRCPSEASGRITVSGKVYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTFNIPPGPF 661  
Db 570 APPRCPSEASGRITVSGKVYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTFNIPPGPY 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721  
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689  
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
Db 690 SEAVYEFTQDAQHSDLRDPHS -RRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 748  
QY 782 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLVYGPFGYIKNPYN 841  
Db 749 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLVYGPFGYIKNPYN 808  
QY 842 IFDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATF 901  
Db 809 IFDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATF 868  
QY 902 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 961  
Db 869 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 928  
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATSESEPDFFSPSVD 1021  
Db 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATSESEPDFFSPSVD 988  
QY 1022 GDGRKKRLALVALGEHAELRKSLLPPLI IHTAATPM SHPKSSSTGVEALGSGSRRTSS 1081  
Db 989 GDGRKKCLALVSLGHEPBLRKSLLPPLI IHTAATPM SLPKSTSTGLGALGPASRRTSS 1048  
QY 1082 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141  
Db 1049 SGSAEPGAA -HEMKSPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1107  
QY 1142 LLSGEGQESQDEEESSEEDRAS PAGSDHRRHRSILEREAKSSFDLPDTLQVPLHRTASGR 1201  
Db 1108 LLSGEGQESQDEEESSEEDRAS PAGSDHRRHRSILEREAKSSFDLPDTLQVPLHRTASGR 1167  
QY 1202 SSASEHQDCNGKKSASGRRLARTLRTDDPOLDGDNDDEGNLSKGERIQAWVRSLPACCRE 1261  
Db 1168 GSASEHQDCNGKKSASGRRLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACCLE 1227  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPKIDPHSAERIFL 1321  
Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIFLNCITIAMERPKIDPHSAERIFL 1287





QY	422	CLVVIATQFSETKORESOLMRQVRFLSNASTILASFSEPGSCYEBELLKYLVIYLRKAAR	481	QY	1479	NFDNLGOALMSLFLVASKDQWVDIMYDGLDAVGVDQOQIMNHNPNWMLLYFISFLLIIVAFF	1538
Db	390	CLVVIATQFSETKORESOLMRQVRFLSNASTILASFSEPGSCYEBELLKYLVIYLRKAAR	449	Db	1468	NFDNLGOALMSLFLVASKDQWVDIMYDGLDAVGVDQOQIMNHNPNWMLLYFISFLLIIVAFF	1527
QY	482	RLAQVSRAGVRAGLLSSPVARSQOEPQPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN	541	QY	1539	VLANMFVGVVVENFHKCRQHOBEEEEARRRREKRLEKRR-----SKEQMAE	1587
Db	450	RLAQVSRAGVRAGLLSSPVARSQOEPQPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN	509	Db	1528	VLANMFVGVVVENFHKCRQHOBEEEEARRRREKRLEKRR-----SKEQMAE	1587
QY	542	GTLRVPASPEIQDRDANGSRRLMLPPPSTPTPSGPPRGAESVHSFYHADCHLEPVRQ	601	QY	1588	AOCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMAMEHYQQOILDEALKICN	1647
Db	510	GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRQ	569	Db	1588	AOCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMAMEHYQQOILDEALKICN	1647
QY	602	APPRCPSEASGRTVSGKVYPTVHTSPPPEILKDKALVEVAPSPGPTLTSTNIPPGPF	661	QY	1648	YIFTVIFVFEVFKLVAFARFFQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTI	1707
Db	570	APPRSPSEASGRTVSGKVYPTVHTSPPPETLKEKALVEVAASSGPTLTSLNIPPGPY	629	Db	1648	YIFTVIFVLESVFKLVAFGRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTI	1707
QY	662	SSMHKLETOSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD	721	QY	1708	IRIMRVLRIRARVLKLLKMAVGMREALLHTVMQALPOVGNLGLLFFLFFIFAALGVLEFGD	1767
Db	630	SSMHKLETOSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD	689	Db	1708	IRIMRVLRIRARVLKLLKMAVGMREALLDTVMQALPOVGNLGLLFFLFFIFAALGVLEFGD	1767
QY	722	SEAVYEFTQACHSDLRDPHSRRRQSLGPDAPESPVLAFWRLLICDTFRKIVDSKYFGRG	781	QY	1768	LECDETHPCGELGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPSCRDCQESTCYNTVIS	1827
Db	690	SEAVYEFTQACHSDLRDPHS-RRQRSLGPDAPESPVLAFWRLLICDTFRKIVDSKYFGRG	748	Db	1768	LECDETHPCGELGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCQESTCYNTVIS	1827
QY	782	IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN	841	QY	1828	PIYFVSFVLTQAQFVLNVNVIIVLVMKHEESNKEAKEEAELEAELEEMKTLSPQHSPLG	1887
Db	749	IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN	808	Db	1828	PIYFVSFVLTQAQFVLNVNVIIVLVMKHEESNKEAKEEAELEAELEEMKTLSPQHSPLG	1887
QY	842	IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDNVATF	901	QY	1888	SPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPT-----	1927
Db	809	IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDNVATF	868	Db	1888	SPFLWPGEVGNSTDSPKPGALHPAAHARSASHFSLHPTDRQLFDTISLLIQGSLEWEL	1947
QY	902	CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSILLWAIIVTVFQIILTQEDWNKV	961	QY	1928	-----	1927
Db	869	CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSILLWAIIVTVFQIILTQEDWNKV	928	Db	1948	KLMDELAGPGQPSAPPSAPSLGSGDPQIPLAEMEALSTSEIVSEPSCSLALTDDSLDP	2007
QY	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAE-----	1003	QY	1928	-----NVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEBSL	1974
Db	929	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEISKREDASGQLSCIQLP	988	Db	2008	DMHTLLLSALESNMQPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPL	2064
QY	1004	-----GDATKSESEPDFFPSVDGDRKKRLALVALGEHAELKSLLPPLIHTAATPM	1058	QY	1975	HRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLOPHGAPTWGAIPKLPPPGRSP	2034
Db	989	VDSQGGDANKSESEPDFFPSLDGDRKKLALVALVSLGEHPELKSLLPPLIHTAATPM	1048	Db	2065	HRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLOPHSAPTWTGTIPKLPPPGRSP	2124
QY	1059	SHPKSSSTGVGEALGSGRRRTSSSGSAEPGAHHEMKCPPSARSSPHSPWSAASSTSR	1118	QY	2035	LAQPLRRQAAIRTDSDLVQGLSREDLISEVSGPCPLTRSSFWGGSSIQVQQRSGIQ	2094
Db	1049	SLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA-HEMKSPPSARSSPHSPWSAASSTSR	1107	Db	2125	LAQPLRRQAAIRTDSDLVQGLSREDLLAEVSGSPPLARAYSFWGQSSTQAQQHRSRSH	2184
QY	1119	SSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEEESSEEDRASPAGSDHRRHRSLERE	1178	QY	2095	SKVSKHIRLPAPCPGLEPSWAKPPETRRSSLELDTLSWISGDL-PSQQEPLFPRDLK	2153
Db	1108	SSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEEESSEERASAPAGSDHRRHRSLERE	1167	Db	2185	SKLSKHTTPPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDLPPPGQEEPPSPRDLK	2244
QY	1179	AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARLTURTDLPQLDGDNDDE	1238	QY	2154	KCVSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPLRCPSPSSLGQPLGGGSRPKK	2213
Db	1168	AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKSASGRLARLARLPDDPPLDGDADDDE	1227	Db	2245	KCVSVEAQSCORRPTSWLDEQRRHSIAVSCLDGSGQPLHGTDPNLSGQPLGGGSRPKK	2304
QY	1239	GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHVVLVIF	1298	QY	2214	KLSPSISIDPPESQSGSRPPCPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKOTLS	2273
Db	1228	GNLSKGERVRAWIRARLPACCLERDSWSAYIFPPQSRFRLLCHRIITHKMFHVVLVIF	1287	Db	2305	KLSPSITIDPPESQSGPRTPPSPGICLRRRAPSSDSKDLASGPPDSMAASPSPKDVLS	2364
QY	1299	LNCITTIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCQGEQAYLRSSWN	1358	QY	2274	LSGLSDPTDMDP	2286
Db	1288	LNCITTIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCQGEQAYLRSSWN	1347	Db	2365	LSGLSDPADLDP	2377
QY	1359	VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRVISRAQGLKLVVETLMS	1418				
Db	1348	VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRVISRAQGLKLVVETLMS	1407				
QY	1419	SLKPIGNIWVICCAFFIIFGILGVQLFKGFFVCQGEDTRNITNKSDCAEASYRWRHKY	1478				
Db	1408	SLKPIGNIWVICCAFFIIFGILGVQLFKGFFVCQGEDTRNITNKSDCAEASYRWRHKY	1467				

RESULT 5  
US-10-408-765A-1128  
; Sequence 1128, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Boin D.  
; APPLICANT: Zhang, Bing

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; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1128

Query Match      51.7%; Score 6222; DB 16; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1370; Conservative 208; Mismatches 529; Indels 310; Gaps 62;

QY 25 PPGLRARGWTRRRMERAPRSDSP--VASRSSTTCGPGAGAGSTEKDPGSADSEAG 82
Db 19 PPGPAALVG-----ASPESGAPGREAGERGSELGVSPSEPAERGAELGA--DEEQR 69

QY 83 LPYPALAPWVFFYLSQDSRPRSWCLRTVCNPWFERSVLMVILLNCVTGLMFRPCEDIACD 142
Db 70 VPYPALAAATVFFCLGQTRPRSWCLRLVCNPFVHVSMLVIMLNCVTGLMFRPCEDVECG 129

QY 143 SQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLLDFFIVTAGMLEYSLD 202
Db 130 SERCNILEAFDAFIFAFFAVEMVVKMVALGLFGQKCYLGDTWNRLLDFFIVVAGMMEYSLD 189

QY 203 LQNVFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDLPMLGNVLLLCFFVFFIFGIVGV 262
Db 190 GHNVSLSAIRTVRVLRLRAINRVPSMRILVTLTLLDLPMLGNVLLLCFFVFFIFGIVGV 249

QY 263 QLWAGLLNRNRCFLPENFSLPSVD-LEPYQOTENEDSPFICSQPRENGMRSCRSVPTLR 321
Db 250 QLWAGLLNRNRCFLDSAFVRNNLTFLRPYYQTEEGEENPFICSSRRRDNMGKQCSHIP--- 306

QY 322 GEGGGPPCSLDYETYN-----SSNTTCVNWNQYNTNCSAGEHNPFKGAINFEDNIGY 374
Db 307 GRRELMPCTLGWEAYTQPAEGVGAARNACINWNQYNTNCRSGDSNPHNGAINFEDNIGY 366

QY 375 AWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETK 434
Db 367 AWIAIFQVITLEGWVDIMYVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETK 426

QY 435 QRESQLMREQVRFLSNASTLASFSEPGSCYEELLLKLVYLILRKAARRLAQVSRRAIGVRA 494
Db 427 QRESQLMREQVRARHLNSDSTLASFSEPGSCYEELLLKLVYGHIFRKVKRRSLRLYARWQSRW 486

QY 495 GLLSSPVARSQEQPQPSGSCSTRSHRR-----LSVHHLV-HHHHHHHHHYHLNGTILRV 546
Db 487 RKKVDPASVQGGQP-----GHRQRRAGRHTASVHHLVYHHHHHHHHYHFSHGSPRR 538

QY 547 PRASPEIQDRDANGSRRRLML--PPPTSTPSGGPPRGAEVSHSFYHADCHLE--PVRQQA 602
Db 539 PGPEPGACD-----TRLVRAGAPPSPSPGRGPP-DAESVHSIYHADCHIEGPQERARV 591

QY 603 PPRPCPSEASGR-TVSGKV-YPTV-----HTSPPEILKOKALVEVAPSP----- 646
Db 592 AHAATAAASRLATGLGTMYNPTILPSGVGSGKSTSPGPK-----GKWAGPPPGTG 644

QY 647 --GPPTLTSPNIPPGPFSSMHKLLLEQTQSTGAC--HSS-----CKISSPCS KADSGACGPD 697
Db 645 GHGPLSLNS-----PDPYEKIPIHVVEGHLGQAPGHLGSLSVPCPLPSP--PAGTLTCELK 698

QY 698 SCPYCART-GAGEPEASADHVPDSDSEAVYEFTQDAQHSDLRDP----- 740
Db 699 SCPYCTRALEDPEGELSGSESGSDGRGVYEFTQDVHRGDRWDPTRPPRATDTPGPGPGS 758
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QY 741 HRRRQRS LGPD AEPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQ 800
Db 759 PQRRAQRAAP-GEPGWMGRLLWVTFSGKLRRIVDSKYFSRGIMAILVNTLSMGVEYHEQ 817
QY 801 PEELTNALEISNIVFTSLFALEMLLKLIVYGPGFYKPNYPINFDGVIVVISWEIVGQOG 860
Db 818 PEELTNALEISNIVFTSMFALEMLLKLACGPLGLYRNYPINFDGIIVVISWEIVGQAD 877
QY 861 GGLSVLRTFRLMRVLKLVRELPALQRLVLMKTMNDVATFCMLLMLFIFIFISILGMHLF 920
Db 878 GGLSVLRTFRLRLVLKLVRELPALRRQLVVLVKTMDNVATFCTLLMLFIFIFISILGMHLF 937
QY 921 GCKFASERD-GDTLPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIA 979
Db 938 GCKFSLKTDGTVPDRKNFDSLLWAIIVTVFQILTQEDWNVVLVNGMASTSSWAALYFVA 997
QY 980 LMTFGNYVLNLLVAILVEGQAEGDATKSESEPDFSPSPVDGDRKRLALVAL---- 1035
Db 998 LMTFGNYVLNLLVAILVEGQAEGDANRSDTDEKTSVHFEEDFKLRELQTELKMC 1057
QY 1036 -----GEHAELRKSLPLLIHTAATPM SHPKSS-TGVGEALGSGSRRTSSSGSABPGA 1089
Db 1058 LAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGSSSGSDPPLG- 1116
QY 1090 AHHEMKCPPSARSSPHSPWSAASSWTSSRSSRNSLGRAPSLKRRSPSGERRSLLSGEQE 1149
Db 1117 ---DQKPPASLRSSPCAPWPGSGAWSSRRSSWSLGRAPSLKRRGQCGERESLLSGEGKG 1173
QY 1150 SQDEESSEEDRASPA--GSDHRHRGSLEREAKSSFDLPDTL-----QVPLGH-----R 1196
Db 1174 STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDQGVVALPSDFFLR 1231
QY 1197 TAGRSSASEHQDCNGKSASGRLARLTRTDDPQLDGGDDNDENGLSKGERIQAWVRSLP 1256
Db 1232 IDSHREDAAEELDDSEDSCLRLHKVLEPKPQ-----W----- 1265
QY 1257 ACCRERDSWSAYIFPPQSRERLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSA 1316
Db 1266 --CRSREAWALYLFSPQNRFRVSCQKVITHKMFHDHVLVIFLNCVTIALERPDIDPGST 1323
QY 1317 ERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEGQAYLRSSWNVLGLLVLISVIDILVSM 1376
Db 1324 ERVFLSVSNYIFTAIFVAENMVKVVALGSLGSEHAVALQSSWNLLDGLLVLSLVDIVVAM 1383
QY 1377 VSDSGTKILGMLRVLRLRLRLPLRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFII 1436
Db 1384 ASAGGAKILGVLRLRLRLRLPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFII 1443
QY 1437 FGILGVQLFKGKFFVCOGEDTRNITNKS DCAEASVRWRHKYNFDNLGOALMSLFLVASK 1496
Db 1444 FGILGVQLFKGKYCEGPDTRNISTKAQCAAHYWRVRKYNFDNLGOALMSLFLVSSK 1503
QY 1497 DGWVDIMYDGLDVGVDQOPQNHNPWMLLYFISFLIIVAFFVLNMFVGVVVENPHKCRQ 1556
Db 1504 DGWVNIMYDGLDVGVDQOPQNHNPWMLLYFISFLIIVSFFVLNMFVGVVVENPHKCRQ 1563
QY 1557 HQEEERARRREKRLRLREKRRSKEKQMAEAQCKPYYSYDYSRFRLLVHHLCTSHYLDLF 1616
Db 1564 HQAEERARRREKRLRLRERRRSTFPS-PEAQRPPYADYSPTRRSIHSLCTSHYLDLF 1622
QY 1617 ITGVIGLVNVTMAMEHYQQQILDDEALKICNYIFTVIFVESVFKLVAFARFRFPQDRWN 1676
Db 1623 ITFIICVNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVEAALKLVAFGRFRFPQDRWN 1682
QY 1677 QLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVRIARVLKLLKMAVGMRLHLTV 1736
Db 1683 QLDLAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVRIARVLKLLKMATGMRLALDVT 1742
QY 1737 MQALPQVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLF 1796
Db 1743 VQALPQVGNLGLLFLMLFFIYAALGVLELFGRLCESDNPCEGLSRHATFSNFGMAFLTLF 1802
QY 1797 RVSTGDNWNGIMKDP SRDC---DQESTCYNTVISPIYFVSFVLTAQFVLNVNVIAMK 1853
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Db 1803 RVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPVYFVTFVLVAQFVLNVVVAVLMKH 1862  
QY 1854 LEESKEAKEAEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTA 1913  
Db 1863 LEESKEAREDAELDAEIELEMA-----QGPSARRVDADRP----- 1899  
QY 1914 HIGASGFSLEHPTMTVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--- 1970  
Db 1900 -----PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVASAP 1943  
QY 1971 -----ERSLHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVH-----YLLQP 2015  
Db 1944 HRPPLQEVEMETYAGTP---LGSVASVHSPPAESCASLQIPLAVSSPARSGEPLHALSP 2000  
QY 2016 HGAPTWGAIPKLP PPPGRSPLAQRPRLRQAAIRTDSDLVQGLGSRDILLSEV-----SGPSC 2071  
Db 2001 RGT-----ARSPSLRLLCRQEAHVHTDSLEGK-IDSPRDTLDPAPGPKTPVR 2047  
QY 2072 PLTRSSSPWGGSSIQVQQRSGIQSKV--SKH-----IRLPAPCPGLEPSWAKDPPETRS 2123  
Db 2048 PVTQ-----GSLQSPRSPRPAASVTRKHTFGQHCVSRRPAPPGGEEABASDP----- 2096  
QY 2124 SLELDTLSWISGDLPLP--SSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDE 2173  
Db 2097 ---ADEEVSHITSSACPWQPTAEPHGPEASPVAGGERDLRLYSVDAQGLDKPG-RADE 2152  
QY 2174 QRRHSIAVCLDSGSPRLCPSPSLGGQPLGGP--GSRPKKLSPPSISIDPP-ESQGS 2230  
Db 2153 QWRPSAE---LGSGE-----PGEAKAWG-PEAEPALGARRKKMSPPCISVEPPAEDEGS 2203  
QY 2231 -RPPCSPG--VCLRRRAPA-----SDSKDPSVSSPLDSTAAS-----PSPKKOTLSL 2274  
Db 2204 ARPSAAEGGSTTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGOASCRAEHLTV 2263  
QY 2275 SGLSSDPTDM-----DP 2286  
Db 2264 PSFAFEPLDLGVPSGDP 2280

RESULT 6

US-10-930-301-52  
; Sequence 52, Application US/10930301  
; Publication No. US20050026207A1  
; GENERAL INFORMATION:  
; APPLICANT: Issa, Jean-Pierre  
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: JHU1590  
; CURRENT APPLICATION NUMBER: US/10/930,301  
; CURRENT FILING DATE: 2004-08-30  
; PRIOR APPLICATION NUMBER: US/09/398,522  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 1207  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel  
US-10-930-301-52

Query Match 48.8%; Score 5872; DB 17; Length 1207;  
Best Local Similarity 95.2%; Pred. No. 0;  
Matches 1123; Conservative 11; Mismatches 44; Indels 2; Gaps 2;  
QY 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFWRVSML 121  
Db 30 GRPFGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFWRVSML 89  
QY 122 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 181

Db 90 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 149  
QY 182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRLRAINRVPSMRILVTLTLLDTP 241  
Db 150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRLRAINRVPSMRILVTLTLLDTP 209  
QY 242 MLGNVLLLCFFVFFIFGIVGVQWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDESPF 301  
Db 210 MLGNVLLLCFFVFFIFGIVGVQWAGLLRNRCFLPENFSLPLSVDLERYQTENEDESPF 269  
QY 302 ICSQPRENGMRSRCSVPTLRGEGGGPPPCSLDYETYNSSNTTCVWNQYTYNCSAGEHN 361  
Db 270 ICSQPRENGMRSRCSVPTLRGEGGGPPPCGLDYEAYNSSNTTCVWNQYTYNCSAGEHN 329  
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421  
Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 389  
QY 422 CLVVIATQFSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 481  
Db 390 CLVVIATQFSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 449  
QY 482 RLAQVSRRAIGVRAAGVRLSSPVARSGQEPQPSGCTSRSHRRLSVHHLVHHHHHHHHVHLGN 541  
Db 450 RLAQVSRRAIGVRAAGVRLSSPVARSGQEPQPSGCTSRSHRRLSVHHLVHHHHHHHHVHLGN 509  
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601  
Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 569  
QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTFNIPGPF 661  
Db 570 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTFNIPGPF 629  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACPDSCPCYARTGAGEPESADHVMPDSD 721  
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACPDSCPCYARTGAGEPESADHVMPDSD 689  
QY 722 SEAVVEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
Db 690 SEAVVEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 748  
QY 782 IMTAILVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 841  
Db 749 IMTAILVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 808  
QY 842 IFDGVIVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATF 901  
Db 809 IFDGVIVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATF 868  
QY 902 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 961  
Db 869 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 928  
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVD 1021  
Db 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVD 988  
QY 1022 GDGRKKRLALVALGEHAEIRKSLPLPIIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1081  
Db 989 GDGRKKRLALVALGEHAEIRKSLPLPIIHTAATPMHSPKSSSTGVGEALGSGSRRTSS 1048  
QY 1082 SGSAEPGAAHEMKCPPSARSSPHSPWASAASWTSSRNLSGRAPSLKRRSPSGERRS 1141  
Db 1049 SGSAEPGAAHEMKCPPSARSSPHSPWASAASWTSSRNLSGRAPSLKRRSPSGERRS 1107  
QY 1142 LLSGEGQESQDEEESSEEDRASPGSDHRRHRSLEAKSSFDLPDQLVPGHLHTASGR 1201  
Db 1108 LLSGEGQESQDEEESSEEDRASPGSDHRRHRSLEAKSSFDLPDQLVPGHLHTASGR 1167  
QY 1202 SSASEHQDCNGKXSASRLARTLRTDDPQLDGDDEGNDENGL 1241  
Db 1168 GSASEHQDCNGKXSASRLARTLRTDDPQLDGDDEGNDENGL 1207





Db 1572 ALLDTVVQALPOVGNLGLLPMLLFFIYAALGVLFGLKVCNDENPCEGMSRHATFENFGM 1631  
QY 1791 AFLTLFRVSTGDNWNGIMKDPSPRDC-DQESTCYNV--ISPIYFVSFVLTAQFVLNVVVI 1847  
Db 1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHDSRSCSLQFVSPLYFVSFVLTAQFVLINVVV 1691  
QY 1848 AVLKMLEESNKEAKEAELEAELELEM-KTLSQPHSPGLSPFLWPG-----1894  
Db 1692 AVLKMLHDDSNKEAQEDAEMDAELELEMAHGLGPGRLPTGSPGA-PGRGPGGAGGGDT 1750  
QY 1895 -----VEG-VNSTDSPKPGAPHHTTAHGAASG-----1920  
Db 1751 EGGLECRRCYSPAQDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHHDKQEVQLAETEA 1807  
QY 1921 -----FSLEHPTMVP-----HPEEVV-PLGPDLLTVRKSGVS 1952  
Db 1808 FSLNSDRSSILLGDDLSLEDPTACPPGRKOSKGLDPPPEPMRVGDLGECFFPLSSTAVS 1867  
QY 1953 RTHSLPN-DSYMCNRNGSTAERSILGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHY 2011  
Db 1868 -----PDENFLCEMEEIPFNPV--RSW--LKHDSSQAPSPSPDASSPLLPMPAEFFH 1918  
QY 2012 -----LLQPHGAPTGAIPKLPPPG-----RSLAQRLRQAAIRTDSDLVQGLGSRE 2060  
Db 1919 PAVSASQKPEKGTGTGLPKIALQGSWASLRSPRVNCTLLRQATGSDTSILDAS-----1972  
QY 2061 DLLSEVSGPSCPLTRSSSFWGGSSIQVQORSIGIQSVSKHIRLPAPCPGLEPSPWAKDPPE 2120  
Db 1973 -----PSSAGSLQTTLEDSDLTSDSPRALGPPAPAG-----2006  
QY 2121 TRSSELDTELWSIGDLLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIA 2180  
Db 2007 -----PRAGLSPAARRL-----SLRGRGLFSLRGLRAHQRS 2038  
QY 2181 VSCLDSGSPQLCPSPSSL-----GGQPLGGPGRPKKLSPPSIS----IDPPESQG 2229  
Db 2039 HS--SGGSTSPGCTHHDSMDPSDEGRGGAGGGAGSEHSETLSLSLTSLECPPP-----2092  
QY 2230 SRPPCSPGVCLRR-----RAP---ASDSKDPVSVSSPLDSTA 2262  
Db 2093 --PPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKODPPGRAPLPMGL 2150  
QY 2263 ASPSPKDTLSLSGLSSDPTDMDP 2286  
Db 2151 GPLAPPPQPL-----PGELEP 2166

RESULT 8  
US-10-425-800-2  
; Sequence 2, Application US/10425800  
; Publication No. US20030180886A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/10/425,800  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US/09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2175  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-425-800-2

Query Match 45.0%; Score 5409; DB 14; Length 2175;  
Best Local Similarity 50.5%; Pred. No. 0;  
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

QY 51 ASRSSTTCPGGAAGAGSTKDPG--SADSEAGL-----PYPALAPVVFVLS 97  
Db 5 ASPSSSSAAP-AAEPGVTTTEQGPSPSPSPSGLEELDGADPHVPHDLPAPAFCLR 63  
QY 98 QDSRPRSCLRTVCNPNWFERVSMVLVILLNCVTLGMFRPCEDIAQDSQRCRILQAFDDFIF 157  
Db 64 QTTSRPNWCIMVCNPNWFECVSMVLVILLNCVTLGMYQPCDDMDCLSDRCKILQVFFDFIF 123  
QY 158 AFFAVEMVVMVALGIFGKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVL 217  
Db 124 IFFAMEMVLKVALGIFGKCYLGDTWNRLDFFIVMAGMVEYSLDLQNLNSAIRTVRVL 183  
QY 218 RPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCLPE 277  
Db 184 RPLKAINRVPSMRILVNLTLTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCLPE 243  
QY 278 NFSPLSVLDLEPYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL-----332  
Db 244 NFTIQGDVALPYQPEEDEMPPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300  
QY 333 -DYETYNSSNTT--CVNWOYITNCAGEHNPFKGAINFNDITGYAWIAIFQVITLEGWV 389  
Db 301 YDFGAGRQDLNASGLCVNWNRYNVCRTGSANPHKGAINFNDITGYAWIVIFQVITLEGWV 360  
QY 390 DIMYFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQRLMREQVRFL 449  
Db 361 EIMYYVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYL 420  
QY 450 SNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAIGVRAGLLSPPVARSQEPQ 509  
Db 421 S-SSTVASYAEPGDCYBEIFQYVCHILRAKR-----RALGLYQALQS-----462  
QY 510 PSGSCTRSHRRLSVHHLVHHHHHHHHVHLNGTLRVPRASPEIQDRDANGSRRLMLPPP 569  
Db 463 -----RRQAL-----GPE-----APAP 474  
QY 570 STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRVSGKVYPTVHTSP 629  
Db 475 AKPGP-----HAK---EPRHYQLCPQHSPLDA-----TPHT--502  
QY 630 PBEILKDKALVEVAPSPGPTLTSTFNIPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK 688  
Db 503 -----LVQ-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGS 534  
QY 689 ADGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVVEFTQDAQHSDLRDPHSRRRQRS 748  
Db 535 TDSQEGSGS-----GSSAGGEDEA-----DGDGA---RSSEDGASSELGKEEEEEQ--579  
QY 749 LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTN 806  
Db 580 ----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRMIMAILVNTVSMGIEHHEQPEELTN 635  
QY 807 ALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIVIVISWEIVCQGGGLSVL 866  
Db 636 ILEICNVVFTSMFALEMILKLAAGFLFDYLRNPYINFDISIIVISWEIVCQADGGLSVL 695  
QY 867 RTERLMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKPAS 926  
Db 696 RTERLLRVLKLVRFMPALRRQLVLMKTMNDNVATFCMLLMFLFIFISILGMHIFGCKFSL 755  
QY 927 ERD-GDTLPDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAAFYFIALMTFGN 985  
Db 756 RTDTGDTVPDRKNFDSLWAIWTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGN 815  
QY 986 YVLFNLLVAILVEGFAEGDATKSESEPDFFSPSV-----DGDGRKKRLALVAL 1035  
Db 816 YVLFNLLVAILVEGFAEGDANRSYDEQSSNIEHFDKLEGLDSSGDPK--LCPIM 873  
QY 1036 GEHAELRKSLLPPLIHT---AATPMSHPKSSSTGVGEALGSGRRRTSSSGSAEPGAH 1091  
Db 874 TPNGLHLDPSL--PLGGHLGPAGAAGPA--PRLSLQDPMLVALGSRKSSVMSL---GRMS 926  
QY 1092 HEMKCPFSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE-QGES 1150

Db 927 YDQSLSSRSYYGPGWGRSAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGA 980  
QY 1151 QDEEESSEE--DRASPAGSDH-----RHRGSLEREAKSSFDLPTLQVPG 1193  
Db 981 RVCEVADEGPPRAAPLHTPHAHHHGPHLAHRHRHRTLSLDRSDSVDLAELVPAVG 1040  
QY 1194 LHRTASGRSS--ASEHQDCNGKASGRRLARTLRTD-DPQLDGGDDNDEGNLSKGERIQAW 1250  
Db 1041 AHPRAAWRAAGPAPGHEDCNGRMPs--IAKDVFTKMGDRGRGEDEEIDYTLCFRVRKM 1098  
QY 1251 VRSRLPACRERDSWSAYIIFPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERP 1310  
Db 1099 IDVKPDWCEVREDWSVLFSPENRFRVLCQTIIAHKLPDYVVLAFIFLNCITIALERPQ 1158  
QY 1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKWALGWCFCGQAYLRSSWNVLGGLVLSVI 1370  
Db 1159 IEAGSTERIFLTVSNYIFTAIFGEMTLKVVSLGLYFGQAYLRSSWNVLGGLVFSVII 1218  
QY 1371 DILVMSVSDSGTKILGMLRVLLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVIC 1430  
Db 1219 DIVVSLASAGGAKILGVLRLTLRLPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278  
QY 1431 CAFFIIFGILGVQLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFNLGQALMSL 1490  
Db 1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRWVHKYNFNLGQALMSL 1338  
QY 1491 FVLASKDGWVDIMYDGLDAVGVDQOPIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVEN 1550  
Db 1339 FVLASKDGWVIMYNGLDVAVDQOPVTNHNPMWLLYFISFLLIIVSFFVLNMFVGVVEN 1398  
QY 1551 FHKCRHOBEERREKRLRLLEKRRSKEKQMAEACQKPYSDYSRFRLLVHHLCTS 1610  
Db 1399 FHKCRHQEAEERREKRLRLLEKRR-----KAQRLPYATYCHTRLLIHSMTCS 1451  
QY 1611 HYLDLFTIGVIGLNVVTMAMEHYQQOQILDEALKICNYIFTVIFVFESVEFKLVAFARFR 1670  
Db 1452 HYLDLFTIFILCLNVVTMSLEHYNQPTSLETALKYCNMTFTVFVLEAVLKLVAFLRLR 1511  
QY 1671 FQDRWNQDLALIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMR 1730  
Db 1512 FKDRWNQDLALIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIRARVLKLLKMATGMR 1571  
QY 1731 ALLHTVMQALPQVGNLGLLMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGM 1790  
Db 1572 ALLDTVVQALPQVGNLGLLMLFFIYAALGVLEFGKLVNDENPCCEGMSRHATFENFGM 1631  
QY 1791 AFLTLFRVSTGDNWNGIMKDPKSDC-DQESTCYNTV--ISPIYFVSFVLTAQFVLNVWVI 1847  
Db 1632 AFLTLFQVSTGDNWNGIMKDTLRDCTHRSCLSSQLQVSPLYFVSFVLTAQFVLNVVV 1691  
QY 1848 AVLMKHLEESNKEAEAELEAELEEM-KTLLSPQHSPLGSPFLWPG-----1894  
Db 1692 AVLMKHLDDSNKEAQEDAEMDAELEMAHGLPGPRLPTGSPGA-PGRGPGGAGGGGDT 1750  
QY 1895 -----VEG-VNSTDSPKPGAPHTTAHIGAASG-----1920  
Db 1751 EGGLECRRCYSPAQDSLEGELTIIDNLSGSIH---HYSSPAGCKKCHHDKQEVQLAETEA 1807  
QY 1921 -----FSLEHPTMVP-----HPEEVPV-PLGPDLLTVRKSGVS 1952  
Db 1808 FSLNSDRSSSILGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGECFPPLSSTAVS 1867  
QY 1953 RTHSLPN-DSYMCNRNGSTAERSILGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHY 2011  
Db 1868 -----PDENFLCEMEEIPFPNV--RSW--LKHDSSQAAPPSPFSPDASSPLPMPAEFFH 1918  
QY 2012 -----LLQPHGAPTWGAIPKLPFPG-----RSPLAQPLRRQAAIRTDSDLVQGLSRE 2060  
Db 1919 PAVSASQKPEKGTGTGLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS-----1972  
QY 2061 DLLSEVSGPSCPLTRSSSFWGSSSIQVQORSIGIQSKVSKHIRLPAPCPGLEPSWAKDPPE 2120

Db 1973 -----PSSAGSLQTTLEDLSLSDSPRRALPPAPAG-----2006  
QY 2121 TRSSLELDTELSWISGDLPLPSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRHSIA 2180  
Db 2007 -----PRAGLSPAARRRL-----SLRGRGLFSLRGLRAHQRS 2038  
QY 2181 VSCLDGSGQPRLCPSPSL-----GGQPLGGPGSRPKKLSPPSIS---IDPPESQG 2229  
Db 2039 HS--SGGSTSPGCTTHDSMDPSDEEGRGGAGGGAGGSEHSETLSLSLTSLFCPPP---2092  
QY 2230 SRPPCSPGVCLRR-----RAP---ASDSKDPVSVSSPLDSTA 2262  
Db 2093 --PPAPGLTPARKFSSSTSLAAPGRPHAAALAHGLARSPSWAADRSKDPGGRAPLPMGL 2150  
QY 2263 ASPSPKDOTLSLSGLSSDPTMDP 2286  
Db 2151 GPLAPPQPL-----PGELEP 2166  
RESULT 9  
US-09-935-541-4  
; Sequence 4, Application US/09935541  
; Patent No. US20020150911A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/935,541  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-541-4  
Query Match 44.9%; Score 5405.5; DB 9; Length 2188;  
Best Local Similarity 50.3%; Pred. No. 0;  
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;  
QY 51 ASRSSTTCPGGAAGAGSTEKDPG--SADSEAEGL-----PYPALAPVVFYLS 97  
Db 5 ASPSSSAAAP-AAEPGVTEQPGPRSPSSPPGLEPLDGADPHVPHDLAPIAFFCLR 63  
QY 98 QDSRPSRWCLRTVCNPNWFERVSMVLVLLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIF 157  
Db 64 QTTSPRNWCIKWCNPNWFECVSMVLVLLNCVTLGMVQPCDDMDCLSDRCKILQVDDFIF 123  
QY 158 AFFAVEMVVMVALGIFGKKCYLGDTWNRDLDFIIVAGMLEYSLDLQNVFSFAVTVRVL 217  
Db 124 IFFAMEMVLKMVALGIFGKKCYLGDTWNRDLDFIIVAGMVEYSLDLQNLINLSAIRTVRVL 183  
QY 218 RPLRAINRVPSMRILVTLDDTLPLMLGNVLLLCFFVFFIFIGIVGVQLWAGLLNRNRCFLPE 277  
Db 184 RPLKAINRVPSMRILVNLDDTLPLMLGNVLLLCFFVFFIFIGIIGVQLWAGLLNRNRCFLEE 243  
QY 278 NFSPLSVLDLEPPYYQTENEDESPFFICSPRENGMRSCRSVPTLRGEGGGPPCSL-----332  
Db 244 NFTTQGDVALPPYYQPEEDEMPPFICSLSGDNGIMGCHIEPPLKEQ---GRECLSKDDV 300  
QY 333 -DYETYNSSSNTT--CVNWNQYVTCNSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWV 389  
Db 301 YDFGAGRQDLNASGLCVNWNRYNVCRTGSANPHKGAINFNDNIGYAWIVIFQVITLEGWV 360  
QY 390 DIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFL 449  
Db 361 EIMYVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYL 420

Qy	450	SNASTLASFSEPGSCYEELLKYLVLILRKAARLAQVSRRAIGVRAGLSSPVARSQEPQ	509
Db	421	S-SSTVASYAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQALQS-----	462
Qy	510	PGSCTRSHRRRLSVHHLVHHHHHHHHYHLGNGTLRVPRAPEIQDRDANGSRRRLMLPPP	569
Db	463	-----RRQAL-----GPE-----APAP	474
Qy	570	STPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPRCPSEASGRVTGSGKVYPTVHTSP	629
Db	475	AKPGP-----HAK-----EPRHYQLCPQHSPLDA-----TPHT--	502
Qy	630	PPEILKDKALVEVAPSPGPPTLTFSNIPPGPFSSMHKLLTQSTGAC-HSSCKISSPCSK	688
Db	503	-----LVQ-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGS	534
Qy	689	ADSGACGPDSCPYCARTGAGEPESADHVMPPDSDEAVYEFTQDAQHSDLRDPHSRRRQRS	748
Db	535	TDSGQEGSGS---GSSAGGEDEA---DGDGA---RSSEGDGASSELGKEEEEEQ--	579
Qy	749	LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFCRGIMIAILVNTLSMGIEYHEQPEELTN	806
Db	580	----ADGAVMLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN	635
Qy	807	ALEISNIVFTSLPALEMLLKLVLVYGPFGYIKNPYNI FDGVIIVISVWEIVGQGGGLSVL	866
Db	636	ILEICNVVFTSMFALEMILKLAAGFLFDYLRNPYNIFDSIIIVISWEIVGADGGLSVL	695
Qy	867	RTFRLMRVLKLVRFPLPALQRLVLMKTMNDNVATFCMLLMFLIFIFSILGMHLFGCKFAS	926
Db	696	RTFRLRLVLKLVRFMPALRRQLVLMKTMNDNVATFCMLLMFLIFIFSILGMHIFGCKFSL	755
Qy	927	ERD-GDTLPDRKNPDSLLWAIIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGN	985
Db	756	RTDGTGTVPDRKNPDSLLWAIIVTVFQILTOEDWNKVLYNGMASTSPWASLYFEVALMTFGN	815
Qy	986	YVLFNLLVAILVEGFAEGDATKSESEPFFPSV-----DGDGDRKKRLALVAL	1035
Db	816	YVLFNLLVAILVEGFAEGDANRSYDEQSSNIEEFDKLQEGLDSSGDPK--LCPIPM	873
Qy	1036	GEHAELKSLPLPIIHT---AATPM SHPKSSSTGVGEALGSGRRRTSSSGSAEPGAH	1091
Db	874	TPNGHLDPSL--PLGGHLGPAGAAGPA--PRLSLPQDPMVLVALGSRKSSVMSL---GRMS	926
Qy	1092	HEMKCPPSARSSPHSPWSAASWTSSRRSRNSLGRAPSLKRRSPSGERRSLLSGE-QGES	1150
Db	927	YDQRSLSRRSSYYGPWGRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGA	980
Qy	1151	QDEEESSEE--DRASPAGSDH-----RHRGSLEREAKSSFDLPDTLOVPG	1193
Db	981	RVCEVAADEGPPRAAPLHTPHAHIIHHGPHLAHRHRHRRHTLSLDRDSVDLAELVPAGV	1040
Qy	1194	LHRTASGRSS--ASEHQDNGKKSASGRLARLTRD-DPQLDGDNDDEGNLSKGERIQAW	1250
Db	1041	AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEIDYTLCFRVRKM	1098
Qy	1251	VRSLRPACCRERDSWSAXIFPPQSRFRLLCHRIITHKMPDHVVVLVIFIPLNCITIAMERP	1310
Db	1099	IDVYKPDWCVEWDSVLPSPENRFRVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQ	1158
Qy	1311	IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCQAYLRSSWNVLDDLVLISVI	1370
Db	1159	IEAGSTERIFLTVSNYIFTAIFVGEMTLKVSLGLYFGQAYLRSSWNVLDFLVPVSI	1218
Qy	1371	DILVSMVSDSGTKILGMLRLVRLRLTLRPLRVLISRAOGLKLVVETLMSLKPIGNIVVIC	1430
Db	1219	DIVVSLASAGGAKILGLVRLVRLRLTLRPLRVLISRAPGLKLVVETLISLKPIGNIVLIC	1278
Qy	1431	CAFFIIFGILGVQLFKGKFFVCOGEDTRNITNKSDCAEASRYRVRHKYNFDNLGQALMSL	1490
Db	1279	CAFFIIFGILGVQLFKGKFFHCLGVDTNRNITNRSDCMAANYRVRVHKKYNFDNLGQALMSL	1338
Qy	1491	FVLASKDGVWDIMYDGLDAVGVDQQPIMNHNPWMLLYFTISFLIIVAFFVLMMFVGVVVEN	1550

Db	1339	FVLASKDGNWIMYNGLD	DAVADQPVTNHNPWMLLYFISFLLI	VSFFVLNMFVG	VWVEN	1398		
Qy	1551	FKHCKHQHEEEARRR	EKKRLRLEKKRRSKEKQMAEAQCKPYSDY	SRFRLLVHHL	CTS	1610		
Db	1399	FKHCKHQHEAEEARRR	EKKRLRLEKKRR-----KAQRLPYATY	CHTRLLIHS	MCTS	1451		
Qy	1611	HYLDLFTIGVIGLNV	VTNAMEHYQQPILDEALKICNIYFTVTFV	FESVFKLVAF	ARRF	1670		
Db	1452	HYLDLFTITII	CLNVVMSLEHYNQPTSLETALKYCNYMFTT	VFVLEAVKLVA	FGLRRF	1511		
Qy	1671	FQDRWNQDLAIVLLS	IMGITLEEIEVNL	SLPINPTIIRIMRVLR	IAVLKLLKMAV	GMR	1730	
Db	1512	FKDRWNQDLAIVLLS	VMGITLEEIEINAALPINPTIIRIMRVLR	IAVLKLLKMA	TGMR	1571		
Qy	1731	ALLHTVMQALPQVGN	LGLLFMLFFIFAALGV	VELFGDLECDETHPCEGLGR	HATFRNFGM	1790		
Db	1572	ALLDTVVQALPQVGN	LGLLFMLFFIYAALGV	VELFGKLV	CNDENPCBGM	SRHATFENFGM	1631	
Qy	1791	AFLTFLFRVSTGDN	WNGIMKDP	SRDC-DOESTCYNTV--ISPIYFVS	FVLTAQFVL	VNVVI	1847	
Db	1632	AFLTFLFQVSTGDN	WNGIMKDTLRDCTH	DRSCLSSLOQFVSPLYFVS	FVLTAQFVL	INVVV	1691	
Qy	1848	AVLMKHLEESKEAE	EALEALEM-KTLPSPQHS	PLGSP-----		1889		
Db	1692	AVLMKHLLDSNKEA	QEDAEMDAELEMAHGLGPGPRLPTGSPG	AGRPGGAGGG	GDTE	1751		
Qy	1890	-----FLW-----	PGVEG-VNSTDSPKPGAPHTTAHIGA	AASG-----		1920		
Db	1752	GGLCRRCYSPAQEN	WLDSVSLIIKDSLEGELTIIDNL	SGSIFH---HYSSPAGCK	KCHH	1808		
Qy	1921	-----	FSLEHPTMVP-----	HPEEVPV-PLG		1940		
Db	1809	DKQEVQLAETEA	PSLNSDRSSILLGDDLSLEDPTACPPGR	KDKSGELDEPEP	MVGDLG	1868		
Qy	1941	PDLLTVRKSGVSR	THSLPN-DSYMCN	RGSTAERSLGHRCWGLPKAQSGS	ILSVHSQ	PADT	1999	
Db	1869	ECFFPLS	TAVS-----PDPENFLCEMEIEI	PFNPV--RSW--LKHDSSQ	APPSPF	PDAS	1919	
Qy	2000	SCILQLPKDVHY	-----LLQPHGAP	TWGAIPKLP	PPPG-----RSPLAQRLRR	QAAIRT	2048	
Db	1920	SPLLMPAEFFH	PAVSASQKPEKGTGTGLPKIALQGS	WASLRSPRVNCTLLR	QATGSD		1979	
Qy	2049	DSLVDQGLSRED	LLSEVSGP	CLTRSSSFWGGSSIQVQORS	GIOQKVS	KHIRLPAPCP	2108	
Db	1980	TSLDAS	-----PSSSAGSLQTTLED	SLTSDSPRRALG	PPAPAP		2018	
Qy	2109	GLEPSWAKOPP	ETRSSL	ELDTLSWISGDL	LLPSSQEEPLFPRDLK	KCYSVETQ	CSRRRPG	2168
Db	2019	G-----	-----PRAGLS	PAARRRL-----SLR	GRGL		2039	
Qy	2169	FWLDEQRRHS	IAVSLD	SGSQPRLCPSP	SSL-----GGQPLGGP	SGSRPKKL	SPSI	2220
Db	2040	FSLRGLRAHQ	RSHS--SGGSTSPGCTH	HDSDMPDSDEGRG	GAGGGAGSEH	SETLS	LSL	2097
Qy	2221	S---	IDPPESQGS	RRPCCPGVCLRR-----	-----RAP---	ASDSK	2250	
Db	2098	TSLFCPPP	-----PPFAPGLT	PARKFSS	TSSLAAPGRPHAAALAHGLARS	SPSWA	DRSK	2151
Qy	2251	DPSVSSPLD	STAASPSK	DTLSLGLSSD	PDTMDP	2286		
Db	2152	DPPGRAPL	PMGLP	APPQPL-----	PGELEP	2179		

RESULT 10  
US-10-425-800-4  
; Sequence 4, Application US/10425800  
; Publication No. US20030180886A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES



[illegible]



Db 1752 GGLCRCYSPAQENLWDSVSLIIKDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCH 1808  
QY 1921 -----FSLHPTWVP-----HPEVPV-PLG 1940  
Db 1809 DKQEVQLAETEAFLNSDRSSILLGDDLSLEDTACPPGRKDKSGELDPPEMRVGD LG 1868  
QY 1941 PDLLTVRKSGVSRTHSLPN-DSYMCNRNGSTAERSLGRWGWLPKAQSILSVHSQPADT 1999  
Db 1869 ECFFPLSSTAVS-----PDENFLCEMEEIPFNV--RSW--LKHSSQAPSPFSPDAS 1919  
QY 2000 SCILQPKDVHY-----LLQPHGAPTWGAIPKLPFG-----RSPLAQRP LRRQAART 2048  
Db 1920 SPLPMPAEFFHPAVSASQGEKGTGTGLPKIALOGSWASLRSRPNCTILLRQATGSD 1979  
QY 2049 DSLDVQGLGSRREDLLSEVSGPCLTRSSSFVGGSSIQVQQRSGIQSKVSKHIRLPAPCP 2108  
Db 1980 TSLDAS-----PSSAGSLQTTLEDLSLSDSPRRALGPPAPAP 2018  
QY 2109 GLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQBEPLFPRDLKKCYSVETQSCRRRPG 2168  
Db 2019 G-----PRAGLSPAARRL-----SLRGRGL 2039  
QY 2169 FWLDEQRHRSIAVCLDSGQPRICPSPSSL-----GGQPLGGPGGRPKKLSPPSI 2220  
Db 2040 FSLRGLRAHQRSHS--SGGSTSPGCTHDSMDPSDEGRGGAGGGAGSEHSETLSLSL 2097  
QY 2221 S---IDPPESQGRPPCSPGVCLRR-----RAP---ASDSK 2250  
Db 2098 TSLFCPPP-----PPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSK 2151  
QY 2251 DPSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP 2286  
Db 2152 DPPGRAPLPMGLGLAPPPQPL-----PGELEP 2179

RESULT 11  
US-09-935-541-5  
; Sequence 5, Application US/09935541  
; Patent No. US20020150911A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/935,541  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1835  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-935-541-5

Query Match 44.4%; Score 5345; DB 9; Length 1835;  
Best Local Similarity 55.4%; Pred. No. 0;  
Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

QY 43 PRSRDSPVASRSSTTCPPGGAAGAGSTKDPGSADSEAE-----LPYPALAPVVFVLSQ 98  
Db 8 PSSAAAPAPEPGITEQGP-----RSPPSPPGLEPLEGTNPDVPHDLPAPVAFCLRQ 62  
QY 99 DSRPRSWCLRTVCNPFERVSMLVILLNCVTLGMFRPCEDIACQRCRILQAFDDFIFA 158  
Db 63 TTSFPRNCIKVCNPFECVSMVILLNCVTLGMYPQCDMECLSDRCKILQVFFDFIFI 122  
QY 159 FFAVEMVVKWALGIFGKKCYLGDTWNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVLR 218  
Db 123 FFAVEMVVKWALGIFGKKCYLGDTWNRLDFFIVAGMVEYSLDLQNLNSAIRTVRLR 182

QY 219 PLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFIGIVGVQWAGLLRNRCLFLEN 278  
Db 183 PLKAINRVPSMRILVNLLDTPMLGNVLLLCFFVFFIFIGIVGVQWAGLLRNRCLFLEN 242  
QY 279 FSLPLSVLEPYQYQTENEDESPFICQSPRENGMRSRVSPTLRGEGGGPPCSL----- 332  
Db 243 FTIQDVALPPYYQPEEDEMFPICSLTGDNGIMGCHEIPPLKEQ---GRECLS KDDVY 299  
QY 333 DYETYNSSNTT--CVNWNQYTYNC SAGEHNPFKGAINFNDNIGYAWIAIFQVITILEGWD 390  
Db 300 DFGAGRQDLNASGLCVNWNRYYNVCRGTGNANPHKGAINFNDNIGYAGIVIFQVITILEGWE 359  
QY 391 IMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMRQVRFLS 450  
Db 360 IMYVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQYLS 419  
QY 451 NASTLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRRAIGVRAGLLSSPVARSQEQPQ 510  
Db 420 -SSTVASYAEFGDCYEEIFQYVCHILRKAKR-----RALGLYQAL----- 458  
QY 511 SGSCTRSHRRLSVHHLVHHHHHHHHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPS 570  
Db 459 -----QNRROA-----MGPGT-----PAPA 473  
QY 571 TPTSPGGPPRGAEVSHFYHADCHLEPVRCQAPPPRCPSEASGRTVSGKVYPTVHTSPP 630  
Db 474 KGP-----HAK---EPHCKLCPRHSPD-----PTPHT--- 500  
QY 631 PEILKDKALVEVAPSGPPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISSPCSKAD 690  
Db 501 -----LVQ-----PISAIL----- 509  
QY 691 SGACGPDSCPYC-----ARTGAGEPESADHVPDSDSEAVYEFTDAQH 734  
Db 510 --ASDPSSCPHCQHEAGRRPSGLSTDSGQEGSGSGSAE---AEANGDGL-QSSE DGVS 563  
QY 735 SLDLPHSRRRRQSLGPDAPSSVLA-----FWRLICDTFRKIVDSKYFGRGIMAILVN 789  
Db 564 SD-----LGKEEQEDGAARLCGDVWRETRKLRGIVDSKYFNRGIMMAILVN 611  
QY 790 TLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVGPFYIKPNYNIFDGVIV 849  
Db 612 TVSMGIEHHEQPEELTNALEICNVVFTSMFALEMILKAAFGFLDYLRPNYNIFDSIIVI 671  
QY 850 ISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATFCMLLMFI 909  
Db 672 ISIWEIVGQADGGLSVLRTFRLLRVLKVRFLPALRRQLVLMKTMNDNVATFCMLLMFI 731  
QY 910 FIFSLGMHLFGCKFASERD-GDTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGMAS 968  
Db 732 FIFSLGMHIFGCKFSLRTDGTVPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGMAS 791  
QY 969 TSSWAALYFIALMTFGNVVLFNLLVAILVEGFAEGDATKSESEPDFFSPSVDG----- 1022  
Db 792 TTPWASLYFVALMTFGNVVLFNLLVAILVEGFAEGDANRSCDEQSSNLEEFDKLPE 851  
QY 1023 --DGRKKRLALVALGEHAELRKSLLPPLIHH--TAATPM SHPKSSSTGVGEALGSGRR 1078  
Db 852 GLDNRDLKLCPIPMTPNGHLDPSL--PLGAHLGPA GTMTAPRLSLQDPVLVALDSRK 909  
QY 1079 TSSGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGE 1138  
Db 910 SSVMSL---GRMSYDQRLSSSRSSYYGPGWGSCTWASRRSWN-----SLKHKPPSAE 960  
QY 1139 RRSLLSGEQES--QDEESSEE--DRASPA GSDH-----RHRGSLEREA 1179  
Db 961 HESLLSGEGGSCVRACEGAREEAPTRTAPLAPHAHHAHGHPLAHPHHRHRTLSLDT 1020  
QY 1180 KSSFDPDLTQVPGHLRTAS--GRSSASEHQCCKGKSASGLARTLRTD-DPQLDGD DDDN 1236  
Db 1021 RDSVDLDELVPVVGASHRAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDRRDRGEDE 1078





Db 639 -----KPGPHAKEPRH 649

Qy 577 GPGRGAESVHSFYHADCHLEPVRQAPPPRCPSSEASGRVTGSGKVYPTVHTSPPEILKD 636

Db 650 YPLTWESILGRQAECTL---RAAAHP-----SSGASHPGVSGSEAPELCPQ 694

Qy 637 KALVEVAP---SPGPPTLTSTFNIPPGPFSSMHKLLLEQTOSTGAC-HSSCKISSPCSKADS 691

Db 695 HSPLDATHTLVQIPATLAS-----DPASCPCQHEHGRRPSGLGSTD 739

Qy 692 GACGPDSPYCARTGAGEPESADHVPDSDSEAVYEFQDAQHSDDLDPHRRRQRLGP 751

Db 740 QOEGSGS-----GSSAGGEDEA-----DGDGA---RSESDGASSELGKEEESEQ----- 781

Qy 752 DAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPE----- 802

Db 782 -ADGAVMLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQASAAQPGRA 840

Qy 803 -----ELTNALE-----ISNIV----- 814

Db 841 CGRGONPDLGWTLKAPCLCHNVPSPGQVLSHPVTPHTAPWRMETGKQHGCGEGPGQR 900

Qy 815 FTSLFALEMLLKLLVYGPFGYIKNPYNIQFDGVIIVISVWEIVGQGGGLSVLRTFRLMRV 874

Db 901 SSDMFALEMILKLAAGFLDYLRNPYNIFDSIIIVISWEIVGADGGLSVLRTFRLRV 960

Qy 875 LKLVRFLPALQROLVLMKTMNDVATFCMLLMFLIFISILGMHLFGCKFASERD-GDTL 933

Db 961 LKLVRFPALRQLVLMKTMNDVATFCMLLMFLIFISILGMHIFGCKFSLRTDGTDTV 1020

Qy 934 PDRKNFSLMLWAIVTVFQILTQEDWNKVLYNGMASTSWAALYFIALMTFGNYVLFNLLV 993

Db 1021 PDRKNFSLMLWAIVTVFQILTQEDWNKVLYNGMASTSPWASLYFVALMTFGNYVLFNLLV 1080

Qy 994 AILVEGFOAE-----GD 1005

Db 1081 AILVEGFOAEVTVVLAEEAPPOGLRKTGRGRGLDGGGLQFKLLAGNLSLKEGVADEVGD 1140

Qy 1006 ATKSESEPDFFPSV-----DGDGDRKKRLALVALGEHAELRKSLLPLLIHT-- 1053

Db 1141 ANRSYDEQSSSNIIEEFDKLQGLDSSGDPK--LCPIPTPNHGLDPSL--PLGGHLGP 1196

Qy 1054 --AATP-----MSHPKSSSTGVG-----EALGSGSRRTSSSGSA----- 1085

Db 1197 AGAAGAPRSLSLQPDPMVLALGSRKSSVMSLGRMSYDQSRSLVGGLRATAGVQAAGHLVP 1256

Qy 1086 EP-----GAAHHEMKCPPSARSPHSPWSAASWTSSRSRNSLGRAPSLKRSPSGERR 1140

Db 1257 QPWWCLWGADPNGNSFQSSRSRYGPGWRSAAWASRRSSWN-----SLKHPPPSAEHE 1310

Qy 1141 SLLSGE--GQESQDEESSEE--DRASPAGSDH-----RHRGSLEREAKSS 1182

Db 1311 SLLSAERGGGARVCEVADEGPPRAAPLHTPHAHVHGHPLAHRHRRHTLSLDNRDS 1370

Qy 1183 FDLPTTLQVGLHRTASGRSS--ASEHQDCNGKSASGRILARTLT--DDPQLDGGDDND- 1237

Db 1371 VDLAELVPAVGAHPRAAWRAAGAPAGHEDCNGRMPS--IAKDVFYTKMGDRGDRGEDEEI 1428

Qy 1238 -----EGNLSKGERIQAWVRSLPACCRRERDSWSAYIFPPQSRFR-----LLC--- 1280

Db 1429 DYVSGGGAEGDLTLCFRVRKMDIVYKPDWCVEVREDWSVLSFSPENRLRLDGLWVSLCQKG 1488

Qy 1281 -----HRIITHKMFHDHVVLVIFLNCITTAWERPKIDPHSAERIFLTLSN 1325

Db 1489 VGDLVVVYGQRRQRQTIIAHKLFDYVVVLAFLFNLNCITTALEPQIEAGSTERIFLTVSN 1548

Qy 1326 YIFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGDLVLSVIDILVMSVSDSGTKIL 1385

Db 1549 YIFTAIFVGEWTLKVVSGLYFGEQAYLRSSWNVLGDLVLSVIDIVVSLASAGGAKIL 1608

Qy 1386 GMLRVLRLLRLPLRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVOLF 1445

Db 1609 GVLRVLRLLRLPLRVISRAPGLKLVVETLISSLKPIGNIVVICCAFFIIFGILGVOLF 1668

Qy 1446 KGKFFVCQGEDTRNITNKSCAEASYSRWVRHKYNFNDNLQALMSLFVLASKDGVVDIMYD 1505

Db 1669 KGKFYHCLGVDTNRNITNRSDCMAANYRWVHHKYNFNDNLQALMSLFVLASKDGVNIMYN 1728

Qy 1506 GLDAVGVDQQPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHQBEEARR 1565

Db 1729 GLDAVAVDQQPVTNHNPMMLLYFISFLLIIVSFFVLNMFVGVVVENFHKCRHQHQBEEARR 1788

Qy 1566 REEKRLRRLEKRRSRKEKQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNV 1625

Db 1789 REEKRLRRLEKRR-----KAQRLPYATYCHTRLLIHSMTCTSHYLDIFITFICLNV 1841

Qy 1626 VTMAHEHYQQP 1636

Db 1842 VTMSLEHYNQP 1852

RESULT 14

US-10-369-493-6836

; Sequence 6836, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6836

; LENGTH: 1657

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6836

Query Match 29.5%; Score 3553; DB 15; Length 1657;

Best Local Similarity 42.2%; Pred. No. 2.7e-226;

Matches 800; Conservative 234; Mismatches 436; Indels 426; Gaps 42;

Qy 66 AGSTKDPG-----SADSEAEGLPYPALAPVFFYLSQDSRPSRWCLRTVCN 112

Db 88 ASSSEASPSRWEGRIEWGNEEQIEESE-LPYPGFAEPALRCFYQARPPRKVALQVMS 146

Qy 113 PWFERSMLVILLNCVTLMFRPCED-IACDSQRCRILOAFDDFIFAFFAVEMVVMVAL 171

Db 147 PWFDRITMAVIMINCVTLMYRPCEDGDCDTRCQILDIDNCIFVFYFAFEMVIMKAL 206

Qy 172 GIFGKCYLGDTWNRLDFFIVLAGMLEYSLDLQ---NVSFSAVRTVRLRPLRAINRVPS 228

Db 207 GFYGPAAVMSDTWNRLDFFIVMAGIAEFVLYHEYLGNINLTAIRTVRLRPLRAVNRIPS 266

Qy 229 MRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCF--LPENFS-----L 281

Db 267 MRILVNLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCVINLPKTISENQSA 326

Qy 282 PLSVDLEPYQOTENEDESPFICQPRENGMRSCRSVPTLRGEGGGPPCSLDYETNSSS 341

Db 327 FNNVKLTRFYIPE-DTSLEYICSQPDANGLHTCSNLPPTYVD---GVKCNLTLDYDKVT 382

Qy 342 NTTCVNWNQYTNCSAG-----EHNPFKAINFDNIGYAWIAIFQVIT 384

Db 383 NDSCINWNIIYNECQVNIYPSLMTIAISCFIKVMQRNPFQGSVFDNIGFAWVAIFLVIS 442

Qy 385 LEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQIMREQ 444

Db 443 LEGWTDIMYVQDAHSFVNWIYFVLLIIVIGAFFMINCLVVIATQFAETKRRETERMLQE 502





QY 343 TTCVNNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFMD-AHSF 401  
Db 281 TEC---REYWP-----GPNFGITNFDNIFAILTVQCITMEGWTIDILYNTNDAAGNT 330  
QY 402 YNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQRVFLSNASTL 455  
Db 331 WNLWYFIPLIIIGSFFMLNLVLGVLGSEFAKERERVENRRAFLKLRRQQIE----- 382  
QY 456 ASFSEPGSYEEELLYLVILRKAARRLAQVSRAGIVRAGLSSPVARSGEQEPQSGSCT 515  
Db 383 -----RELNGYLEWIFKAEEVMAEED-----RNAEKSPLDVLK 417  
QY 516 RSHRRLSVHHLVHHHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRRLMLPPPTPTPS 575  
Db 418 RAATKKSRLNLIH-----AEEGEDRPAD----- 440  
QY 576 GPPRPGAESVHSFYHADCHLEPVRCQAPPPRCPPSEASGRVTGSGKVYPTVHTSPPEILK 635  
Db 441 ----- 440  
QY 636 DKALVEVAPSGPPTLTSTFNIPGPFSSMHKLTQSTGACHSSCKISSPCSKADSGACG 695  
Db 441 -----LCAVGSPPFARAS----- 452  
QY 696 PDSCPYCARTGAGEPESADHVMPSDSEAVYEFTQDAQHSDLRDPHSRRRQBSLGPDAEP 755  
Db 453 -----LKSGETESSYF-----RRKEK----- 469  
QY 756 SSVLAFWRLICDTFRKIIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVF 815  
Db 470 --MFRFF-----IRRMVKAQSFYVVVLCVVALNTLVCAMVHYNQPRRLTTTLYPAEFVF 521  
QY 816 TSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGLSVLRTFR 870  
Db 522 LGLFLTEMSLKMYGLGRSRYFRSSFNCFDFGVIIVGSVFVWAAIKPGSSFGISVLRALR 581  
QY 871 LMRVLKLVRELPALORQLVLMKTMNDNVATFCMLMLFIFIFSILGMHLFGCKFASERDG 930  
Db 582 LLRIFKVKYWSLLRNVLVSLNSMKSIISLLFLFLFVIVFALLGMQLFGGQFNQDET 641  
QY 931 DTLPRDKNFDLSLLWAIVTVFQILTQEDWNKVLYNGM-----ASTSSWAAALYFIALMTFGN 985  
Db 642 PT-----TNFDTFPAAILTVQILTGEDWNAVMYHGIESQGVSKGMFSSFYFIVLTFLGN 697  
QY 986 YVLFNLLVAILVEGFAEGDATAKSESEPDFFPSVSDGDGDKRKRLALVALGEHAELKSL 1045  
Db 698 YTLNVLAIADVNLANAQELTKDEEEMEEAA-----NQKLALQAKEVAEV--SP 746  
QY 1046 LPPLIIHTAATPMSPKSSSTGVGEA----- 1071  
Db 747 MSAANISIAARQONSAKARSVWEORASQLRLQNLRASCEALYSEMDPEERLRFATTRLHLR 806  
QY 1072 -----LGSGRRITSSSGSAEPGAA-----HH-----EMKCP----- 1097  
Db 807 PDMKTHLDRPLVVELGRDGRGARGPVGGKARPEAAEPEGVDPPRRHRRHRDKDTPAAGDQ 866  
QY 1098 -----PSARSS-----PHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSL 1142  
Db 867 DRAEAPKAESGEPGAREERPRPHRSKSEA--GPPEARSERGRGP-----GPEGRRHH 919  
QY 1143 LSQEGQESQDEE-----ESSEEDRASPAQSDHRRHRSLE---REAKSSFDLPDTL 1189  
Db 920 RRGSPESAAREPRRHRHRHQDPSPKCECAGAKGERARRHRRGGPRAGPREAESG----- 972  
QY 1190 QVPG-LHRTASGRSSASE--HODCNGKSGASGRLA-----RTLRTDDPQLDGGDDNDE 1238  
Db 973 EEPARRHARHKAQPAHEAVEKEETEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032  
QY 1239 GNLSKGERIQAWVRSRLPACCRER-----DSW----- 1265  
Db 1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQNRVTRMGSPQPPDPTIVHIPVMLTG 1086  
QY 1266 -----SAYIFPPQSRFRLLCHRI 1283

Db 1087 PLGEATVVPSCNVLDLESQAEGKKEVEADDMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146  
QY 1284 ITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343  
Db 1147 VTWRYFEVILVIALSSIALAAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVIKMDL 1205  
QY 1344 GWCPEQAYLRSSWNVLDGLLVLSIVDILVSMV-SDSGTKILMLRVLRLRLRPLRV 1402  
Db 1206 GLLLHPGAYFRDLWNILD----FIVWSGALVAFAPSGSGKDINTIKSLRVLRLRPLKT 1261  
QY 1403 ISRAQGLKVVELTMSLSKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCOGE-----D 1456  
Db 1262 IKRLPKLKAVFDCVVSNSLKNVLNIIIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERD 1321  
QY 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFLVASKDGVWDIMYDGLDVGVD 1513  
Db 1322 CRGQILDYEKEEVEAQPROWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381  
QY 1514 QQPMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHOOEEEEARRRREKRLRR 1573  
Db 1382 QGSPGMYRMELSIFYVYVVFVFPFFFNIFVALIITF-----QEQDKVMSE-----CS 1431  
QY 1574 LEKRRSKEKQMAEAQCKPYYSYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTMAME 1631  
Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFOYKWTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491  
QY 1632 HYQOQILDEALKICNIYIFTVIFVFESVFKLVAFARFRFQDRWNQLDLALVLLSIMGIT 1691  
Db 1492 FYDAPYEVELMKCLNIVFTSMFSMECVLKIIAFGLVNLVFRDANWVDFEFTVLGSDITDIL 1551  
QY 1692 LEEIE-----VNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRALLHTVMQALPQVGNL 1746  
Db 1552 VTEAETNNFINLS-----FLRLFRAARLLIKLRQGYTIRILLTWTFFVQSFKALPYV 1602  
QY 1747 GLLFMLLFFIFAALGVELFGDLECDETHPCGEGLRHATFRNFGMAFLTILFRVSTGDNWNG 1806  
Db 1603 CLLIAMLFFIYAIIGMQVFNIALDDD---TSINRHNFRFTLOALMLLFRSATGEAWHE 1659  
QY 1807 IMKD--PSRDCQE--STCVNTVISPIYFVSFVLTAQFV-----LVNV 1845  
Db 1660 IMLSLSNQACDEQANATECGSDFAFYFYFVSFIFLCSFLRLVRMNMPISNEDMTVHTST 1719  
QY 1846 VIAVLMKHLE-----ESNKEAKEAEAELEAEL-----ELEMKTLS--PQHPSP-----LGSP 1889  
Db 1720 LMALIRTALEIKLAPAGTKHQHQCDAELRKEISVVWANLPKQTLDLLVPPHKBDEMTVGKV 1779  
QY 1890 F----LWPGVEGVNSTDSPKPGAPHTTAHIGAAAGSFSLEHPTMTVPHPEEVPVPL-GPDLL 1944  
Db 1780 YAALMIFDFYKONKTTTRDQMQQAPGGLSQMGPSVLF--HPLKATLEQTQPAVLRGARVF 1836  
QY 1945 TVRKSGVSRTHSLPNDSYMCNRNGSTAERSLGRHGWGLPKAQSGSILSVHSQPADTSCILQ 2004  
Db 1837 LRQSSST---SLSNGGAIQNOESGIKESV---SWGTQRTQDA----- 1872  
QY 2005 LPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRLRRQAARTD----- 2049  
Db 1873 -----PHEA-----RPPLERGHSTEIPVGRSGALAVDVQMOSITRRGPDGEP 1914  
QY 2050 --SLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGSSSIQVQORSIGQSKVKHRLPAPC 2107  
Db 1915 QPGLESQG---RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG-----THLCSTTP- 1964  
QY 2108 PGLEPSWAKDPPETRS-----SLELDTELSWISGDLPLSPSQEPLFP- 2149  
Db 1965 -----DRPPPSQASSHHHHHRRRRDRKQSRLEKGPSSL-ADMDGAPSSAVGGLPP 2016  
QY 2150 -----RDLKKCYSVETQSCRRRPPGFWDDEQRHSIAVSCLDSDSGSQRLCPSPS---- 2197  
Db 2017 GEGTGCRRRERRRQERGRSQRRRQPPSSSSSEKQRF---YSCDRFGGREPPPKPPLSSSH 2073  
QY 2198 -----SLGGQPL-----GGGSRPKKLSLSP-PSISIDPPES 2227

Db	2074	PTSPTAGQEPGPHPGQSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITYKTANS	2133
Qy	2228	-----QGSRRPPCSPG-----VCLRRRAPASD-----SKDPSVSSPLDSTA	2262
Db	2134	SPIHFAGAQTSLPAFSPGRLSRGLSEHNALLQRDPLSQPLAPGSRIGSDPYLGQRLDSEA	2193
Qy	2263	ASPSPKKDTLSL-----SGLSS	2279
Db	2194	SVHALPEDTLTFEEAVATNSGRSS	2217

Search completed: April 13, 2005, 19:30:57  
Job time : 243 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 18:36:39 ; Search time 71 Seconds  
(without alignments)  
3099.264 Million cell updates/sec

Title: US-09-611-257A-24  
Perfect score: 12028  
Sequence: 1 MLPHRVPRCVRTPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11657	96.9	2254	2 T09053	low voltage-activa
2	3553	29.5	1657	2 T15838	hypothetical prote
3	1720.5	14.3	1810	2 T31092	probable voltage-g
4	1676	13.9	2339	2 A42566	omega-conotoxin-se
5	1665.5	13.8	2259	2 S29236	calcium channel pr
6	1653.5	13.7	2272	2 C54972	voltage-dependent
7	1652.5	13.7	1891	2 T43262	calcium channel al
8	1652.5	13.7	2178	2 S29237	calcium channel pr
9	1650.5	13.7	2288	2 S41080	calcium channel al
10	1642	13.7	2223	2 A47447	calcium channel pr
11	1640.5	13.6	2237	2 T45115	N-type calcium cha
12	1638	13.6	2251	2 B54972	voltage-dependent
13	1637.5	13.6	2270	2 A54972	voltage-dependent
14	1636	13.6	1993	2 T30902	sodium channel SCA
15	1632.5	13.6	2222	2 A37490	voltage-dependent
16	1632.5	13.6	2336	2 A45386	omega-conotoxin-se
17	1631	13.6	2181	2 A38198	calcium channel al
18	1628	13.5	1873	2 A30063	dihydropyridine re
19	1622	13.5	2161	2 JH0564	calcium channel al
20	1619.5	13.5	1911	2 T43048	calcium channel al
21	1616	13.4	1852	2 A37860	calcium channel pr
22	1614.5	13.4	1977	2 S54771	sodium channel alp
23	1613	13.4	2203	2 T42742	voltage-dependent
24	1610	13.4	2143	2 JH0427	voltage-dependent
25	1603	13.3	1610	2 A46227	voltage-dependent
26	1595.5	13.3	1783	2 T37258	probable voltage-d
27	1595	13.3	2166	2 S11339	calcium channel pr
28	1592.5	13.2	2139	2 A44467	voltage-dependent
29	1587.5	13.2	1646	2 JH0422	voltage-dependent

30	1587.5	13.2	1873	2 A55645	calcium channel, v
31	1585.5	13.2	2016	2 A38195	sodium channel pro
32	1580	13.1	1917	2 C88728	protein C48A7.1 (i
33	1577.5	13.1	1559	2 T30535	calcium channel al
34	1574	13.1	2171	2 S05054	calcium channel al
35	1573	13.1	2108	2 S72458	sodium channel pro
36	1567.5	13.0	1687	2 S41742	calcium channel al
37	1565	13.0	1957	2 S68453	sodium channel pro
38	1557.5	12.9	2220	2 A45290	calcium channel pr
39	1556	12.9	2019	2 A33996	sodium channel pro
40	1551.5	12.9	1840	1 CHRTM1	sodium channel pro
41	1549	12.9	1976	2 I56555	sodium channel pro
42	1546.5	12.9	1983	2 A60054	sodium channel pro
43	1546	12.9	2262	2 T30890	calcium channel al
44	1544.5	12.8	1951	2 S00320	sodium channel pro
45	1544.5	12.8	2005	2 A46269	sodium channel alp

ALIGNMENTS

RESULT 1

T09053

low voltage-activated, T-type calcium channel alpha chain - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: T09053

R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox

Nature 391, 896, 1998

A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium

A;Reference number: Z16538; MUID:98154730; PMID:9495342

A;Accession: T09053

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2254 <PER>

A;Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3

A;Experimental source: strain Sprague-Dawley; brain

C;Genetics:

A;Map position: 17

A;Note: CACNA1G

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: calcium channel; voltage-gated ion channel

Query Match	96.9%;	Score 11657;	DB 2;	Length 2254;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 2219;	Conservative	0;	Mismatches	6;
			Indels	0;
			Gaps	0;
Qy	62	GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPSWCLRTVCNPFERSVSM	121	
Db	30	GRQPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPSWCLRTVCNPFERSVSM	89	
Qy	122	VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	181	
Db	90	VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	149	
Qy	182	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSPMRILVTLLDTLP	241	
Db	150	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSPMRILVTLLDTLP	209	
Qy	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVDLEPYQTENEDSPF	301	
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVDLEPYQTENEDSPF	269	
Qy	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDETYNSSNTTCVNNQYNTNCSAGEHN	361	
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDETYNSSNTTCVNNQYNTNCSAGEHN	329	
Qy	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL	421	
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL	389	
Qy	422	CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELKLYLVILRKAAR	481	

Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

QY 482 RLAQVSRRAIGVRAGLLSSPVARSQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 541

Db 450 RLAQVSRRAIGVRAGLLSSPVARSQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGN 509

QY 542 GTLRVPRAPEIQDRDANGSRRLMLPPPSTPTSPGGPRGAESVHSFYHADCHLEPVRCQ 601

Db 510 GTLRVPRAPEIQDRDANGSRRLMLPPPSTPTSPGGPRGAESVHSFYHADCHLEPVRCQ 569

QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPPILTFSNIPPGPF 661

Db 570 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPPILTFSNIPPGPF 629

QY 662 SSMHKLETSQSTGACHSSCKISSPCSKADSGACGPDSPYCARTGAGEPEPADHVMPDSD 721

Db 630 SSMHKLETSQSTGACHSSCKISSPCSKADSGACGPDSPYCARTGAGEPEPADHVMPDSD 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKI VDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKI VDSKYFGRG 749

QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKL LVYGPFGYIKNPYN 841

Db 750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKL LVYGPFGYIKNPYN 809

QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATF 901

Db 810 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATF 869

QY 902 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAI VTVFQILTQEDWNKV 961

Db 870 CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAI VTVFQILTQEDWNKV 929

QY 962 LYNGMASSTSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPPFFSPSVD 1021

Db 930 LYNGMASSTSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPPFFSPSVD 989

QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRRRTSS 1081

Db 990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRRRTSS 1049

QY 1082 SGSAEPGAAHENKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141

Db 1050 SGSAEPGAAHENKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1109

QY 1142 LLSGEGQESQDEBESSEEDRASPA GSDHRRHGRSLEREAKSSFDPD LTVPGHLRTASGR 1201

Db 1110 LLSGEGQESQDEBESSEEDRASPA GSDHRRHGRSLEREAKSSFDPD LTVPGHLRTASGR 1169

QY 1202 SSASEHQDCNGKSASGR LARTLRDTPQLDGGDDNDDEGNLSKGERIQA WVRSLRPACCRE 1261

Db 1170 SSASEHQDCNGKSASGR LARTLRDTPQLDGGDDNDDEGNLSKGERIQA WVRSLRPACCRE 1229

QY 1262 RDSWSAYIFPPQSRFLLCHRIIITHKMFHDHVVLVII FLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFLLCHRIIITHKMFHDHVVLVII FLNCITIAMERPKIDPHSAERIFL 1289

QY 1322 TLSNYIFTAVFLAEMTVKVVALGWC FGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVALGWC FGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLLRLTLRPLRVISRAQGLKLVVETLMSLKP GNIVVICCAFFIIFGILG 1441

Db 1350 TKILGMLRVLLRLTLRPLRVISRAQGLKLVVETLMSLKP GNIVVICCAFFIIFGILG 1409

QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEAS YRWRHKNYFNFDNLGQALMSLFLVASKDGWVD 1501

Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEAS YRWRHKNYFNFDNLGQALMSLFLVASKDGWVD 1469

QY 1502 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLI VAFVFLNMFVGVVVENFHKCRQHQBEE 1561

Db 1470 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLI VAFVFLNMFVGVVVENFHKCRQHQBEE 1529

QY 1562 EARRREEKRLRLEKKRRSKEKQMAEAQCKPYYSYDRFRLLVHHLCTSHYLDL FITGVI 1621

Db 1530 EARRREEKRLRLEKKRRSKEKQMAEAQCKPYYSYDRFRLLVHHLCTSHYLDL FITGVI 1589

QY 1622 GLNVVTMAMEHYQQPQIILDEALKICNYIIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLDA 1681

Db 1590 GLNVVTMAMEHYQQPQIILDEALKICNYIIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLDA 1649

QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGM RALLHTVMQALP 1741

Db 1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGM RALLHTVMQALP 1709

QY 1742 QVGNLGLL FMLLFFIFAALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLT LFRVSTG 1801

Db 1710 QVGNLGLL FMLLFFIFAALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLT LFRVSTG 1769

QY 1802 DNWNGIMKOPSRDCQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861

Db 1770 DNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1829

QY 1862 KEEAELEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTT AHIGAASGF 1921

Db 1830 KEEAELEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTT AHIGAASGF 1889

QY 1922 SLEHPTMVPHPPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH RWGWL 1981

Db 1890 SLEHPTMVPHPPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH RWGWL 1949

QY 1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041

Db 1950 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2009

QY 2042 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSF WGGSSIQVQORSGIOQSKVSKHI 2101

Db 2010 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSF WGGSSIQVQORSGIOQSKVSKHI 2069

QY 2102 RLPAPCPGLEPSWAKDPPETRSSL ELDTEL SWISGDLLPSSQEEPLFP RDLKKCYSVETQ 2161

Db 2070 RLPAPCPGLEPSWAKDPPETRSSL ELDTEL SWISGDLLPSSQEEPLFP RDLKKCYSVETQ 2129

QY 2162 SCRPPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSSLGGQPLGGPSRPKKLSPPSIS 2221

Db 2130 SCRPPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSSLGGQPLGGPSRPKKLSPPSIS 2189

QY 2222 IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVS SPSPLDSTAASPSPKDTLSLGLSSDP 2281

Db 2190 IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVS SPSPLDSTAASPSPKDTLSLGLSSDP 2249

QY 2282 TDMDP 2286

Db 2250 TDMDP 2254

RESULT 2

T15838  
hypothetical protein C54D2.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Mar-2000  
C;Accession: T15838  
R;Minx, P.  
submitted to the EMBL Data Library, October 1995  
A;Description: The sequence of C. elegans cosmid C54D2.  
A;Reference number: Z18415  
A;Accession: T15838  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1657 <MIN>  
A;Cross-references: EMBL:U37548; NID:gl017804; PID:gl017809; PIDN:AAA79201.1; CESP:C54D2  
C;Genetics:  
A;Gene: CESP:C54D2.5  
A;Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 513/  
C;Superfamily: sodium channel protein

Query Match		29.5%;	Score 3553;	DB 2;	Length 1657;
Best local similarity		42.2%;	Pred. No. 1.3e-217;		
Matches 800;		Conservative 234;	Mismatches 436;	Indels 426;	Gaps 42;
Qy	66	AGSTEKDPG-----	SADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCN	112	
Dd	88	ASSEASPRWEGRIEWGNEEQIEESE-LPYPGFAEPALRCFYQARPPRKALQVMVS	146		
Qy	113	PWFERVSMVLNVCVTLMFRPCED-IACDSQRCRILQAFDDFIFAFAFVEMVVMQVAL	171		
Dd	147	PWFDRITWAVIMINCVTLGMYRPCEDGPDCTYRCQILDIDNCIFVYFAFEMVIMKIMAL	206		
Qy	172	GIFGKKCYLGDWTNRLDFFIVIAAGMLEYSLDLQ---NVSPSAVRTVRVLRPLRAINRVPS	228		
Dd	207	GFYGPAAVMSDTWNRLDFFIVMAGIAEFVLHEYLGGINLTAIRTVLRPLRAVNRIPS	266		
Qy	229	MRILVTLLDTPMLGNVLLLCFFVFVFFIGIVGVQLWAGLLRNRCF--LPENFS-----L	281		
Dd	267	MRILVNLLDTPMLGNVLLLCFFVFVFFIGIVGVQLWAGLLRNRCVINLPKTTISENQSAL	326		
Qy	282	PLSVDLEPYQTENEDESPFCISQPRENMRSCRSVPTLRGEGGGGPPCSDLYETYNSSS	341		
Dd	327	FNNVKLTRFIPE-DTSLEYICSPDANGLHTCSNLPPTYVD---GVKCNLTLEIDYDKVT	382		
Qy	342	NTTCVNNWNYTNCAG-----	EHNPFKAGNFDNIGYAWIAIFQVIT	384	
Dd	383	NDSCINWNIYNECQVNIYPSLMTIAISCFIKVMQRNPFQGSVFDNIGFAMVAIFLVIS	442		
Qy	385	LEGWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQIMREQ	444		
Dd	443	LEGWTDIMYVQDAHSFNNWIYFVLLIIVIGAFFMINCLVVIATQFAETKRRETERMQE	502		
Qy	445	RVRFLSNASTLASFSEPG-----	SCYEELLKYLVLKRAARRLAQVSRAIGVRAG	495	
Dd	503	RKMLLNRSISCTGSEIGGASSKEEGDTVYAAFVRFIGHTFRRTKRAAKKYYTAY-----	557		
Qy	496	LLSSPVARSQEPQPSGSTRSHRRLSVHHLVHHHHHHHHLGNGTLRVPRASPEIQD	555		
Dd	558	-----	MEERAERKSSERQORRKSCL-----	DDMATLSRIEKAED	592
Qy	556	RDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCAQPPPCPSEASGRT	615		
Dd	593	EE-----	DETTITRENGDDQIEQN-----	611	
Qy	616	VGSGKVPTVHTSPPEILKOKALVEVAPSPGPTLTSTFNIPGPFSSMHKLETQSTGA	675		
Dd	612	-GDGVRIKRVKIEEPI-----	628		
Qy	676	CHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHS	735		
Dd	629	-----	KIGNGNSNGPHYKHSSSDEES-----	DEdgeED	656
Qy	736	DLRDPHSRRQRSLGPDAPSSVLAPWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGI	795		
Dd	657	QVYDGEBAKK-----	STPSKL--WW--	FREKIQKFVICDHFTRGILVAILVNTLSMGV	706
Qy	796	EYHQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISVWEI	855		
Dd	707	EYHQPEILTVILEYSNLFFTALFALEMLLKIIASGLFGYLAGDGNLFDGGIVALSVLEL	766		
Qy	856	VGOQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFIFSIL	915		
Dd	767	FQEGKGLSVLRTFRLRLKLVRFMPALRYQLVLMRLTMDNVTVFFGLLVLFIFIFSIL	826		
Qy	916	GMHLFGCKFASERD---GDTLP--	DRKNFDSLWAIWTVTFQILTQEDWNKVLNMGMASTS	970	
Dd	827	GMNLFCKFKVEEKFGLGLAKKCKERNFDTLWALITVFQILTQEDWNMVLNFMGAQTN	886		
Qy	971	SWAALYFIALMTFGNYVLFNLLVAILVEGFQAECDATKSESEPDFFSPSVDGDGRKRL	1030		
Dd	887	PWAALYFVALMTFGNYVLFNLLVAILVEGFQESKEEBKRLQLEEDARKQAVEEEDERKREL	946		

Qy	1031	ALVALGEHAELRKSLPLPLIIHTAATPMSHPKSSSTGVGEALGSGRRSTSSSGSAEPGAA	1090
Db	947	ELII-----AKTSPAFNNGVA	963
Qy	1091	HHEMKC--PPSARSSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSG-----ERRSLL	1143
Db	964	PAECTCQRPSSPEESP-SPRLLSANY-----HPSPERKHSANLDAIDKRLVL	1010
Qy	1144	SGEGESQDEEESSEEDRASPAQSDHRRHRSGLEREAKSSFDLPDTLQVGLHRTASGRSS	1203
Db	1011	-----RNSAPFDR-SPV-SEGRDDSLRNRHA--SLVLPVANGVP-----	1045
Qy	1204	ASEHQDCNGKSASGRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSL--PACCRER	1262
Db	1046	-YRRQVHSWKASQELKQALAEERKEAKQN-----TFVRKLLKKTCLHNR	1091
Qy	1263	DSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIFLNCITIAMERPKIDPHSAERIFLT	1322
Db	1092	TEFSLFLMGPKNPLRIKLOTTQKKWFDYTVLFFIGINCITLAMERPSIPPDSEFERQFLH	1151
Qy	1323	LSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDLGLLVLISVIDILVSMVSDSGT	1382
Db	1152	ISGYIFTVIFTGEMMK-----	1168
Qy	1383	KILGMLRVLRLTLRPLRVISRAQGLKLWVETLMSLKPIGNIVVICCAFFIIFGILGV	1442
Db	1169	-----VSHRIPTLKPIGNIVLICCTFFIIFGILGV	1198
Qy	1443	QLFKGKFFVCQGEDTRNITNKSDCAEASYR--WVRHKYNFDNLGOALMSLFLVLASKDGWV	1500
Db	1199	QLFKGMVYHCIGPEVGNVTTKADCIIE-DYRNKWNHRYNFDNLGOALMSLFLVLSSKDGWV	1257
Qy	1501	DIMYDGLDAVGVDQOPIMNHNPMWLLYFISFLLIVAFFVLNMFVGVVVENFHKCRHQEE	1560
Db	1258	SIMYQIGIDAVGVVQPIENYNEWRMIYFISFLLLVGFFVLNMFVGVVVENFHKCKEALEK	1317
Qy	1561	EEARRREKRLRLEKRRSKEKQMAEAQCK-----PYSDYSRF	1600
Db	1318	EMREKEKEKRLKR-KLKQKFEESMAGKRRKNRIVWAGSAIKSIFSVERNYPYHYDYHT	1376
Qy	1601	RLLVHHLCTSHYLDLFTITGVIGLVNVTMAMEHYQQOILDEALKICNYIFTVIFVESVF	1660
Db	1377	RLFLHGIVTSKYFDLAIAAVIGINVISMAFEYMPMPGLKYVLKALNYFFTAVTTLEAAM	1436
Qy	1661	KLVAFAFRFFQDRWNQDLALVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIARVL	1720
Db	1437	KLIALGFKRFFIEKNRDLDMFVILSIAGIIFEEFEA-LLEPINPTIIRVMRVLRIARVL	1495
Qy	1721	KLLKMAVGMRALLHTVMQALPOVGNLGLLFLMLFFIFAALGVELFGDLECDETHPCGLG	1780
Db	1496	KLLKMAKGIIRSLDVTGEALPOVGNLGSLLFFLLFFIFAALGVELFGKLECEDHPCDGLG	1555
Qy	1781	RHATFRNFGMAFLTFLFRVSTGDNWNGIMKOPSR-DCD-----QESTCYNTVISPIYFVSF	1834
Db	1556	EHAHFKNFGMAFLTFLRIATGDNWNGIMKDALRDDCSDSDHCETNCCVDPILAPCFFVIF	1615
Qy	1835	VLTAQFVLNVNVIAMKHLSESNKEAEAEAEAE	1870
Db	1616	VLISQFVLNVVVAVLMKHLEESN---KRDAEGPAE	1648

RESULT 3  
T31092

probable voltage-gated sodium channel - Aiptasia pallida

C;Species: Aiptasia pallida

C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004

C;Accession: T31092

R;White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.

submitted to the EMBL Data Library, January 1998

A;Description: Structure of a putative sodium channel from the sea anemone Aiptasia pall

A;Reference number: 220975

A;Accession: T31092

A;Status: preliminary; translated from GB/EMBL/DBJ



A;Molecule type: mRNA  
A;Residues: 1-1810 <WHI>  
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:G2791840; PID:G2791841; PIDN:AAB9  
C;Genetics:  
A;Gene: Nal  
C;Superfamily: sodium channel protein

		Query Match	14.3%	Score	1720.5	DB 2	Length	1810		
		Best Local Similarity	25.8%	Pred. No.	6.2e-101					
		Matches	509	Conservative	342	Mismatches	694	Indels	429	Gaps
QY	110	VCPNPFERVSMVLVILLNCVTLGMRPCEDIAQDSQCRILQAFDDFIF-AFFAVEMVVKM	168							
DB	110	ITNQFFEFILLTIIVNCIFLAL-----RDAPEQPEYVFAIYTFEMLLKI	155							
QY	169	VALG-IFGKCYLGDTWNRLDFEIVIAQMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVP	227							
DB	156	IAKGLVMHEYAYLRDPWNWLDVFFVILGYVTLVPNVANL--SGIRIFRVLRLRTISAVE	213							
QY	228	SMRILVTLTLLDTLPLMGNVLLCPFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDL	287							
DB	214	GLKTMVNALLKSMKMLSDVLLITLTFPFCVVALVGMQLFVGLSRNKCVCPLPLNTTIDYDS	273							
QY	288	---EPYYQTEDESPFICSPRENGMRSCRSVPTLREGGGGPPCSDLVETYNSSNT	343							
DB	274	FVTNESHWHYHPTDTPITC-----GNSTAGPCPLNY-----	306							
QY	344	TCVWNQYTYNCAGEHNPFPKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN	403							
DB	307	TCL-----ANIG-NPNNGYTNLDNFGWAVITAFQLVTLDYWENVYNYVLSMGSWY	357							
QY	404	FIYFILLIIVGSFPMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGS	463							
DB	358	IFYFFMVIFFGSFYLLNLVAVAVSY-----QDEVLAQDRENYNNLKGVASLYSFHG	412							
QY	464	CYBELLKYLVIYLKAAARLAQVSRAIGVRAGL-LSSPVARSGEQPQPSGSCFTRSHRRLS	522							
DB	413	C-----VVPKLLRNSKSKTKSLASKCKMSFCVPCFSIGKQPEHSNG-----	453							
QY	523	VHHLVHHHHHHHHLGNGTLRVPRASPE---IQDRDANGSRRLMLPPPSTPTPSGGPP	579							
DB	454	-----HASDNESHASTG-GTIRVDSTALEMKMLNDKNEVRTNGHSLPEPKT-----	499							
QY	580	RGAESVHSFYHADCHLEBPVRCQAPPPRCPSEASGRTVGSGKVPTVHTSPPPPEILKDKAL	639							
DB	500	-----SSFF-----SVSSDN---SIH-----IRMNSS	518							
QY	640	VEVAPSPGPTLTSP--NIPPGPFSSMHKLTQSTGACHSSCKISSPCSKADSGACGPD	697							
DB	519	TEVMPQ-----TSKFDNI-----LTKTLDVKS-----SFLKLSAISEQSS-----	555							
QY	698	SCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHRRRRQSLGPDAPESP	757							
DB	556	-----TDGVDNNEINNTQPKQSVFIARV-----LTPRGSLARQTSTGSATHHKT	601							
QY	758	VL---APWRLICDTRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPEELTNALEISNIV	814							
DB	602	ITKQDTKNRIRRMISKIVLHGMDTFITFCTMVNTLFLSLEYHNMDSNYLMVLEIGNKV	661							
QY	815	FTSLFALEMLLKLIVYGPFGYIKPNYIFDGVIVVISWVE-----IVGQGGGLSVLRTF	869							
DB	662	FTWVFLLEMLKITAFGFKGYIKSRWNIFDGFIVVISMVDLMVELLDHDSGLSVLRTF	721							
QY	870	RLMRVLKVRFLPALQRLVVLMTMDNVATFCMLMLFIFIFSILGMHLFGCKFASERD	929							
DB	722	RLLRVFKLAQSWQTMMLLSTIARSVGQLNLTLVLGIVYMLAVVGVLFDQYYTTKNF	781							
QY	930	GDTLPDRKNPDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLF	989							
DB	782	NGDVP-RWNFTDFWHSFMMIFRVLGGE-WIEPLYDCMRASTSWATLFFLTVLVIGNFLVL	839							
QY	990	LLLVAILVEGFQAG---DATKSESEPDFFSPSVDGDGRKKRLALVALGEHAELRKS--	1044							

RESULT 4  
A42566

DB	840	NFLALLNAPARESLQEAKKTKKPSKFAQGV-----SKLSR-ALRFRSTVSKTTQ	891
QY	1045	LLPPLIHTAATPMHPKSSSTGVGEALGSGSRSTSSGSAEPGAHHEMKCPPSARSSP	1104
DB	892	VLPTIRVHD-----GENATDGDK-----APTQVNGL	917
QY	1105	HSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGE-----RRSLLSGEGQESQDEESES	1158
DB	918	ESKTSDSAISTSSNASNAMISAVTAFQGNKKGKLNDRDTFRRLSLAIE-----	965
QY	1159	EDRASPGSDHRHRGSLEREAQSSFDLPDTLQVPLGHLRTASGRSSASEHQDCNCKSASGR	1218
DB	966	-----TANSDNTSNVLMAAASST-----SITGR	989
QY	1219	LARTLRDTPQLDGGDDNDDEGNLSKGERIQAWRSRLPACCRERDSWYI-FPPQSRFR	1277
DB	990	-----QDHGTSDDPPDPMTVEDECPCWCMKMTGCGITR--WKASDGYRSWRNLR	1037
QY	1278	LLCHRIITHKMFHDVVLVIIFLNCITAME-----RPKIDPHSAERIFLTLSNYIFTAV	1331
DB	1038	LAVKKEVHKFEWTLAIIMASSIALTTFEDINLPSRPKL-----KEYLQYLNIFPAVT	1091
QY	1332	FLAEMTVKVVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTK--ILGMLR	1389
DB	1092	FSIEFLKVLGL---GVVSYFRNCWCLDVLIFFVPV---SSVIADSSNQDSSLSSLR	1143
QY	1390	VLRLRLTLRPLRVISRAQGLKLVETLMSSSLKPIGNIVVIVICCAFFIIFGILGVQLPKGF	1449
DB	1144	SLRTLALRPLRAISRWEGRVNVNSLLFAIPGIGNVLLVCMVFWLIFSIMGVQFFGGRF	1203
QY	1450	FVCQGEDTRN-----ITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGVVDIMY	1504
DB	1204	PKCVDNNKERLPISIVQNRSECIQGYRWVNSDINFNLSNGFMALFOVATFEGWIEVMR	1263
QY	1505	DGLDAVGVDQQPINNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRHQHEE---	1560
DB	1264	DAVDAREVDQPSDGYNFSAYAYFVVFIIVGSFNTLNFIFIGVIDNFNRLKKQYEDFGAL	1323
QY	1561	---EEARRREKRLRLEKRRSKEKQMAEAOCKPYSDY---SRFRLLVHHLCTSHYL	1613
DB	1324	DVLLTPSORAWFGTIRKAATKPKKVISRPENSPMAWLFVDIHSRFFETLI-----	1374
QY	1614	DLFITGVIGLVNVTWAMEHYQQPQILDEALKICNYIFTVIVFVESVFKLVAFARRFFQD	1673
DB	1375	-MFF---ICLNILVMMIQHYGQKPAVEQALMIINLVFTGLFTLEAILRIVLRL-HYFRE	1429
QY	1674	RNQDLALVLLSIMGITLEEIEVNLSLPINFTIIRMRVLRIARVLLKLMQAVGMALL	1733
DB	1430	PMNVDFVIVVLSILGIILEHLEYELFITPSPF---VARFRIGRLLRFPYKAGKIRRL	1486
QY	1734	HTVMQALPQVGNLGLLFLMFLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFL	1793
DB	1487	FALLISLPALLNIGALLFLIMFIYAIIGMSSFGYVK-----KTGALDSVVNFETFGNSML	1541
QY	1794	TLFRVSTGDNWNGIMKD---PSRDCDQE-----STCYNTVISPIYFVSFVLTAQFVLVN	1844
DB	1542	LLFRLSTAGWNDVLKPLLLKPPDCDKLWCIPNGNCSTPWLAVVYFTTFTFLIINI	1601
QY	1845	VVIAVLMKHLEESNKEAEAELEAELEEMKTLSPQSPHSPGLSPFPGVEGVNSTDSP	1904
DB	1602	MYIAIILENLSQAH-EQEEVGVTDDDLDMFY-----YHWERFD-----	1638
QY	1905	KPGAPHTTAHGAASGF--SLEHPTMVPHPEE-----VPVPLGPDLLTVRKSGVSRTH	1955
DB	1639	-PGATQYIPH-SALSDFDVGLDHLRLIPQPNKFACINLNIPIKQG-----DRVH	1685
QY	1956	SLPNDSYMCRN--GSTAERSLGRGWGLPKAQSGSILSVHSQPADTSCILQLPK	2007
DB	1686	CFDVMQALVRRVLGDIEDGLG-----SSSVAYTLMKSKMEQHCISTEPK	1730

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively spliced)  
C;Species: Homo sapiens (man)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Sep-1998  
C;Accession: A42566  
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McQuinn, J.; et al.; Science 257, 389-395, 1992  
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type calcium channel alpha-1 chain  
A;Reference number: A42566; MUID:92335886; PMID:1321501  
A;Accession: A42566  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-2339 <WIL>  
A;Experimental source: IMR32, hippocampus  
A;Note: sequence extracted from NCBI backbone (NCBIP:109168)  
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.9%; Score 1676; DB 2; Length 2339;  
Best Local Similarity 24.0%; Pred. No. 6e-98;  
Matches 638; Conservative 364; Mismatches 827; Indels 824; Gaps 88;

QY	59	PGPGAAGAGSTEKDPGSADSEAGLPYPALAPV-----VFFYLSQDSRRPSWCLRT	109
DB	32	PGPGGLQPGQVLYKQSIQAQRARTWALYNPIPVKQNCFTVNRSLFVSESDNVVRKYAKRI	91
QY	110	VCNPFERFVSMVILLNCVTLMGFRPCEDIACDSQRCRIQAADD---FIFAFVEMVV	166
DB	92	TEWPPFEYMLATIIANCIVLAL-----EQHLPDGDKTPMSERLDDTEPYFIGFCFEAGI	147
QY	167	KMVALG-IPGKKCYLGDWTNRLLDFEIVIAGMLEYS---LDLQNVSFSAVRTVRVLRPLRA	222
DB	148	KIIALGFVFKHGSYLRNGWNVMDVYVVLVTGILATAGTDFDLR-----TLRAVRVLRPLKL	202
QY	223	INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVLWAGLLRNRCFLPENFSLP	282
DB	203	VSGIPSLQVVLKSIKAMVPLQLGLLFFAILMFAIIGLEFYMGKFHKAFC-----P	255
QY	283	LSVDLEPYQTENEDESPFICSPRENGMRSRVSPTLRGEGGGPPCSLDYETYNSSN	342
DB	256	NSTDAEPV-----GDFPCQKEAPARLCEGD	280
QY	343	TTCVNMNQYTNCSAGEHNPFKGAINDNIGYAWIAIFQVITLEGVVDIMYFVMD-AHSF	401
DB	281	TEC---REYWP-----GPNFGITNFDNLFALITVFCITMEGTDLTYNTNDAAGNT	330
QY	402	YNFIYFILLIIVGSFFMINCLVVIATQPSQKES-----QLMREQVRFLSNASTL	455
DB	331	WNWLYFIPLIIGSFFMLNLVLGVLSGEFAKERERVENRRAFLKLRQQQIE-----	382
QY	456	ASFSEPGSCYBEELLKYLVIILKAAARLAQVSRAGVRAIGLSSPVARSQGEPPSGSCT	515
DB	383	RELNGYLEWIFKAEVMLAED-----RNAEKSPLDVLK	417
QY	516	RSRRRLSVHHLVHHHHHHHHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS	575
DB	418	RAATKKSRLDIH-----AEEGEDRFAD-----	440
QY	576	GGPPRGAESVHSFYHADCHLEPVRQAPPPRCPSEASGRIVGSGKVYPTVHTSPPEILK	635
DB	441	-----	440
QY	636	DKALVEAPSPGPPTLTSFNIPPGPFSSMHKLLLETSQSTGACHSSCKISSPCSKADSGACG	695
DB	441	-----LCAVGSPPFARAS-----	452
QY	696	PDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAP	755
DB	453	-----LKSGKTESSSYF-----RRKEK-----	469
QY	756	SSVLAFLRLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALRISNIVF	815
DB	470	-----IRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTTLYFAEFVF	521
QY	816	TSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVG---QQGG---GLSVLRTRF	870

DB	522	LGLFLTEMSLKMVYGLGPRSYFRSSPFCDFGVIVGSVFVVWAAIKPGGSFGISVLRALR	581
QY	871	LMRVKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLIFITFSILGMHLFGCKFASERDG	930
DB	582	LLRIFKVTKYWSSRLNLVSVLLNSMKSIISLLFLFLFVIVFALLGMQLFGQGFQDET	641
QY	931	DTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIALMTFGN	985
DB	642	PT----TNFDTFPAAILTVFQILTGEDWNVAVMYHGIESQGVSKGMFSSFYFIVLTFLGN	697
QY	986	YVLFNLVAILVEGFAEGDATKSESEPDFFSPSVDGDKRKKRLALVALGEHAELRKS	1045
DB	698	YTLNVLFLAIVDNLANAQELTKDEEEMEEAA-----NQKLALQAKEVAEV--SP	746
QY	1046	LPPLIIHTAATPMSPKSSSTGVGEA-----	1071
DB	747	MSAANISIAARQONSAKARSVMQBRASQLRLQNLRASCEALYSEMDPEERLRFATTHLR	806
QY	1072	-----LGSGSRRRTSSSGSAEPGAA-----HH-----EMKCP-----	1097
DB	807	PDMKTHLDRPLVVELGRDARGPVGKGARPEAAEAPEGVDPPRRHHRHRDKKTPAAGDQ	866
QY	1098	-----PSARSS-----PHSPWSAASWTSSRSLGRAPSLKRRSPSGERSL	1142
DB	867	DRAEAPKAESGEPGAREERPRHRSHSKEAA--GPPEARSEGRGP-----GPEGGRHH	919
QY	1143	LSGEGQESQDEE-----ESSEEDRASPAAGSDHRRHRSLE--REAKSSFDLPDPTL	1189
DB	920	RRGSPPEAAEREPHRAHRHQDPSPKECAGAKGERRARRHRRGPRAGPREAESG-----	972
QY	1190	QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE	1238
DB	973	EEPARRHRAHKAQPAHEAVEKEETEKEAEIVEADKELRNHQPPEPHCDLETS	1032
QY	1239	GNLSKGERIQAWVRSRLPACCRER-----DSW-----	1265
DB	1033	GTVTVG-----MHTLPSTCLQKVEEQPEDADNQNRNVRMGSPDPDNTIVHIPVMTG	1086
QY	1266	-----SAYIFPPQSRFRLLCHRI	1283
DB	1087	PLGEATVVPNGVNDLESQAQKEVEADDMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI	1146
QY	1284	ITHKMFHDVVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVAL	1343
DB	1147	VTMRVFEVILVIALSSIALAEDP-VRTDSPRNNAKLYDYIFTGVFTFEMVIMKIDL	1205
QY	1344	GWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMV-SDSGTKILGMLRVLRLLRTRPLRV	1402
DB	1206	GLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRPLKT	1261
QY	1403	ISRAQGLKLVVETLMSLKLPIGNIVVICCAFFIIFGILGVQLFKGKFFVCCGE-----D	1456
DB	1262	IKRLPKLKAVIDCVVNSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELE	1321
QY	1457	TRN--ITNKSDCAEASYR-WVRHKYNFDNLQALMSLFVLASKDQWVDIMYDGLDAVGVD	1513
DB	1322	CRGGYLDYEKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE	1381
QY	1514	QQPIMHNPNWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQQEERREERKLRR	1573
DB	1382	QGPSGYRMELSIYVYVYVFPFVFFVNFVIFVALIITF-----QEQQDKVMSE---CS	1431
QY	1574	LEKRRSKEQMAEAQCKPYYSYSR--FRLLVHLCCTSHYLDLFTITGVLGNVVTMAME	1631
DB	1432	LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTTWTFVSPPEFFYFIMAMIALNTVVLMMK	1491
QY	1632	HYQQPQILDALKICNYIFTVVFVESVFKLVAFARFRFQDRWNQDLAIIVLLSIMGIT	1691
DB	1492	FYDAPYEYELMLKCLNIVFTSMFMECVLKIIAFGLVNLFRDAWNVDFVTVLGSITDIL	1551
QY	1692	LEEIE-----VNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMALLHTVMQALPQVGNL	1746

Db 1552 VTEIAETNNFINLS-----FLRLFRAARLIKLRQGYTIRILLMTFVQSFKALPYV 1602

QY 1747 GLLFMLEFFIPAAALGVLEFGLCEDETHPCEGLGRHATERNFGMAFLTLFRVSTGDNWNG 1806

Db 1603 CLLIAMLEFFIYAIIGMQVFGNIALDDD---TSINRHNNERTFLQALMLLFRSATGEAWHE 1659

QY 1807 IMKD--PSRDCQE--STCVNTVISPIYFVSFVLTAQFVLNVNVIATLKMHLKEESKEAK 1862

Db 1660 IMLSCLSNQACDEQANATECGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1719

QY 1863 -----EAELEAELE-----LEM-KTILSPQPHSLG-----SPFLWPGV 1895

Db 1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSp-----PLGLGKKCPARVAYKRL 1775

QY 1896 EGVNSTDSPKPGAPHTTAHIGASGFSLE-----HPTMVPHPEEVPV----- 1937

Db 1776 VRNMPISEDNMTVHTSTLMALIRTALEIKLAPQTKQHQCDAELRKEISVVWANLPQK 1835

QY 1938 -----PLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLHGRGWGLPKAQSGSIL 1990

Db 1836 TLDLLVPPHKDEMVTGVKYAA---LMIFDFY--KQNKTRDQMQAQGG--SQMGVPS 1888

QY 1991 SVH-----SQPA-----DTSCILQ-----LPKDVHYLLQ-----P 2015

Db 1889 LFHPLKATLEQTPAVLRGARVFLRQKSSTLSNGGAIQNESGIKESVSWQTQTDAP 1948

QY 2016 HGAPTWGAIPKPPGRSPLAQRPLRQAARTDSDLVQ-----GLGSRE 2060

Db 1949 HEA-----RPPLERGHSTEIPVGRSGAL---AVDVMQMSITRRQPDQEPQGLSQ 1997

QY 2061 DLLS--EVGSGCPLTRSSFWGSSIQVQORSQKSHIRLPAPCPGLEPSPWAKDP 2118

Db 1998 RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG-----THLCSTTP-----DRPP 2043

QY 2119 PETRS-----SLELDELWSIGDILLPSQEEPLFP-----RDL 2152

Db 2044 PSQASSHHHHHRCHRRDRKQRSLEKGFSLs-ADMDGAPSSAVGGLPPGEQPTQCRERR 2102

QY 2153 KKYSVETQSCRRRPGFWLDEQRHSAVSCLDGSGQRLCPSPS----- 2197

Db 2103 ERROGRSQERRQPSSSSEKQRF---YSCDRFGGREPPKPKPSLSHPTSPTAGQEPG 2159

QY 2198 -----SLGGQPL-----GGGSR---PKKLSLSP-PSIS-----IDPESQGS 2230

Db 2160 PHPGSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITYKTANSSPIHFAQAQTS 2219

QY 2231 RPPCSPG-----VCLRRRAPASD-----SKDPSVSSPLDSTAASPPKDKTLS 2273

Db 2220 LPAFSPGRLSRLGSLSEHALLQDPLSQPLAPGSRIGSDPYLQRLDSEASVHALPEDTLT 2279

QY 2274 L-----SGLSS 2279

Db 2280 FEEAVATNSGRSS 2292

RESULT 5

S29236

calcium channel protein BII-1, brain - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S29236

R:Nidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.

FEBS Lett. 308, 7-13, 1992

A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit b

A:Reference number: S29236; MUID:92354772; PMID:1379552

A:Accession: S29236

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2259 <NII>

A:Cross-references: UNIPROT:Q02343; EMBL:X67855; NID:g1472; PIDN:CAA48040.1; PID:g1473

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C:Keywords: transmembrane protein

Query Match 13.8%; Score 1665.5; DB 2; Length 2259;

Best Local Similarity 23.8%; Pred. No. 2.6e-97;

Matches 606; Conservative 379; Mismatches 844; Indels 719; Gaps 87;

QY 62 GAAGAGSTEKDPGSADS--EAEGLPYPALA-----PV----- 91

Db 5 GEAAAGRPASGEGSDSQGRNLPGTPVPASGSAAYKQSKAQRARTMALYNPIPVRQNCFT 64

QY 92 ---VFFYLSQDSRPSRWCLRTVCNPFERVSMLVILLNCVTLMFR--PCEDIAQDSQRC 146

Db 65 VNRSLFIFGEDNIVRYAKKLIDWPPFEYMLATIIANCIVLALAEQHLPEDDKTPMSRR- 123

QY 147 RILQAFDDFIFAFFAVEMVVMVALG-IFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQN 205

Db 124 --LEKTEPYFIGIFCFEAGIKIVALGFIFHKSYLRNGWVMDFIWVLSGILATAGTHFN 181

QY 206 --VSFSAVRTVRLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQ 263

Db 182 THVDLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLQLIGLLFFAILMFAIIGLE 241

QY 264 LWAGLLNRNRCFLPENFSLPLSVDLEPYQYQTENEDESPFICSPRENGMRSCRSVPTRLRGE 323

Db 242 FYSGKLHRACFVNN-----SGVLEGF-----DPPHPC----- 268

QY 324 GGGGPPCSLDYETVNSSNTTCVNWQYVYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVI 383

Db 269 --GVQGPCAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFOCI 306

QY 384 TLEGWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMR 442

Db 307 TMEGWTTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVGLVSGEFAKERERV----- 361

QY 443 EQRVRFSLNASTLASFSEPGSCYEELLYVILRKAARRLAQVSRAL-GVRAGLLSSPV 501

Db 362 ENRRAFMK-----LRRQQIERELNGYRAWIDKAE 392

QY 502 ARSQEQPQSGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGS 561

Db 393 VMLAENKNSGTSALEVLRAT-----IKRSRTEAMTRDSS-- 428

QY 562 RRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPPCPSEASGRTVSGKV 621

Db 429 ----- 428

QY 622 YPTVHTSPPPEILKDKALVEVAPSPGPPTLTSTFNIPPGFSSMHKLETSQSTGACHSSCK 681

Db 429 -----DEHCVDIS-----S 437

QY 682 ISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPH 741

Db 438 VGTPLARASIKSAKVDGASY-----FRHKE----- 462

QY 742 SRRRQSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQP 801

Db 463 -----RLLRISVRHAKSVQFYWIWVLSLVALNTACVAIVHNQP 501

QY 802 EELTNALIEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ--- 858

Db 502 QWLTHLLYYAEFLFLGLFLEMSLKMGMGPRLYFHSSFCDFGTVGSIFFVWVAIFR 561

QY 859 --QGGLSLVRLTRFLMRVLKLVRLPALQRLVLMKTMNDVATFCMLMLFIFIFSILG 916

Db 562 PGTSFGISVLRALRLRIFKITKYWASLRNLVLSLSSMSKSIISLLFLFLFIVFALLG 621

QY 917 MHLFGCKFASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLNGM-----ASTSS 971

Db 622 MOLFGGRF-NFNDG--TPSANFDTFPAAIMTVFQILTGEDWNVYNGIRSGQGVSSGM 677

QY 972 WAALYFIALMTFGNYVLFNLVAILVEGFQAEADATKSE-SEPDFS----- 1017

Db 678 WSAVYFIVLTFGNYYTLNVLFAIAVDNLANAQELTKDEQEEAEAFNQKHALQAKEVSP 737

QY 1018 -----PSVDGDGDRKKRLAL-----VALGEHAEL 1041





QY 331 SLDYETNSSNTTCVNWNOYVYNCNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVD 390  
Db 275 PAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGWT 314  
QY 391 IMYFVMDA-HSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQBSQLMRQVRFL 449  
Db 315 VLYNTDAGLATWNLWYFIPLIIGSFVNLVLGVLSGEFAKERERV-----ENRRAFM 369  
QY 450 SNASTLASFSEPGSCYEELLYLYVILRKAARRLAQVSRAI-GVRAGLLSSPVARSGQEP 508  
Db 370 K-----LRRQQIERELNGYRAWIDKAEVMLAEEN 400  
QY 509 QPSGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLEVPTRASPEIQDRANGSRRLMLPP 568  
Db 401 KNSGTSALEVLRAT-----IKRSRTEAMTRDSS----- 429  
QY 569 PSTPTSGGPRGAESVHSFYHADCHLEVPRCQAPPPRCPCSEASGRTVSGKVYPTVHTS 628  
Db 430 ----- 429  
QY 629 PPEILKDKALVEVAPSPGPPTLTLSFNIPPGPFSSMHKLLTQSTGACHSCKISSPCSK 688  
Db 430 -----DEHCVDIS-----SVGTPLAR 445  
QY 689 ADGACGPDSCPCYARTGAGEPESADHVPDSDSEAVYFTQDAQHSDLRDPHSRRQRS 748  
Db 446 ASIKSTKVDGASY-----FRHKE----- 463  
QY 749 LGPDAEPSSVLAFWRLLICTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPEELTNAL 808  
Db 464 -----RLLRISIRHMVKSQVFWYIVLSVVALNTACVAIVHNNQVQLTHLL 509  
QY 809 EISNIVFTSLFALEMLLKLIVGPPGYIKNPYNIFDGVIVVSVWEIVGQ-----QGGGL 863  
Db 510 YYAEFLFLGLFLEMSLKMGMGPRLYPHSSFCDFGVTVGSIFEVWVAIFRGTSGFI 569  
QY 864 SVLRTFRLMRVLKLVRELPALORQLVVLMTMDNVATFCMLLMFLFIFISILGMHLFGCK 923  
Db 570 SVLRALRLRIFKITKYWASLRNLVLSLSSMKSIISLLFLFLFIVFALLGMQLFGGR 629  
QY 924 FASERDGTLPDRKNPDSLLWAIVTVFQILTQEDWNKVLVNGM-----ASTSSWAALYFI 978  
Db 630 F-NFNDG---TPSANEDTTPAAIMTVFQILTGEDWNEVMYNGIRSGGVSSGMWSAIYFI 685  
QY 979 ALMTFGNYVLNLLVAILVEGFAEGDATKSE-SEPDFS-----P 1018  
Db 686 VLTLFNGYTLNVLFAVDNLANAQELTKDEQEEAEAFNQHALQAKEVSPMSAPNMP 745  
QY 1019 SVDGDGDRKKRLAL-----VALGEHAELRKSLLPP 1048  
Db 746 SIERDRRRHHMSMWEPRSSHLRERRRRHHMSVWEQRTSQLRRHMQSSQEALNKEBAPP 805  
QY 1049 LIHTAATPMS-----HP---KSSSTGVGEALGSGRRRTSSGSAEPGAHHEMKCPP 1098  
Db 806 MNPLNPLNPLNPLNPLNPLNPRPIEGLALGLGLEKCEEEERISRGSLKGDIGGLT 865  
QY 1099 SARSSPHSPWSAAS---SW-----TSRRSSRNSLGR 1126  
Db 866 SALDNQRSPLSLGKREPPWLPDRSCHGNCDP IQEAGGGETVVTTFEDRARHRQORRRHR 925  
QY 1127 APSLKRSPSGERRSLLSGEQESQDEEESSEEDRASPAAGSDHRRHRSGLEREAKSSFDL- 1185  
Db 926 RVRTEGKDSASASRS-RSASQERSLDEGVSVGEKEHEPHSSHRSKPTIHEERTQDLR 984  
QY 1186 -PDTLQVP---GL-----HRTASGRSSASEHQDCNGKSASGRL----- 1219  
Db 985 RTNSLMVPRGSLVGALDEAETPLVQPOPELVGKDAALTEQEAEGSEQALLGDVQLDV 1044  
QY 1220 -----ARTLRD-----DPQLD-----GDDNDNENLSKG 1244  
Db 1045 GRGISQSEBDLSGMTANMDKATTESTSVTVAIIPVDPLVDSTVVNISKNTDGEASPLKEA 1104  
QY 1245 E--RIQAVWVSRLPACCRERDSWSA-----YIFPPQSRFRLLCHRIITHQMFHDHVLV 1295

Db 1105 ETKEEEVEKKKKQKKEKRETKAMVPHSSMFISTTNPIRRACHYIVNLFYFEMCILL 1164  
QY 1296 IIFLNCITAMERP KIDPHSABRIFLTLNSYIFTAVFLAEMTVKVVALGWCFCGEQAYLRS 1355  
Db 1165 VIAASSIALAAEDPVLTNSEKRV-LRYFDYVFTGVFTFEMVIKIDQGLILQDGSYFRD 1223  
QY 1356 SWNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLTLRLPLRVISRAQGLKLWVE 1414  
Db 1224 LWNILDFVVVGALVAFALANALGNTKGRDIKTIKSLRVLRLPLTKIKRLPKLKAVFD 1283  
QY 1415 TLMSSLPKIGNIVVICCAFFIIFGILGVQLFKGKFFVC--QGEDTRN-----ITNKSDC 1466  
Db 1284 CVVTSLKNVFNILIVYKLFMPFIFAVIAVQLFKGKFFYCTDSSKDEKECIGNVYVDHEKNK 1343  
QY 1467 AEASYSR-WVRHKYNFDNLGOALMSLFLVASKDGWVDIMYDGLDAVGVDQQPIMNHNPMWL 1525  
Db 1344 MEVKGREWKREHFEHYDNI IWALLTLFTVSTGEGWPQVLQHSVDVTEEDRGPSRSRNMEMS 1403  
QY 1526 LYFISFLLIIVAFVNLVNVFVVENPHKCRHQHEEEARRRREKRLRLEKKRRSKEKQM 1585  
Db 1404 IFYVVYFVFPFVFVNFVALIIITF-----QEQDKMEE---CSLEKNERACIDFA 1453  
QY 1586 AEAQCKPYYSYSR--FRLLVHLCSTSHYLDLFTITGVIGLVNVTMAMEHYQOQOILDEAL 1643  
Db 1454 ISAKPLTRYMPQNRHTFQYRVVHFVVSFSEYTIMAMIALNTVVLMMKYTAPCTYELAL 1513  
QY 1644 KICNYIFTVIFVESVFKLVAFARFRFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPI 1703  
Db 1514 KYLNIAFTWVFSLECVLKVIAFGFLNPRDTWNIFDITVIGSITEIILTDKLVNTSGF 1573  
QY 1704 NPTIIRMRVLRARVLKLLKMAVGMRALLHTVMQALPOVGNLGLLMLLFFIFAALGVE 1763  
Db 1574 NMSFLKLFR--ABLIKLLRQGYTIRILLMTFVQSFKALPYVCLLIAMLFFIYAILGMQ 1630  
QY 1764 LFGDLECD-ETHPCGLGRHATERNFMAFLTLFRVSTGDNNNGIMKD--PSRDCDQEST 1820  
Db 1631 VFGNIKLEESH----INRHNFRSFFGSLMLLFRSATGEAWQEIIMLSCLGEKGCPEPDT 1686  
QY 1821 C-----YNTVISPIYFVSFVLTAQFVLNVVVIIVLAKHLEESKEAK-----E 1863  
Db 1687 APGQNESERCGTDLAVYFVSFIFFCFSLMLNLFVAVIMDNFELYLTRDSSILGPHHLDE 1746  
QY 1864 EAELEAELE-----LEMKTL-SPQHSPLG-----SPLWPGVEGVNSTDSP 1904  
Db 1747 FVRVMAEYDRAACGRIHYTEMYEMLTLMSP-----PLGLGKRCPSKVAYKRLVLMN----- 1797  
QY 1905 KPGAPHTTAH-----IGAASG-----FSLEHPTMV--PHPEE----- 1934  
Db 1798 MPVAEDMTVHFTSTLMALIRTALDIKIAKGGADRQQLDSELOKETLAIWPHLSQKMLDLL 1857  
QY 1935 VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRGWGLPKAQSGSILSVHS 1994  
Db 1858 VPMPKASD-LTVGKIYAA--MMIMDYKQSKVKQRQOL-----EEQXVAPMFQRM 1905  
QY 1995 QPADTSCILQLPKDV-----HYLLQPHGAPTWGAIPKLPPGRSPLAQRPRLRQAIR 2047  
Db 1906 EPS-----SLPQEI IANAKALPYLQD--PVSGLSGRSGYPSMSPLSPQEIFQLACM- 1955  
QY 2048 TDSLVDQGLSREDLLSEVSGPSCPL-----TRSSSFV----- 2080  
Db 1956 -DPADDGQFQEQQLV--VTDPSMRRSFSTIRDKRSNSSLWLEEFMSERSSENTYKRRR 2012  
QY 2081 -GGSSIQVQ-----QRSG-----IQSKVSKHIRLP--APC-----PGLPSW- 2114  
Db 2013 SYHSSRLSAHRLNSDSGHKSDTHRSGRGRGRSKERKHLSPDVSRCSNERGTQADWE 2072  
QY 2115 -----AKDPETRSLSLELDELTELWSIGDLLPSSQEEBPLFPRDLKKCYSVETQSCRRRPG 2168  
Db 2073 SPERRQSRSEGRSQTPNRQGTGSLSESSIPSISDSTPRRSRRLPPVPP---KPRPL 2129  
QY 2169 FWLDEQRHHSIAVCLDSGSGQPRCLCPSPSSLLGQPLGGFCGRPKK-LSPPSISIDPPES 2227



Db 2130 LSYSSLMRHTGGISPPPDGSE-----GGSPLASQALLESNSACLTESSNSLHPQOG 2179

Qy 2228 QGSRPP---CSPGVCLRRRAPASD 2248

Db 2180 QHPSPQHYISEPYLALHEDSHASD 2203

RESULT 7

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C;Species: Stylophora pistillata

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T43262

R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J

Gene 227, 157-167, 1999

A;Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylo

A;Reference number: 222375; MUID:99148007; PMID:10023047

A;Accession: T43262

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1891 <ZOC>

A;Cross-references: UNIPROT:O97017; EMBL:U64465; NID:G4204977; PID:G4204978; PIDN:AAD114

C;Genetics:

A;Gene: CACHL

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.7%; Score 1652.5; DB 2; Length 1891;

Best Local Similarity 24.8%; Pred. No. 1.4e-96;

Matches 523; Conservative 331; Mismatches 623; Indels 633; Gaps 60;

Qy 115 FERVMLVILLNCVTGLMFRPCEDIACDSQRCRILQAFDDIF-AFFAVEMVMVMALG- 172

Db 83 FDMILITIFANCAALAAFEPLPE--KDSSEINDNLEVAEYVFLAVFTMEAVLKIAYGF 140

Qy 173 IFGKKCYLGDWNRDLDFIVIAG----MLEYSLDLQNVSPSAVRTVRLRLRAINRVPS 228

Db 141 LFHPGAYLRNGWNILDFIVVVGATILVKATLSSGSFVKALRAFRVLRPLRVSGVPS 200

Qy 229 MRILVTLTLLDPLMGLNVLLLCFFVFFIFGIVGVQLWAGLNRNRCFLPENFSLPSVDLE 288

Db 201 LQVVLNSIIKALIPLFHIALLVFVVIYAIIGVELFMGRHKTCY--DNVTGAESEFE-E 257

Qy 289 PYYQTENEDESPFICSQPRENGMRSRCSVPTLRGEGGGGPPCSLDYETYNSSNTTCVNW 348

Db 258 PH-----PCS-----SGSSGFQCDKA 273

Qy 349 NOYITNCAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDA-HSFYNIYF 407

Db 274 AGQV--CEGGWKGPNHGITNFDNIGLACMTVFQCITLEGTDVLYWINDAVGNSWPVYF 331

Qy 408 ILLIIVGSFWMINCLVVIATQFSETKQ-----ESQLMREQR-----VRFLSNAS 453

Db 332 VTLLIIGSFFVLNLVLGVLGSEFAKARRQKSGEFQKREKQVEDAYNGYLDWITQAE 391

Qy 454 TLASFSEPGSCYEELLKYLVIILKAAARRLAQVSRIGVRAGLLSSPVARSGQEPQSGS 513

Db 392 DIEGDSSESGDES-----KASKK-----TSSRQRT-----EDIEM 423

Qy 514 CTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPT 573

Db 424 IDRNERQDSI-----SQDTHY----- 441

Qy 574 PSGGPPRGAEVSHSFYHADCHLEPVRCQAPPPRCPEASGRTVSGKVPTVHTSPPEI 633

Db 442 ----- 441

Qy 634 LKOKALVEAPSPGPTLTSTFNIPGPFSSMHKLLTQSTGACHSSCKISSPCSKADSGA 693

Db 442 -----GWCHNEKV----- 450

Qy 694 CGPDSCPYCARTGAGEPESADHVMPSDSEAVYEFTQDAQHSLDRDPHSRRRRQSLGPD 753

Db 451 -----LKKWHRRRQTE----- 461

Qy 754 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 813

Db 462 -----LRKAVKTOAFYWIIVVVFNSLTLELHYDQPDWLTAKFLDIANK 506

Qy 814 VFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVV-----ISVWEIVGQGGGLSVLRT 868

Db 507 LFLGIFTIEMIVKMYCLGFHGFASLFRNFRDCLVVISSLELAITEALKQPPIGISVLR 566

Qy 869 FRLMRVLKLVRLPALQRLVVLMTMDNVATFCMLLMFLIFIFISILGMHLFGCKFASER 928

Db 567 IRLLRIFKVTTRYWSSLSNLVASLNSMRISAGLLLLLSLFMLICSLLMQIFGGKF--NT 624

Qy 929 DGDTPDRKNFDSLLWAIVTVFQILTQEDWNKVLNGMAS-----TSSWAALYFIALM 981

Db 625 DDDEIP-RSNFDSFWRALITVFQILTGEDWNAVMDYDGIKAWGGIGEGGSAIALLYFIFLV 683

Qy 982 TFGNYVLFNLVAILVEGFQAEADATKSESEPDFFSPSDGDRKRLALVALGEHAEL 1041

Db 684 VVGNVILLNVFLAIAVDNLADAENLTEMEE-----KKKK-----EKARE 724

Qy 1042 RKSLLPPLIHTAATPMSPHPSSTGVGEALGSGRRRTSSSGSAEPGAHHKMPSPSAR 1101

Db 725 KEAL-----KMGSVDSQG-----RIDQDAIVPN----- 749

Qy 1102 SSPHSPWSAASWTSSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEDR 1161

Db 750 --HS-----SASRSNVTLDKSTQELHSTG----- 771

Qy 1162 ASPAGSDHHRGSLEREAKSSFDPDPTLQVPLHRTASGRSSASEHQDCNGKSASGRLAR 1221

Db 772 -----TLNGNVARTAS-----HDDVEAQS----- 791

Qy 1222 TLRTDDPOLDG-----DDNDENGLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRP 1276

Db 792 ---TDISEIVGSKSAVSNNSASASSDDID---RAPMP-----PESALFIFSPNTIF 839

Qy 1277 RLLCHRIITHKMFHDVVLVIIFLNCITIAMERPDKIDPHSABRIFLTLSNYIFTAVFLAEM 1336

Db 840 RVVCYKIATNTYFVNFILCLIIVSSILLAAEDP-LNASAKRNQVNLNYFDYFFTSVTFEI 898

Qy 1337 TVKVVALGWCFFGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILMLRVLRLRT 1396

Db 899 LVKFISYGLILHKGFCRFAFNLDLLVSVSVISISLR-----TSQFSVVRILRLRV 952

Qy 1397 LRPLRVISRAQGLKLVETLMSLKPIGNIVVICCAFFIFGILGVQLFKGKFFVCQGED 1456

Db 953 LRPLRAINRAKGLKHVVQSVFVAVKTIKLVTLMLFQFLFAVIGVQLFKGTFSCNDE- 1011

Qy 1457 TRNITNKSDCAEASY-----RWRHKNYFNLQALMSLVFLASKDGWV 1500

Db 1012 --KILTAEEC-QGNYIDFKGPGLSNPVVKERWRHRHDFNVDVGNAMLTFTVMTFEGWP 1068

Qy 1501 DIMYDGLDAVGVDQOQIMNHNPMWLLYFISFLLIVAFVFLNMVGVVVENFHKCRQHEE 1560

Db 1069 GILENSIDSTEVKGPNNQNRPMVAIYIIYIIIAFFMVNIFVGFVIVTF----- 1119

Qy 1561 EEARREKRLRRLEKRRRSKEKQMAEAQCKPYYSYDYSRFRLLVHHLCTSHYLDLFTGV 1620

Db 1120 -QSEGREBFKGCGLDKNQRCIEFALKAKPLKRYIPENRLQPHIWPVVTSAFEYLIFAF 1178

Qy 1621 IGLNVVTMAHEHYQQPQILDEALKICNYIFTVIFVESVFVKLVAFARRFFQDRWNQDL 1680

Db 1179 IVCNTVVLMMQYQEPKLYTRVLDGFNIGFTAVFLECLIKLIAFKPKNYFTDRWNLPDF 1238

Qy 1681 AIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRLHVTM--- 1737

Db 1239 IIVVGSIIDITMNEVSSEMQMFAFG-----FFRLFRALRLVKLLNQSGIKTLLWTFKSF 1293

Qy 1738 QALPQVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPCGLGRHATFRNFGMAFLTLFR 1797

Db 1294 QALPYV---ALLIVMFFIYAVIGMQMFGRIAINS-----TAINRNNNFQTFPQSLMVLFR 1347

QY	1798	VSTGDNWNGIMK-----DPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVVI	1847
Db	1348	SATGENWQOIMLACTHRDDVKDQADPQEPGLGSDFAFYFVSFISCSFLIINLFV	1407
QY	1848	AVLMKHLSESNKEAKEAELEAELEMKTSLPQPHSPLGSPFLWPGEVGNSTDSPKPG	1907
Db	1408	AVIMDNFDYLTRD-----WSILGPHHL---DEYVRVWSEYDPD	1442
QY	1908	APHTTAHGAASGFSLEHPTM-----VPHPEE---VPVPLGPDLLTVRKSGV-----	1951
Db	1443	AHGCVKHVDIVTVLKRIAPPLGFGKFCPHREACKRLVTMNMG-----LTKDGMVDFNATL	1497
QY	1952	-----SRTHSLPNDSYMCRNGSTAERSLGRGWGLPKAQSGSILSVHSQPADTSCILQL	2005
Db	1498	FGLIRSSLNKRPECKGSIDKANEVRNIILRIW--PKT-SMELLDKVVQPSGVRDDVTV	1554
QY	2006	PK-DVHYLLQ-----PHGAPTWGAIPKLP-PP-PGRSPLAQRPLRRQAA	2045
Db	1555	GKFYATYLIQYFRRFKARQKAQANEPHGNSITMALQAGLRTLHGLGPQLRRRAISGQLG	1614
QY	2046	I-----RTDSLVDVQGLGSRDILLSEVS-GPSCPLTRSSSF-----WGGSSIQVQQ	2089
Db	1615	SDDDELFLKEDDSQKAHDKGFWESLKSASVSPRHSFRSASFRLSAFLKGNGSGLETKK	1674
QY	2090	RSGIQSKVSK 2099	
Db	1675	KSSMSNLSE 1684	
RESULT 8			
S29237			
calcium channel protein BII-2, brain - rabbit			
C:Species: Oryctolagus cuniculus (domestic rabbit)			
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004			
C:Accession: S29237			
R:Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.			
FEBS Lett. 308, 7-13, 1992			
A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit h			
A:Reference number: S29236; MUID:92354772; PMID:1379552			
A:Accession: S29237			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-2178 <NII>			
A:Cross-references: UNIPROT:Q02343; EMBL:X67856; NID:g1474; PIDN:CAA48041.1; PID:g1475			
A:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
C:Keywords: transmembrane protein			
Query Match 13.7%; Score 1652.5; DB 2; Length 2178;			
Best Local Similarity 23.8%; Pred. No. 1.7e-96;			
Matches 601; Conservative 376; Mismatches 850; Indels 699; Gaps 83;			
QY	62	GAAGAGSTEKDPGSADS--EAEGLPYPALA-----PV-----	91
Db	5	GEAAAGRPASGEGDSQGRNLPGETVPVPSAGSAAAYKQSKAQRATIMALYNPIPVQRNCF	64
QY	92	---VFFYLSQDSRPRSWCLRTVCNPWFERSVLMVILLNCVTLGMFR--PCEDIACDQR	146
Db	65	VNRSLEIFGEDNIVRKYAKKLDWPPFYMILATIANCIVLALEQHLPEDDKTPMSRR-	123
QY	147	RILQAFDDFIAFFAVEMVVKMVALG-IFGKKCYLGDWTNRLDFFIVTAGMLEYSLDLQN	205
Db	124	--LEKTEPYFIFGFCFEAGIKIVALGFIFHKGSILRNGWNVMDFIVLSILATAGTFN	181
QY	206	--VSFSAVRTVRLRPLRAINRVPSMRILVTLLLDPLMLGNVLLICFFVFFIFGIVGVQ	263
Db	182	THVDLRLAVRVLRLPLKLVSGIPSLQIVLKSIMKAMVPLQIGLLFFAILMFAIIGLE	241
QY	264	LWAGLLNRNRCFLPENFSLPLSDLEPYQYQ TENEDSPFICQPRENGMFSRCSVPTLRGE	323
Db	242	FYSGKLHRACFVNN-----SGVLEGF-----DPPHPC-----	268
QY	324	GGGPPCSLDYETYNSSNTTCVNNNQYNTNCSAGEHNPFKGAINFDNIGYAWIAIFQVI	383

Db	269	--GVQCGPAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCI	306
QY	384	TLEGWVDIMYFVMDA-HSFYNPIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMR	442
Db	307	TMEGWTTVLNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLGSEFAKERERV-----	361
QY	443	EQRVRFSLNASTLASFSEPGSCYBELLKYLVIILRKAARRLAQVSRAI-GVRAGLLSSPV	501
Db	362	ENRRAFMK-----LRRQQIERELNGYRAWIDKAE	392
QY	502	ARSGQEPQPSGSCSTRSHRRLSVHHLVHHHHHHHHVHLNGTLRVPRASPEIQDRDANGS	561
Db	393	VMLAEENKNSGTSALEVLRAT-----IKRSRTEAMTRDSS--	428
QY	562	RRLMLPPSPPTPSGGPPRGAESVHSFYHADCHLEPVRQCAPPPRCPSSEASGRTVSGKV	621
Db	429	-----DEHCVDIS-----S	437
QY	682	ISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPPDSSEAVYEFTQDAQHSDLRDPH	741
Db	438	VGTPLARASIKSAKVDGASY-----FRHKE-----	462
QY	742	SRRRQSLGPDABPSSVLAFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIEVHEQP	801
Db	463	-----RLLRISVRHAVKSQFYWIIVLSLVALNTACVAIVHNQP	501
QY	802	BELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISWEIVGQ---	858
Db	502	QWLTHLLYYAEFLGLFLLEMSLKMVGMPRLYFHSSFCNCFDGVTVGSIFEVWALFR	561
QY	859	--QGGLSVLRTFRMLRVLKLVRFLPALQRLVVLKTMNDNVATFCMLLMFLFIFISILG	916
Db	562	PGTSFGISVLRALRLRIFKITKYWASLRNLVSLMSSMKSIISLLFLFLFIVVFALLG	621
QY	917	MHLFGCKFASERDGTLPDRKNFDSLLMAIVTVFQILTQEDWNKVLYNGM-----ASTSS	971
Db	622	MLFGGRF-NFNDG---TPSANFDTFPAAIMTVFQILTGEDMNEVMYNGIRSQGGVSSGM	677
QY	972	WAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSE-SEPDPFS-----	1017
Db	678	WSAVFIVLTLFGNYTLNLVFLAIAVDNLANAQELTKDEQEEEAFAFNQKHALQAKEVSP	737
QY	1018	-----PSVDGDGDRKKRLAL-----VALGEHAEL	1041
Db	738	MSAPNVPSIERDRRRRHMSMWEPRSSHLRERRRRHHMSVWEQRTSQLRRHMQSSQEAL	797
QY	1042	RKSLPLLIHTAATPMS--HPKSSSTGV-----GEALGSGRRRTSSSGSAEPGAHHE	1093
Db	798	NKEEAPPNNPLNPLNPLNPLNAHPSLYRRPRPMEGLALGLEKCEEHVSRGGSLLKGA	857
QY	1094	MKCPPS-----ARSSPHSPWSA-----ASSWT-----SRRSSRNSLGR	1126
Db	858	LDCQRSPLSLGRREP--PWLARPCGNCEPALQETAGGETVVTFFEDRARHRQSQRSSRHR	915
QY	1127	APSLKRSPSGERRSLLSGEGESQDEEESSEEDRASPGSDHRRGS-----LERE	1178
Db	916	RVRTEAKESSASRS-----RSVQSERSLDEGASTEGEDHEARGSHGCKEPTIHEEE	968
QY	1179	AKSSFDPDLPTLQVP-----GLHRTAS-----GRSSASEHQDCNKSASGRL--	1219
Db	969	RAQDLRRTDLSLMVPKSGLAGGLDEAGTPLVLSPEGVGKEAAPTEQHADGSGEPALLGH	1028
QY	1220	-----ARTLRDTPQL-----DGDDDDNDE-----GNLSKGE--	1245
Db	1029	VQLDVGRAISQSEPDLSCVTATTDKVTTESTDVTVAIPDAEPLVDSTVVHIGNKTDGEAS	1088
QY	1246	-----RIQAWVRSLPACCRERDSWSA-YIFPPQSRFRLLCHRIITHKMFHDHV	1292
Db	1089	PFOEAMKEABQETEKQKKKERPASGKAMVPHSSMFIPTSTNPIRRACHYVNVNRYFEMC	1148



QY 737 LRDPHSRRQRSLGPDAPSSVLAFWRLLCDTFRKIVDSKYFCRGIMAILVNTLSMGIE 796  
Db 465 -----RRKEK-----MRF-----IRMVKAQSFYVWVLCVVALNTLCVAMV 502  
QY 797 YHEQBELTNALEISNIVTSLPALEMLLKLVLVGPFGYIKNPYNIPDGVIVVISVWEIV 856  
Db 503 HYNQPORLTTALYFAEFVLGLFLEMLSKMYGLGPRSYFRSSFCDFGVIVGSIFEVV 562  
QY 857 GQ-----QGGLSVLRTFRMRVLKLVRLPALQRLVLMKTMNDVATFCMLLMFLFIFI 911  
Db 563 WAAIKPCTSGISVLRALRLRIKFKVTKYWNSLRNLVSLNSMKSIISLLFLFLFIVV 622  
QY 912 FSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIWVVFQILTQEDWNKVLYNGM----- 966  
Db 623 FALLGMQLFGGFNFQDETPT-----TIFDTFPAALITVFQILTGEDWNAVMYHGIESQGG 678  
QY 967 ASTSSWAAIFYALMTFGNYVLNLLVAILVEGFOAEGDATKSESEPDFFSPSVDDGDR 1026  
Db 679 VSKGMFSSFFIVLTTFGNVTLNVLFLAIVDNLANAQELTKDEEEMEEAA----- 729  
QY 1027 KKRLALVALGEHAELKSLPLLIHTAATPMHPKSSSTGVGEALGSGR----- 1077  
Db 730 NOKLALQAKEVAE-----VSPMSAANISIAAQNSAKARSVWEQASQLRLQNLRASCE 784  
QY 1078 -----RTSSSGSAEPGAAHH-----EMKCPPSARSPPHSPWSAASS 1113  
Db 785 ALYSEMDPEERLYASTHRVRPDMKTHMDRPLVVEPGDGLRGPVGSKSKPEGTEATESA 844  
QY 1114 WTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASP-----A 1165  
Db 845 DLPRRHRHR--DRDKTSATAPAG-----GEQDRTETETGPREERARPRRSHKETP 895  
QY 1166 GSD-----HRRHGSLE----- 1176  
Db 896 GADTVQRCERSRRHRRSGPEATEREPRCHRAHRHAQSSKEGTVPLVPKGBERRARHR 955  
QY 1177 -----REAKSPD-----LPDTLQVPLGHRAS-----GRSSASEHQDCNG 1212  
Db 956 GPRTGPREAENBEPTRRHRARHKVPPTLQPP--EREAESKNPVEGDKETRHNQPKPE 1013  
QY 1213 KSASGLART-----LRDTPQLDGDND----- 1237  
Db 1014 HCDLEAIAVTVGLHMLPSTCLQVDEQEDADNQRNVTRMGSPSDPSTTVHVPVTLT 1073  
QY 1238 -----EGNL-----SKGER-----IQAWVRSRLPACCRERDSWSAYIFPPQSR 1275  
Db 1074 GPPGETPVVPSGNMLEGQAEGKKEAEADVLRRGPRPIVPS-----SMFCLSPNTL 1126  
QY 1276 FRLLCHRIITHKMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAE 1335  
Db 1127 FRFCHYIVTMRYLEMVILVIALSSIALAAEDP-VRTDSFRNALALEMDYIFTGVPTCE 1185  
QY 1336 MTVKVVALGWCFCGEQAVLRSSWNVDGLLVLSVIDILVSMV-SDSGTKILGMLRLVRL 1394  
Db 1186 MVIKMIDLGLLHPGAYFRDLWNILD-----FIVVSGALVAFESGSKGKDINTIKSLRVL 1241  
QY 1395 RTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGLGVQLFKGKFFVCOG 1454  
Db 1242 RVLRPLKTIKRLPKLPVFDVSVNSLKNVLNLIIVMLFMFIFAIVAVQLFKGKFFYCTD 1301  
QY 1455 E-----DTRN--ITNKSDCAEASYR-WVRHKYNFDNLGOALMSLVFLASKDGWVDIMVD 1505  
Db 1302 ESKELERDCRGQYLDYEKEVEEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKH 1361  
QY 1506 GLDVGVDQOPIMNHNPNWMLLYFISFLLIYAFVFLNMFVGVVVENHKKRQHOREEARR 1565  
Db 1362 SVDATYEEQGSPSGFRMELSILYVYFVVFPPFFVNFVALIIITF-----QEQQDKVM 1415  
QY 1566 REEKRLRLEKRRSKEKQMAEAQCKPYYSYSR--FRLLVHLCTSHYDLFITGVIGL 1623  
Db 1416 SE----CSLEKNERACIDFAISAKPLTRYMPQNQSQFYKTTWTVVSPPFYFIMAMIAL 1471  
QY 1624 NVVTWAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQLDLAIV 1683

Db 1472 NTVVLMKFDYDAPYEYELMLKCLNIVFTSMFSEMECILKIIAFGLVNLFRDAMNVDFVTV 1531  
QY 1684 LLSIMGITLEEIE-----VNLSPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQ 1738  
Db 1532 LGSITDILVTEIAETNNFINLS-----FLRLFRAARLIKLLRQGYTIRILLWTFVQ 1582  
QY 1739 ALPOVGNLGLLFFLFFFAALGVLEFGLDECDETHPCCEGLGRHATERNFMAFLTLFRV 1798  
Db 1583 SFKALPYVCLLIAMLFFIYAIIGMQVFGNSALDDD---TSINRHNHNFRTFLQAIMLLFRS 1639  
QY 1799 STGDNWNGIMKD--PSRDCD---QESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKH 1853  
Db 1640 ATGEAWHEIMLSCLDNACDPHANASEC-GSDFAFYFVSFIFLCSFLMLNLFVAVIMDN 1698  
QY 1854 LEESNKEAK-----EEAELEAELE-----LEM-KTLSPOPHSPLG----- 1887  
Db 1699 FEYLTRDSSILGPHHLDEFIRVWAEYDPAACGRISYNDMEMLKHMSP---PLGLGKKC 1754  
QY 1888 -SPFLWPGEVGNSTSPKPGAPHTTAHIGAASGFSLEHPTWVPHPPEVPVPLGP-DLLT 1945  
Db 1755 PARVAYKRLVRNMNMPISNEDMTVHTSTLMALIRTALE-----IKLAPADEMT 1802  
QY 1946 V-----RKSQVSRTHSLPNDSYMCRNGSTAEERSLCHRGWGLPKAQSGSIL 1990  
Db 1803 VGKVAALMIFDYKQNKTRDQTHQAPG-----GL--SQMGPV 1840  
QY 1991 SVHSQPADTSCILQLPKDVHLLQPHGAPTGAIPKLPFGSPPLAQR---PLRRQAIR 2047  
Db 1841 LFHPLKAT-----LEQTQPAVLRG-----RVFLRQKSATSLNSGGAIQ 1879  
QY 2048 TDSLVDVQGLGR-----EDLLSEVSGP-----SCPLTRSSSFVGGSSIQVQOR 2090  
Db 1880 T-----QESGSRSCPGRRGTQDALYEGRAPLERDHSKEIPVQS---GTLVVDVQM 1930  
QY 2091 S-----GIQS--KVSKHIRLPA---PCPGLEP-----SWA 2115  
Db 1931 NMTLRGPDGDPQGLSQGRAASMLRLAAETQAPNAPSPMKRSISTLAPRPGDTQLCSTV 1990  
QY 2116 KDPP-----ETRSSLELDE---LSWISGDLPLPSSQEEPLF 2148  
Db 1991 LDRPPPSQASHHHHRCHRRRDKKQRSLEKGPVSLVDPEGAPSTAAAGPGLPHGEGSTAC 2050  
QY 2149 PRDLKKCYSVETQSCRRRPGFWLDEQRRHSTAVSC--LDGSGQPRLCPSPS----- 2197  
Db 2051 RRDRKQERGRSQE--RRQPSSSSEKQRF---YSCDRLGAGS-PQLMPFSLSSHPTSPAAA 2104  
QY 2198 -----SLGGQPL-----GGPSRPPKKLSP-PSIS-----IDPPE 2226  
Db 2105 LEPAPHPQSGSVNGSPLMSTSGAITPGRGRRQLPQTPLTPRPSITYKTANSSPVHFAE 2164  
QY 2227 SQGSRPPCSPG-----VCLRRRAPASD-----SKOPSVSSPLDSTAASPSPK 2269  
Db 2165 GQSGLPAPFSPGRLSRGLSEHNALLQKEPLSQPLAPGSRIGSDPYLGQRLDSEASHTLPE 2224  
QY 2270 DTLSL-----SGLSS 2279  
Db 2225 DTLTFEEAVATNSGRSS 2241

RESULT 10

A47447  
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)  
C;Species: Discopyge ommata  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A47447  
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.  
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993  
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Disc  
A;Reference number: A47447; MUID:93248175; PMID:7683405  
A;Accession: A47447  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA



A;Residues: 1-2223 <HOR>			
A;Cross-references: UNIPROT:P56699			
A;Note: sequence extracted from NCBI backbone (NCBIP:130671)			
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
Query Match 13.7%; Score 1642; DB 2; Length 2223;			
Best Local Similarity 24.0%; Pred. No. 8.1e-96;			
Matches 598; Conservative 373; Mismatches 841; Indels 682; Gaps 78;			
QY	37	RMERAPRSRDSPVASRSSTTCPPGGAAGAGSTEKDPGSADSBAGLPYPA-----LAPV	91
Db	21	RSRHQVPVTGETAVAAAAAAVAGAAQGSAGFKQTRAQARARTMALYNPIPVRHNCLTANR	80
QY	92	VFFYLSQDSRPRSCLRTVCNPFERVSMLVILLNCVTLMFR--PCEDIACDQSQRCL	149
Db	81	SLFLFGEDNIVRKSARRVIEWPPFEYMLATIIANCVVLALEQHLPNGD---KTPMAKSL	137
QY	150	QAFDDFIFAFFAVEMVVKWVALG-IFGKKCYLGDWTNRLDFFIVIAGMLEYSLDLQNVSF	208
Db	138	EQTEPYFIFGFEAGIKIVALGFVFKGSLRNGWNVMDFIVVLSGLL--ATAATHFNL	195
QY	209	SAVRTVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLCFVFFVIFGIVGVQLWAGL	268
Db	196	RTLRAVRVLRLKLVSGIPSLQIVLKSIMKAMVPLLOIGLLFFAILMFAIIGLEFYGK	255
QY	269	LRNRCFLPENPSLPLSVDLPEYYQTENEDESPFICSPRENGMRSCRVPTLRGGGGGP	328
Db	256	LHRTCYTDDAAABELDQF-----	274
QY	329	PCSLDYETYNSSNTTCVWNQYYTNCAGEHNPFKGAINDNIGYAWIAIQVITLEGW	388
Db	275	PCGTQEPTRLCNGTVCYSW-----IGPNDGITQFDNILFALLTVFQCITMEGW	323
QY	389	VDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVR	447
Db	324	TTILYNTDDALGAMWNWLYFIPLIIGSFVNLVGLVLSGEFAKERERV-----ENRRS	378
QY	448	FLSNASTLASFSEPGSCYEELLKYLVIIRKAARRLAQVSRAL-GVRAGLLSSPVARSQ	506
Db	379	FLK-----LRRQQIERELNGYRAWIDKAEVMLLE	409
QY	507	EPQPSGSCTRSH--RRLSVHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRL	564
Db	410	ENKNAGEKSALHLRRATIK-----KGRMEM-----IQTESSEDQ---444	
QY	565	MLPPSPSTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSQKVPYPT	624
Db	445	-----YTBISVGSPLARASIKS-----	462
QY	625	VHTSPPEILLKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISS	684
Db	463	-----TKLEGSS-----	470
QY	685	PCSKADSGACGPDSCPYCARTGAGEPESADHVMPSDSEAVYEFTQDAQHSDLRDPHSRR	744
Db	471	-----YFRR	474
QY	745	QRSLGPDABESSVLAFWRLICDTRFKIVDSKYFGRGIMTIALVNTLSMGIYHEQPEEL	804
Db	475	KERML-----RI---SIRHMVKSHAFYIWLGLVALNTVCVAVVHYDQPLWL	518
QY	805	TNALEISNIVFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIV-----GQQ	859
Db	519	SNFLYYAEFTFLGLFSSEMFLKMYGCGPRLYFHSSEFCDFCGVIIGSIFDVVWTTIRPET	578
QY	860	GGGLSVLRTFLRLRVLKLVRFLPALQQLVVLMTMDNVATFCMLLMFIFISILGMHL	919
Db	579	SFGISVLRALRLRIFKITKYWASLRNLVSLMSSMKSIISLLFLFLFVIVFALLGMQL	638
QY	920	FGCKFASERDGTLPDRKNFDSLLWAVTVFQILTQEDWNKVLNGMAS-----TSSWAA	974
Db	639	FGQFNFE--GTPP--TNFDTFPAALITVFQILTGEDMNEVNYNGIKSQGGVNSGMWSS	694
QY	975	LYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFSPVDGDRKKRLALVA	1034
Db	695	VYFIVLTLFGNYTLNVLNLAIVDNLANAQELTKSEQEEE-----EA	736
QY	1035	LGEHAELRKSLPLLIHTAATPMShPKSSST-----GVGEALGSGSRRTSSSGS	1084
Db	737	INQKHALQKA-----KEVSPMSAPGFPSTEREFRRHKHMSIWEARTSQLRRRQMSS	788
QY	1085	AE-----PAAAHHEMKCPPSARSSPHSPWSAASSWTSSRSRNSLGRAPSLKRRS---	1134
Db	789	REALFTDALQGLEGSRYRRHSRIFEASLRRLAEQAAESHQLEGEVGRREAFKSRSLRN	848
QY	1135	---PSG---ERRSLSGEQE---SQDEEESSEEDRASPDGSDHRRHRSLEAKSSFDL	1185
Db	849	SWOPAGPDKRSSSIKVNQEQGRALGRSVEAGASFRMAEPIRARRRYR-SLYKEAK--MGL	905
QY	1186	PDTLQVPLHRTASGRSSASEHQDCNGKSASGRLARTLRTDDPQ-----	1229
Db	906	EESAETSLSRPPGKNKEGRLLQQLCE-EQESGQLTOTPEVMDAQGMKAFSWQGEPHSSS	964
QY	1230	---LDGDDNDDEGNLSK-----GERIQA---WVRSRL-----	1255
Db	965	MTRTPDVTDPGGNLEKESGRTPENGKEESANTSEQVNEQSNWLNQLNQATPGDREL	1024
QY	1256	-----PACCRERDSWSAYIFFPQS	1274
Db	1025	TTGTRDTKQDKTQEOTEIDVDCENTETPMDSLVTPGNAYSSSSSVKDEKSKAIIPYS	1084
QY	1275	RF-----RLCHRITTHKMFHVVLVLIIFLNCITIAWERPKIDPHSAERIFLTLSNY	1326
Db	1085	MFLFRKTNPIRRVCHFIIVNLRYFEMCILLVIAASSVALAEDP-IHKDSARNQVLYFDY	1143
QY	1327	IFTAVFLAEMTVKVALGWCFGEQAYLRSSWNVLGLLVLISVIDI-LVSMVSDSGTKIL	1385
Db	1144	VFTGVFTFEMVIKIDIGLVFHEGSYFRDVMNILDIVVSGALVAFATNLIGSSGKDI	1203
QY	1386	GMLRVLRRLTLRPLRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLF	1445
Db	1204	NTIKSLRVLRPLKTIKRLPKLKAFCVDTSLKNVFNILVYKLFMFIFAIVAVQLF	1263
QY	1446	KGKFFVCQGEDTRNITNKSDCAEASRYRWVRHK-----YNFDNLGQALMSLFVL	1493
Db	1264	KGKFFYC--TDSSKMT-KQDC-RGQFVLYRQRTKLSIENGNTVTFHYDNVWVWALLTFTV	1319
QY	1494	ASKDGVDMYDGLDAVGVDQOQIPMHNHPWMLLYFISFLIVAFVFLNMFVGVVVENFHK	1553
Db	1320	STGEGWPQVLOHSVDVTEADQGPDPGNRMEMSIFYIVYVVFVPPFFVNFVVALIITP--	1377
QY	1554	CRHQHEEEARRREKRLRRLEKRRSKEKQMAEAQCKPYSDYSR--FRLLVHLCCTSH	1611
Db	1378	-----QEQGDKMLEES---SLEKNERACIDFAISAKPLTRYMPQNRQTFQYRVWQFVVS	1429
QY	1612	YLDLFTIGVIGLVNVTMAMEHYQOQILDEALKICNYIFTVIFVFESVFKLVAFAFRPF	1671
Db	1430	SFEYTLTMTALNTVVLMMKHSPPGFASVCLKMNIATFTTLECILKIIAFGFLNYF	1489
QY	1672	QDRWNQLDLAIVLLSIMGITLEEIE--VNLSLPINPTIIRIMRVLRIRARVLKLLKMAVG	1728
Db	1490	RDSNVVDFVTVVGSISEIIVTECNLKFNLS-----FLKLFRAARLIKLLRQGIT	1540
QY	1729	MRALLHTVMQALPOVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNF	1788
Db	1541	IRILLWTVQSFKALPYVCLLIAMLFFIYAIIGMQLFNGNLGDDHTP---INRHNHFTF	1597
QY	1789	GMAFTLFRVSTGDNWNGIMKD--PSRDCD--QESTCVNTVISPIYFVSFVLTAQFVLVN	1844
Db	1598	FNALMLLFRSATGESWQEIACLKSGKECEGTREPSG-GTDVAYFYFVSFIFLCSFLMLN	1656
QY	1845	VIAVLMKHLEESNKEAK-----BEAELEAELE-----LEMKTL-SQOPH	1883
Db	1657	LFVAVIMDNFEYLTRDSSILGPHHLDDEFVRVWAEYDRAACGRHYTDMYQMLTLMSP---	1713
QY	1884	SPIGSPFLWPGV-----EGVNSTDSKPKGAPHTTAHIGAASGFSLEHPT	1927



Db	1714	PLGLGKCPKSVAYKRLVLMNMPVTEKTVHFT-STLMGLIRLTALQIKLARGGA-----	1766
Qy	1928	MVPHPEVPVPLGPDLLTVRKSGVSRTHSL--PNDSYMCNRNGSTAESLGHGWLGPKAQ	1985
Db	1767	---DKQQLDAELRKEIMTIWPHLSQKTLDLLVPMHTY-----SDLTVG-----KIY	1809
Qy	1986	SGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGAIPKLPPLPGRSPLAQR---PLR	2041
Db	1810	AAMIMDYKQSKNKKYQKLQEB-----QSRTPMFORMEASSLP	1848
Qy	2042	QAAAIRTDLDV--QGLGSRREDLLSEVSGPCLTRSSSFVGGSSIQVQORSGIOQKVS	2099
Db	1849	PQIISSTKGLPYLQGTGPDVDSRSEFT-PLVPLPPVMFQQGRTSSQGEIHKQRPKEL	1907
Qy	2100	HIRLPAP-----CPGLEPSWAKDPPETRSSLEL-----DTLSWISGDLL	2139
Db	1908	KIKLEYPHYGHYLPNIENQRAVSMRPLEIESAEDTSLKRSLSLTFEAAHNSNLTWNEYS	1967
Qy	2140	PSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRHSAVSCLDGSGPRLCPSSSL	2199
Db	1968	-----ERAGPEDLYKRW-----RRP-----LRP-----PSRSSN	1992
Qy	2200	GGQPLGGPGSRPKKLSPPSISI-----DPPESEQ-----SRPPCSPGVCLRRRAPAS	2247
Db	1993	AGSRRG-RSRRKHLLSPERSVCSTGCAHPSQHRGLDQLRSRP-SPGYSHRPREQVN	2050
Qy	2248	DSKDPVSVPDSTAAASPKKDTLSLSGLSSDP	2281
Db	2051	SSVS---ESPVPSSSGTSPPKQGRQLPQTPSKP	2081
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N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human			
C:Species: Homo sapiens (man)			
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004			
C:Accession: T45115			
R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC			
Science 257, 389-395, 1992			
A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type			
A:Reference number: A42566; MUID:92335886; PMID:1321501			
A:Accession: T45115			
A:Status: preliminary; translated from GB/EMBL/DBD			
A:Molecule type: mRNA			
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A:Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g1797			
A:Experimental source: cell line IMR32; neuroblastoma			
C:Genetics:			
A:Note: CCHL1A2			
C:Function:			
A:Description: calcium influx			
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
Query Match 13.6%; Score 1640.5; DB 2; Length 2237;			
Best Local Similarity 23.5%; Pred. No. 1e-95;			
Matches 614; Conservative 350; Mismatches 815; Indels 839; Gaps 82;			
Qy	59	PGPGAAGAGSTKOPGSADEAGLPPALAPV-----VFFYLSQDSRPSRWCLRT	109
Db	32	PGPGGLQPGQRLYKQSIQARARTMALNPIPVKQNCFTVNRSLFVFESEDNVVRKYAKRI	91
Qy	110	VCNPFERVSMLVILLNCVTILGMFRPCEDIACSQRCLILQAFDD---FIFAFFAVEMVV	166
Db	92	TEWPPFEYMLATIIANCIIVLAL-----EQHLPDGDKTPMSERLDDTEPYFIFGFCFEAGI	147
Qy	167	KWVALG-IFGKCYLGDVTNRDLDFIVIAGMLEYS---LDLQNVSFSAVTRVRLPLRA	222
Db	148	KIIALGFVFKGSLRNGVNMDFVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL	202
Qy	223	INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLP	282
Db	203	VSGIPSLQVVLKSIKMAVPLQLQIGLLFFAILMFAIGLEFYMGKFHKACF-----P	255

Qy	283	LSVDLEPYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSDLTYETNSSN	342
Db	256	NSTDAPV-----GDFPCGKEAPARLCEGD	280
Qy	343	TTCVNWNQYVYTNCSAGEHNPFGKAINFDNIGYAMIAIFQVITLEGWVDIMYFVMD-AHSF	401
Db	281	TEC---REYWP-----GNFGITNFDNILFAILTVFCITMEGTDLTYNTNDAAGNT	330
Qy	402	YNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRFLSNASTL	455
Db	331	WNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENRRAFLKLRQQQIE-----	382
Qy	456	ASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAGLLSSPVARSQEQPSPSGSCT	515
Db	383	RELNGYLEWIFKAEVMLAED-----RNAEEKSPLDVLK	417
Qy	516	RSRRRLSVHLLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS	575
Db	418	RAATKKSRLDLH-----AEEGEDRFAD-----	440
Qy	576	GGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSASGRIVGSGKVPTVHTSPPEILK	635
Db	441	-----	440
Qy	636	DKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLLTETQSTGACHSSCKISSPCKADSGACG	695
Db	441	-----LCAVGSPFFARAS-----	452
Qy	696	PDSCPYCARTGAGEPESADHVPDSDSEAVVEFTQDAHQHSLDRDPHSRRRQORSLGPDAP	755
Db	453	-----LKSGTSSSYF-----RRKEK-----	469
Qy	756	SSVLAFWRLLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVF	815
Db	470	-----MRRFF-----IRRWKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTTLTYFAEFV	521
Qy	816	TSLFALEMLLKLIVGPFYKPNYNIFDGVIVVISVWEIVGQ-----QGGGLSVLRTR	870
Db	522	LGLFTEMSLKMYGLGRSFRSSFCDFGVIVGVFVVVWAAIKPGSSFGISVLRALR	581
Qy	871	LMRVLKLVRFLPALQQLVVLMTMDNVATFCMLMLFIFIFISILGMHLFGCKFASERDG	930
Db	582	LLRIFKVTKYWSSRLNVVSLNSMKSIISLLFLFLFVIVFALLGMQLFGGQNFQDET	641
Qy	931	DTLPDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALFYIALMTFGN	985
Db	642	PT-----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFFIVLTLFGN	697
Qy	986	YVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSVDGDGRKRLALVALGEHAELRKS	1045
Db	698	YTLNVFLAIAVDNLANAQELTKDEEMEEAA-----NQKLALQKAKEVAEV--SP	746
Qy	1046	LPPLIIHTAATPMSPKSSSTGVGEA-----	1071
Db	747	MSAANISIAARQONSAKARSVWEQRAQLRLQNLRASCEALYSEMDPEERLRFATTRHLR	806
Qy	1072	-----LGSGSRRTSSSGSAEPGAA-----HH-----EMKCP-----	1097
Db	807	PDMKTHLDRPLVVELGRDARGPVGKARPEAAEAPGVDPPRRHRRHRDKDKTAAAGDQ	866
Qy	1098	-----PSARSS-----PHSPWSAASSWTSRRSSNSLGRAPSLKRRSPSGERRSL	1142
Db	867	DRAEAPKAESGEPGAREERPRHRSKSEA--GPPEARSERGRGP-----GPEGGRHH	919
Qy	1143	LSGEGQESQDEE-----ESSEEDRASPAQSDHRRHRSLE---REAKSSFDLPD	1189
Db	920	RRGSPPEAAERPRRHRHRHQDPSPKECAGKGERARRHRRGGPRAGPREAESG-----	972
Qy	1190	QVPG-LHRTASGRSSASE--HQDCNGKSSASGRLA-----RTLRTDDPQLDGD	1238
Db	973	EEPARRHRARHKAQPAHEAVEKETEKATEKEAEIVEADKEKELRNHQPREPHCDLETS	1032

QY 1239 GNLSKGERIQAWRSRLPACCRER-----DSW----- 1265  
Db 1033 GTVTGVP-----MHTLPSTCLQKVEQPEDADNQNVNTRMGSPQDPNTIVHIPVMLTG 1086  
QY 1266 -----SAVIFPPQSRFRLLCHRI 1283  
Db 1087 PLGEATVVPNGVDLESQAEGKEVEADVMRSGRPPIVPYSSMFCLSPTNLLRRFCHVI 1146  
QY 1284 ITHKMFHVVIVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1343  
Db 1147 VTMRYFEVVLVIALSSIALAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVIKMDL 1205  
QY 1344 GWCFGQAYLBSSWNVDGLLVLSVIDILVMV-SDSGTKILGMLRVLRLRLRPLRV 1402  
Db 1206 GLLHPGAYFRDLWNILD----FIVVSGALVAFAPSGSGKGDINTIKSLRVLRLPLKT 1261  
QY 1403 ISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE-----D 1456  
Db 1262 IKRLPKLKA VDCVNSLKNVLNILVYMLFMFIFAIVAQVLFKGFYCTDESKELERD 1321  
QY 1457 TRN--ITNKSQCAEASR-WVRHKYNFEDNLGQALMSFLVLASKDGVWDIMYDGLDAVGVD 1513  
Db 1322 CRGQYLDYEXEVEAQRQWKYDFHYDNVWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381  
QY 1514 QQPIMNHNPMMLLYFISFLLI VAFVNLNMFVGVVVENFHKCRQHQEAEARRRREKRLRR 1573  
Db 1382 QGSPSGYRMEISIFYVVVFVFFNFIFVALIITF-----QEGDKVMSE-----CS 1431  
QY 1574 LEKRRSKEQMAEAOCKPYYSYSR--FRLLVHHLCTSHVLDLFTIGVIGLNVVTNAME 1631  
Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491  
QY 1632 HYQPOILDEALKICNIYIFTVIFVESVFKLVAFARFRFFQDRWNQDLAIIVLLSIMGIT 1691  
Db 1492 FYDAPYEYELMKCLNIVFTSMFMECVLKIIAFGLVNLFRDANWVDFVTVLGSIIDIL 1551  
QY 1692 LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMALLHTVMQALPOVGNL 1746  
Db 1552 VTEIAETNNFINLS-----FLRLFRAARLIKLLRQGYTIRILLTWFVQSFKALPYV 1602  
QY 1747 GLLFMLFFIIPAALGVELFGDLECEHPCGLRGRHATFRNFGMAFLTFRVSTGDNWNG 1806  
Db 1603 CLLIAMLFFIYAIIGMQVFGNIALDDD--TSINRHNFRFLQALMLLFRSATGEAWHE 1659  
QY 1807 IMKD--PSRDCQE--STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLM----- 1851  
Db 1660 IMLSCLSNQACDEQANATECGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1719  
QY 1852 ----KHEE----- 1856  
Db 1720 ILGPHHLDDEFIRVWAEYDPAACGRISYNDMFEMLKMSPPLGLGKKCPARVAYKRLVRMN 1779  
QY 1857 -----SNKEAKEAELEAEL-----ELEMKTLS- 1879  
Db 1780 MPISNEDMTVHTSTLMALIRTALEIKLAPAGTKHQCDABLKEISVVWANLPQKTLDL 1839  
QY 1880 -POPHSP----LGSPF----LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVP 1930  
Db 1840 LVPHPKPDGMTVKVYAALMIFDFYKQNKTRDQMQAQPGLSQMGPVSLF---HPLKAT 1896  
QY 1931 HPEEVPVPL-GPDLITVRKSGVSRTHSLPNDSYMCNRNGSTAEERSLHGRGWGLPKAQSGSI 1989  
Db 1897 LEQTQPAVLRGARVFLRQKST---SLNGGAIQNESGIKESV---SWGTRQTDQ-- 1947  
QY 1990 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTGWGAIPLKPPGRSPLAQRPLRRQAARTD 2049  
Db 1948 -----PHEA-----RPPLERGHSTEIPVGRSGALAVD 1974  
QY 2050 -----SLDVQGLGSRDILLSEVSGPSCPLTRSSSFWGSSSIQVQORSQ 2092  
Db 1975 VOMQSI TRRGPDGEPQPGLESQG---RAASMPRLAAETOPVTDASPMKRSISTLAQRPRG 2031  
QY 2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS-----SLEDTELWSWIS 2135

Db 2032 -----THLCSTTP-----DRPPFSQASSHHHHRRCHRRDRKQORSLEKGPSLS-AD 2076  
QY 2136 GDLLPSSQEEPLFP-----RDLKKCYSVETQSCRRRRPGFWLDEQRRHSIAVSClds 2186  
Db 2077 MDGAPSSAVGPGGLPPGEGPTGCRERERRQERGRSQERRQPSSSSEKQRF---YSCDRF 2133  
QY 2187 GSQ--PRLCPSPPSSSLGGQPLGG--PGSRPK-----KKLSP-----PSISIDPPESQ-- 2228  
Db 2134 GGREPPKPKPSLSSHPTSTPTAGQEPGHPQAGSAVGFPNTTTPCCRETSPASWPWLALELA 2193  
QY 2229 -----GS-----RPPCSPGVCLRRRAPASDSKDPSSVSP 2257  
Db 2194 LTLTWGSMVTVRPLSTP--CLTRSLSRRLWPPTRAAP 2229  
  
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C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 24-Sep-1999  
C;Accession: B54972  
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil  
J. Biol. Chem. 269, 22347-22357, 1994  
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel  
A;Reference number: A54972; MUID:94350992; PMID:8071363  
A;Accession: B54972  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-2251 <WIL>  
A;Cross-references: GB:L29384; NID:G495867; PIDN:AAAS9204.1; PID:G495868  
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Query Match 13.6%; Score 1638; DB 2; Length 2251;  
Best Local Similarity 23.7%; Pred. No. 1.5e-95;  
Matches 600; Conservative 391; Mismatches 818; Indels 724; Gaps 86;  
  
QY 73 PGSADSEA-----EGLPYPALA-----PV-----VFFY 95  
Db 12 PGSGDGDSDQSRNRQGTVPASGQAAAYKQTKAQRARTMALYNPIVRQNCFTVNRSLFI 71  
QY 96 LSQDSRPRSWCLRTVCNPFERVSMLVILLNCVTGLMFR--PCEDIACDQSQRILQAFD 153  
Db 72 FGEDNIVRYAKKLLIDWPPFEYMIATIANCIVLALEQHLPEDDDKTPMSRR---LEKTE 128  
QY 154 DFIFAFFAVEMVVKWVALG-IFGKKCYLGDWTNRLDFFIVIAGMLEYSLDLQN--VSFSA 210  
Db 129 PYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHENTHVDLRT 188  
QY 211 VRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLR 270  
Db 189 LRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLIQIGLLFFAILMFAIIGLEFYSGKLH 248  
QY 271 NRCFLPENFSLPLSDVLEPYQYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGGPPC 330  
Db 249 RACFMNN-----SGILEGF-----DPPHPC-----GVQGC 273  
QY 331 SLDYETYNSSSNTTCVNNQYITNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVD 390  
Db 274 PAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGWTT 313  
QY 391 IMYFVMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFL 449  
Db 314 VLYNTNDALGATWNWLYFIPLIIIGSFVFLNLVLGSLGEPAKERERV-----ENRAAFM 368  
QY 450 SNASTLASPSEPGSCYEELLKYLVIILRKAARLAQVSRAT-GVRAGLLSSPVARSQEP 508  
Db 369 K-----LRRQQQIERELNGYRAWIDKAEVVMLEEN 399  
QY 509 QPSGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPP 568  
Db 400 KNAGTSALEVLRRAT-----IKRSRTAMTRDSS----- 428

QY 569 PSTPTSGGPRGAESVHSFYHADCHLEPVRQOAPPPRCPSSEASGRVTGSGKVYPTVHTS 628  
Db 429 -----  
QY 629 PPEILKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISSPCSK 688  
Db 429 -----DEHCVDIS-----SVGTPLAR 444  
QY 689 ADGACGDPSCPYCARTGAGEPESADHVMPPDSBAVYEFTQDAQHSLDRDPHSRRQRS 748  
Db 445 ASIKSAKVDGVSY-----FRHKE----- 462  
QY 749 LGPDAEPSSVLAFWRLICDTFRKIYVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNAL 808  
Db 463 -----RLLRISIRHMVKSQFYWIVLSLVALNTACVAIVHHNQPOWLTHLL 508  
QY 809 EISNIVFTSLFALEMLLKLLVYGPFGYIKPNYNIFDGVIVVSVWEIVGQ-----QGGGL 863  
Db 509 YAEFLFLGLELLEMSLKMGMGPRLYFHSSFCNCFDGVTVGSIFEVVWAIFRPGTSFGI 568  
QY 864 SVLRTFRMLMRVLKVRFLPALQRLVVLMTMDNVATFCMLMLFIFIFISILGMHLFGCK 923  
Db 569 SVLRALRLRIFKITKYWASLRNLVSLMSSMKSIISLLFLFLFIVV FALLGMQLFGGR 628  
QY 924 FASERDGDTLPRKKNFDSLLWAIVTVFQILTQEDWNKVLNMG-----ASTSSWAALYFI 978  
Db 629 F-NFNDG---TPSANFDTTPAAIMTVFQILTGEDWNEVMYNGIRSGGVSSGWSAISYFI 684  
QY 979 ALMTFGNYVLNLLVAILVEGFAEGDATKSE-SEPDPS-----P 1018  
Db 685 VLTFLGNYTLLNVFLAIAVDNLANAQELTKDEQEEEAFAFNQKHALQAKAVEPSMSPANMP 744  
QY 1019 SVDGDDGRKKRLALVALGEHAELRKSL-----LPPLIIHTAATPM-S 1059  
Db 745 SIERERRRRHMS-VWEQRTSQLRKHMOMSSQEALNREEAPTWNPLNPLNLSLNPLNA 803  
QY 1060 HP-----KSSSTGV-----GEALGSGSRTS-----SSGSAEPG 1088  
Db 804 HPSLYRRPRAIEGLALGLALEKFEERISRGSLKGDGDRSSALDNQRTPLSLQOREPP 863  
QY 1089 --AAHEMKCPPSARSSPHSPWSAASWTSSRNLSGRAPSLKRRSPSGERRLLSGE 1146  
Db 864 WLAPPCGNCPTQOE- -GGGEAVTFEDRARHRQSRRS---RHRVRTEGKSSAS 918  
QY 1147 QGESQDEEESSEEDRASPDSDHRRG-----SLEREAKSSFDLPDTLQVPLHRTAS 1199  
Db 919 RSRASQERSLDEAMPTGEKDHELRCNHGAKEPTIQEERAQDLRRTNSLMVSRGSLAG 978  
QY 1200 GRSSAS-----EHQDCNGKSASGLAR-----T 1222  
Db 979 GLDEADTPLVLPHPELEVCKHVVLTEQEPEGSEQALLGNVQDMGRVISQSEPDLSCT 1038  
QY 1223 LRTD-----DPQLDG-----DDNDEGNLSK 1243  
Db 1039 ANTDRKATTESTSVTVAIPVDPLVDSTVVHISNKTIDGEASPLKEAREDEEEVEKKQK 1098  
QY 1244 GERIQAWVRSLRPACCRERDSWSAYIFPPQSRFLCHRIITHKMFHVVVLIIFLNCIT 1303  
Db 1099 KEKRETG-KAMVPHS-----SMFIFSTTNPIRRACHYIVNLRYFEMCILLVIAASSIA 1150  
QY 1304 IAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVL DGL 1363  
Db 1151 LAEEDPVLNTERNKV-LRYFDYVFTGVFTFEMVTKMIDQGLIQLDGSYFRDLWNILDFV 1209  
QY 1364 LVLIISVIDI-LVSMVSDSGTKILGMLRLVRLRLTRPLRVISRAOGLKLVVETLMSLKP 1422  
Db 1210 VVVGALVAFALANALGNTKGRDINKTIKSLRVLRLVRLPLTKIKRLPKLKA VDFCVVTSKN 1269  
QY 1423 IGNIVVICCAFFIIFGILGVQLFKGFFVC--QGEDFTN-----ITNKSDCAEASR-W 1473  
Db 1270 VFNILIVYKLFMFIFAVIAVQLFKGFFYCTDSSKDTEKECIGNYVDHEKNKMEVKGREW 1329  
QY 1474 VRHKYNFDNLGQALMSLFLVALSKDGWVDIMYDGLDAVGVDQQPIMNHNPNWMLLYFISFLL 1533

Db 1330 KRHEFYDNIWALLTLFTVSTGEGWPQVLQHSVDVTEEDRGPSRNRMEMSIFYVVYFV 1389  
QY 1534 IVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRLRLLEKKRRSKEKQMAEAQCKPY 1593  
Db 1390 VFPFFVNFVALIITF-----QEQGDKWME--CSLEKNERACIDFAISAKPLTR 1439  
QY 1594 YSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLVNVTWAMEHYQQPQILDEALKICNYIFT 1651  
Db 1440 YMPQNRHTFYRVWHFVVSPEYTIMAMIALNTVLMMKYISAPCTYELALKYLNIAFT 1499  
QY 1652 VIFVFESVKLAVAFARRFFQDRWNQDLAI VLLSIMGITLEEIEVNLSLPINPTIIRIM 1711  
Db 1500 MVFSLECVLKVIAFGFLNYFRDTWNIFDFTVIGSITEILLTDSKLVNTSGFNMSFLKLF 1559  
QY 1712 RVLRIARVLKLLKMAVGMRALLHTVMQALPOVGNLGLLPMLLFFIFAALGVFLFGDLECD 1771  
Db 1560 RA---ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVFGNIKLD 1616  
QY 1772 -ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNNWNGMKD--PSRDCDQESTC----- 1821  
Db 1617 EESH---INRHNFRSFFGSLMLLFRSATGEAWQEI MLSCGKGCPEPTTAPSGQEN 1672  
QY 1822 --YNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLSESNKEAK-----EEAELEAEL 1871  
Db 1673 ERCGTDLAYVYVFSFIFFCFSLMLNLFVAVIMDNFXYLTRDSSILGPHHLDEFVRVWAEY 1732  
QY 1872 E-----LEMKTL-SPQPHSLG-----SPFLWPGEVGNSTDSPKPGAPHTT 1912  
Db 1733 DRAACGRIHYTEMVEMLTLMSP---PLGLGKRCPSKVAYKRLVLMN---MPVAEDMT 1783  
QY 1913 AH-----IGAASG-----FSLEHPTMV--PHPEE-----VPVPLGPD 1942  
Db 1784 VHTSTLMALIRTALDIKIAKGGADROQLDSELOKETTLAIWPHLSQKMLDLLVPMPKASD 1843  
QY 1943 LLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRGWGLPKAQSGSILSVHSQPADTSCI 2002  
Db 1844 -LTVGKIYAA--NMIMDYKQSKVKKQKQQL-----EEQKNAPMFQRMES----- 1886  
QY 2003 LQLPKDV-----HYLLOPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSDLVQG 2055  
Db 1887 -SLPQEIIANAKALPYLOD---PVSGLSGRSGYPSMSPLSPQDIFQLACM--DPADDGQ 1940  
QY 2056 LGSREDLLSEVGPSCPL-----TRSSFWGGSSIOVQQRSGIQSKVSKHIRLPAPC 2107  
Db 1941 FOERQSLV--VTDPSNMRRSFSTIRDKRNSW-----LEEFSEMERSS----- 1981  
QY 2108 PGLPESWAKDPPETRSLELDT-ELSWIG---DLLPSSQEEPLFRDLKKCYSVETQSC 2163  
Db 1982 ---ENTYKSRRRSYHSSLSLAHRLNSDSGHKSDTHPSGGRERRRRKXERKHLSPDVSR 2038  
QY 2164 ---RRRPGFWLDEQRHRSIAVCLDSGSPRLCPSPSSLGQPLGGPSRPPKKLSPPS 2219  
Db 2039 NSEERGTDQADWESPERRQS-----RSPSEGRSQTPNRQGTGSLSESSIPS 2083  
QY 2220 IS--IDPPESQGSRRPPCSPG-----VCLRRRA-----PASDSKD--PSVSSPLDSTAA 2263  
Db 2084 VSDTSTPRSRRLPPVPKPRPLLSYSSLIHAGSISPPADGSEGSPLTSQALESNNA 2143  
QY 2264 -----SPSPKK 2269  
Db 2144 WLTESSNSPHPQQ 2156

RESULT 13  
A54972

voltage-dependent calcium channel alpha 1E-3 - human  
C;Species: Homo sapiens (man)

C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004

C;Accession: A54972

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil  
J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A;Reference number: A54972; MUID:94350992; PMID:8071363  
A;Accession: A54972  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2270 <WIL>  
A;Cross-references: UNIPROT:Q15878; GB:L29385; NID:9495869; PIDN:AAA59205.1; PID:9495870  
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.6%; Score 1637.5; DB 2; Length 2270;  
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Matches 601; Conservative 394; Mismatches 815; Indels 741; Gaps 87;

QY	73	PGSADSEA-----EGLPYPALA-----PV-----VFFY 95
DB	12	PGSGDSDQSRNRQGTVPASGQAAAYKQTKAQRARTMALYNPIPVQRNCFTVNRSLFI 71
QY	96	LSQDSRPRSWCLRTVCNPFVERVSMVLILLNCVTLMFR--PCEDIACDQRCLQAFD 153
DB	72	FGEDNIVRKYAKKLIDWPPFEYMIATIANCIVLALEQHLPEDDKTPMSRR---LEKTE 128
QY	154	DFIFAFFAVEMVVKQVALG-IFGKKCYLGDWTNRLDFFIVTAGMLEYSLDLQN--VSFSA 210
DB	129	PYFIGIFCFEAGIKIVALGFIFHKGYLRNGWNVMDFIVLSGILATAGTHENTHVDLRT 188
QY	211	VRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLR 270
DB	189	LRAVRVLRPLKLVGIPSLQIVLKSIMKAMVPLLOIGLLLPAILMFAIIGLEFYSGKLH 248
QY	271	NRCFLPENFSLPLSDLEPYQOTENEDESPFCISQPRENGMRSCRSVPTLRGEGGGPPC 330
DB	249	RACFMNN-----SGILEGF-----DPPHPC-----GVQGC 273
QY	331	SLDYETYNSSNTTCVNNQYNTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVD 390
DB	274	PAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGWT 313
QY	391	IMYFVMDA-HSFYNFIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQRVFL 449
DB	314	VLYNTNDALGATWNWLYFIPLIIGSFVNLVGLVSGEFAKERERV-----ENRRAFM 368
QY	450	SNASTLASFSEPGSCYEEELLKYLVIILRKAARLAQVSRAT-CVRAGLLSSPVARSQEP 508
DB	369	K-----LRRQQQIERELNGYRAWIDKAEVVMLEEN 399
QY	509	QPSGSCTRSHRRLSVHHLVHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRLMLPP 568
DB	400	KNAGTSALEVLRRAT-----IKRSRTAMTRDSS----- 428
QY	569	PSTPTPSGGPPRGAESVHSFYHADCHLEPVRCAQPPRCPSASGRTVGSGKVPTVHTS 628
DB	429	----- 428
QY	629	PPPEILKDALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCSK 688
DB	429	-----DEHCVDIS-----SVGTPLAR 444
QY	689	ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS 748
DB	445	ASIKSAKVDGSY-----FRHKE----- 462
QY	749	LGPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL 808
DB	463	-----RLLRISIRHMVKSQVFWYIIVLSLVALNTACVAIVHNPQWMLTHLL 508
QY	809	EISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGIIVVISVWEIVGQ-----QGGGL 863
DB	509	YAEFLFLGLFLEMSLKMVGMPRLYFHSFNCFCDFGVTVGSIFEVVAIFRPGTSPGI 568
QY	864	SVLRTFRLMRVLKLVRLPALQRLVVLMTMDNVATFCMLMLFIFIFSILGMHLPGCK 923
DB	569	SVLRALRLLRIFKITKYWASLRNLVLSMSMKSIISLLFLFLFVIVFALLGMQLFGGR 628
QY	924	FASERDGDTLPRKQNFDSLILWAIIVTVFQILTQEDWNKVLNMG-----ASTSSWAALYFI 978

DB	629	F-NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMMWSAIYFI 684
QY	979	ALMTFGNYVLEFNLVAILVEGFOAEGDATKSE-SEPDFFS-----P 1018
DB	685	VLTLFGNYTLLNVFLAIAVDNLANAQELTKDEQEEEAFAFNQKHALQKAKEVSPMSAPNMP 744
QY	1019	SVDGDGDRKKRLAL-----VALGEH--AELRKSIL----- 1045
DB	745	SIERDRRRRHMSWEPSSHLRERRRRHHMSVWEQRTSLRKHQMSSQEALNREEAPT 804
QY	1046	---LPPLIHTAATPM-SHP-----KSSSTGV-----GEALGSGSRRRT 1079
DB	805	MNPLNPLNPLSSLNPLNAHPSLYRRPRAIEGLALGLEKFEERISRGSLKGDGDRS 864
QY	1080	S-----SSGSAEPG--AAHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAP 1128
DB	865	SALDNQRTPLSLGQREPPWLARPCHGNCDDPTQEA--GGGEAVVTTFEDRARHRQSRRS- 921
QY	1129	SLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRRHG-----SLEREAKS 1181
DB	922	--RHRRVRTECKESSASRSRSASQERSLDEAMPTEGEKDHELGNHGAKEPTIQEERAQ 979
QY	1182	SFDLPDTLQVPGHLHRTASGRSSAS-----EHQDCNGKSASGLAR-- 1221
DB	980	DLRRTNSLMVSRGSLAGGLDEADTPLVLPHPHELEVGHVVLTEQEPESSEQALLGNVQ 1039
QY	1222	-----TLRTD-----DPQLDG----- 1232
DB	1040	LDMGRVISQSEPDLSCTANTDKATTESTSVTVAIPDVPDLVDSTVVHISNKTDGEASPL 1099
QY	1233	-----DDNDEGNLSKGERIQAWVRSLRPACCRERDSWSAYIFPPQSRFRLLCHRIIT 1285
DB	1100	KEABIREDEEEVEKKQKKEKRETC-KAMVPHS-----SMFISTTNPIRRACHYIVN 1151
QY	1286	HKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNVIPTAVFLAEMTVKVVALGW 1345
DB	1152	LRYPFEMCILLVIAASSIALAAEDPVLTNSEKRV-LRYFDYVFTGVFTFEMVIKMDQGL 1210
QY	1346	CFGEQAYLRSSWNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLTLRLPLRVIS 1404
DB	1211	ILQDGSYFRDLWNILDFVVVVGALVAFALANALGNTKGRDIKTKSLRVLRLPLKTIK 1270
QY	1405	RAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFGKFFVC--QGEDTRN--- 1459
DB	1271	RLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFGKFFYCTDSSKOTEKECI 1330
QY	1460	---ITNKSDCAEASR-WVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDVGVDQ 1515
DB	1331	GNVVDHEKXKMEVKGREWKREHFEYDNIWALLTLFTVSTGEGWPQVLQHSVDVTEEDRG 1390
QY	1516	PIMNHNPMWLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEBARRRERKRLRLE 1575
DB	1391	PSRSNRMEMSIFYVVYFVVPFFVFVNIIFVALIITF-----QEQQDKMMEE---CSLE 1440
QY	1576	KKRRSKEKQMAEAQCKPYYSYSR--FRLLVHHLCTSHYLDLFTGTGVLNVVTMAMEHY 1633
DB	1441	KNERACIDPAISAKPLTRYMPQNRHTFYRVVWHFVVSFPEYTIMAMIALNTVLMMKYY 1500
QY	1634	QQPQILDEALKICNYIFTVIFVESVFKLVAFARRFFQDRWNQLDLAIVLLSIMGITLE 1693
DB	1501	SAPCTYELAKYLNIAFTWVFSLECVLKVIAFGFLNYFRDTWNIFDFTVIGSITEIILT 1560
QY	1694	EIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRRALLHTVMOALPOVGNLGLLMLL 1753
DB	1561	DSKLVTNSGFNMSFLKLFR---ARLKLRLQGYTIRILLTWVQSFKALPYVCLLIAML 1617
QY	1754	FFIFAALGVLEFGDLECD-ETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD-- 1810
DB	1618	FFIYAIIGVQVGNIKLDEESH-----INRHNFRSFFGSLMLLFRSATGEAWQEIMLSCL 1673
QY	1811	PSRDCDQESTC-----YNTVISPIYFVSFVLTAQFVLNVNVIIVLMLKHEESNKEA 1861



Db	1674	GEKCEPDTAPSGQNERCGHDLAYVYFVSFIFFCSFLMLNLFVAVIMDNFEYLTRDS	1733
QY	1862	K-----EEAELEAELE-----LEMKTL-SPQHPSPLG-----SPFLWPG	1894
Db	1734	SILGPHHLDEFVRVWAEYDRAACGRHYHTEMYEMLTILMSP----PLGLGKRCPSKVAYKR	1789
QY	1895	VEGVNSTDSPKPGAPHTTAH-----IGAASG-----FSLEHPTMV--P	1930
Db	1790	LVLNM-----MPVAEDMTVHTSTLMALIRTALDIKIAKGADRQQLDSELQKETLAIWP	1844
QY	1931	HPEE-----VPVPLGPDLLTVRKSGVSRTHSLPNDSYNCRNGSTAERSLGRHWGLPKA	1984
Db	1845	HLSQKMLDLLVPMPKASD-LTVGKIYAA---MMIMDYKQSKVKQKQQL-----EE	1892
QY	1985	QSGSILSVHSQPADTSCILQPKDV-----HYLQPHGAPTWGAIPKLPDPGRSPLAQ	2037
Db	1893	QKNAPMFORMEPS-----SLPOEIIANAKALPYLOQD---PVSGLSGRSGYPSMSPLSP	1943
QY	2038	RPLRRQAIRTDSLDVQGLGSRREDLLSEVSGPSCPL-----TRSSFWGSSSIQVQQ	2089
Db	1944	QDIFQLACM--DPADDGQFOERQSLV--VTDPSMRRSFSTIRKRSNSW-----LEE	1993
QY	2090	RSGIQSKVKSHIRLPAPCPGLEPSWAKDPPETRSSLELDT-ELSWISG---DLLPSSQEE	2145
Db	1994	FSMERSS-----ENTYKSRRRSYHSSRLSAHRLNSDSGHKSDTHPSGGRE	2039
QY	2146	PLFPRDLKKCYSVETQSC---RRRPGFWLDEQRRHSIAVSCLDGSGQPRLCSPSSLGG	2201
Db	2040	RRRSKERKHLSPDVSRNCNSEERGTCQADWESPERRQS-----RSPSEGRS	2084
QY	2202	QPLGGPGSRPKKLSPPSIS--IDPPESQGSRRPPCSPG-----VCLRRRA-----PAS	2247
Db	2085	QTPNRQGTGSLSESSIPSVSDTSTPRRSRRQLPPVPPKPRPLLSSYSSLIRHAGSISPPAD	2144
QY	2248	DSKD--PSVSSPLDSTAA-----SPSPKK 2269	
Db	2145	GSEEGSPLTQALSNNAWLTESSNSPHPQQ 2175	
RESULT 14			
T30902			
sodium channel SCAP1 alpha chain - California sea hare			
C;Species: Aplysia californica (California sea hare)			
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004			
C;Accession: T30902			
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.			
DNA Cell Biol. 16, 347-356, 1997			
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.			
A;Reference number: T20929; MUID:97238630; PMID:9115644			
A;Accession: T30902			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-1993 <DYE>			
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474			
C;Superfamily: sodium channel protein			
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Best Local Similarity 25.8%; Pred. No. 1.7e-95;			
Matches 518; Conservative 348; Mismatches 702; Indels 442; Gaps 69;			
QY	94	FYLSQDSRPRSWCLRTVCNPFWRVSMVLVLLNCVTLM--FRPCEDIACDSORCILQA	151
Db	119	FLLSFPNPIIRIAIYILVHPIFSLVMVTILVNCVFAITSYTP-----PA	164
QY	152	FDDFIF-AFFAVEMVMVMVALGIFGKK-CYLGDWTNRLDFFIV-IAGMLEYSLDLQNVSF	208
Db	165	FVEHIFLGIYTVAAVVKVLSRGFVLKPFYTLRDPWNWLDFFVISIAYMTMTVTKSFGNL--	222
QY	209	SAVRTVRLRPLRAINRVPSMRILVTLTLDLTPMLGNVLLLCFFVFFIFGIVGVQLWAGL	268
Db	223	QALRTFRVLRAKTTISVIPGLKTIIVGALLEAVRRLRDMILTVFLSIFALIGMQLYSGA	282
QY	269	LNRCFLPENFSLPLS-----VDLEPYQTENEDESPFICSQPRENGMRSCRSVPT	319

Db	283	LRQKCVLNPVPELGTNITHDEWNDVNNESHQKDFYDEWQ-VC-----	325
QY	320	LRGEGGGPPCSLDYETYNSSNTTCV--WNQYYTNCAGEHNPKGAINFDNIGYAWIA	378
Db	326	--GNGTGAGKCG--NGTINGTAEWLCLPNIGQ-----NPNHDTSFDFNFGMALLC	371
QY	379	IFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRES	438
Db	372	AFRLMTQDFWESLYHLVLRVAVGSAHCLYFVLVILLGSLYVLLNLLAIIVAMSDET-QKQD	430
QY	439	QLMREQVRFLSNASTLASFSFPGSCYEELLYVILRKAARLA-QVSRAGVRAGLL	497
Db	431	QADAEAEA-----AERQE-----EEARKEALSIMTKSPSNSWNNDFEAGVR----	472
QY	498	SSPVARSQEQPQSGSCTRSHRRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRD	557
Db	473	--TAGDKAEKERLSLTSDSATSATSAHLKPSRLNQKRH-----SLSLP-GSPYIHRRN	521
QY	558	ANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPCSEASGRTVG	617
Db	522	SRGSQYSWRKPVPTAKRS-----PYCPDR-----	545
QY	618	SGKYVPTVHTSPPEILKDKALVEVAPSPGPPTLTSF---NIPPG---PFSSMHKLET	670
Db	546	QLVHHTLENLPLP-FADDSA--TPSSEDLCNFSFIRNPNRGRFASFASQRRPDGT	600
QY	671	QSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGE-----PESA-D	714
Db	601	GRSGRRSS--FASNHSRASRTSRG-----SGQDRTKTQTLNLFKKGVDPVVD	649
QY	715	HVMDSDSEAVYEFTQDAQHSDLRDPHSRRR---QRSLGPDAPESPSSVLA-----	760
Db	650	KSKLDDDDQDSV--SSGSGHCPEKDKASEGNFSLSHSPGGPNVEMKDVMLDKILDQASG	707
QY	761	-----FWRLIC-----DTRFKI-----VDSKYFGRGIMIAILVN	789
Db	708	HRRSFVSMTSIHQRTMKDIMWKYFCTWDCHEPNFQKQLRVLVSFIMDAFVDLITICILVN	767
QY	790	TLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIV	849
Db	768	TAFVAMEHYDMEDDLKAVSNAANLVFTAFAVEAFKILALSPVIYFKDGNIFDSIIVA	827
QY	850	ISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLQVLVLMKTMNDVATFCMLLMLEI	909
Db	828	LSLMELSMTKLPGLSVLRAFRLLRVFKLAKSWPTLNMLIAIVGRTMGALNLIIVLGIIL	887
QY	910	FIFSILGMHLFGCKFAS-ERD-----GDTLPDRKNFDSLWALVIVTFQILTQEDW	958
Db	888	FIFAVMGQQLFSSDYKTYEREIDAAGNVTINKDKMP-RWNFNDFLHSMIVFVRLVCGE-W	945
QY	959	NKVLNGMASTSSWAAL-YFIALMTFGNYVLFNLVAILVEGFQAEQ-DATKSESEPDEF	1016
Db	946	IESMW-GCYLVSGWACVPFLLTYVGNLVNLFLALLSSFGSESLQSRSESDDEPSKI	1004
QY	1017	SPSVDDGDRKKRLA-----LVALGEHAELRKSLLPPLIHTAATPMSPKSSSTGVG	1069
Db	1005	AEAI-----DRFKRFGNWKVILVICIKVQLQKQKWRPP-----PTTGQS	1045
QY	1070	EALGSGSRRTSSSGSAEPGAHHEMKCPPSARSSPHSPWSAASWTSRRSRNSLGRAPS	1129
Db	1046	EVNG-----KDPVVVDGTVVSMKTPDDFPDGPCCPAQAIC-----	1082
QY	1130	LKRRSPGERRLLSGEGQESQDEESESSEEDRASAGSDHRHGRGSLEREAKSFDLPDTL	1189
Db	1083	-----SAKKOLKSPSGS-HSNSGS-----	1100
QY	1190	QVPGLHRTASGRSSASEHQDCNGKSASGRLARLTLDTPQLDGGDDNDEGNLSKGERIOA	1249
Db	1101	-----SHCSSCSLSESAQTKKID---LEADHEINEVEI-----V	1132
QY	1250	WVR-----SRLPACCRERDS-----WSAYIFPPQSRFRLLCHRIITHKMFHDVV	1293



Db 1133 YVKEPDDCFYMCYTKRCPWCVCVKVKSIGRAWWA-----VRCFFYRLTENKYFDSFI 1184

Qy 1294 LVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEQAYL 1353

Db 1185 IAMILASSCALEDAYLHEKPILKEILEYLDKVFTAIFIEMLIKWLA----FGFKTYF 1240

Qy 1354 RSSWNVLDGLVLISVIDILVSM-VSDSGTKILGMLRLVRLRLTLRPLRVISRAOGLKLV 1412

Db 1241 TDAWCWLDFIVMLSIIVLVADLTASEEGGSMWSMKSMRTLRALRPLRAVSRWEGRVV 1300

Qy 1413 VETLMSLLPIGNIVVICCAFFIIFGILGVQLFKGKFFVQGE-----DTRNITNKS DCA 1467

Db 1301 VNALFKAIPSI CNVLLVCLVFWLIFGIMGVQLFNGKFHACRDEKGDXYPREEVNKTVCI 1360

Qy 1468 EASYRWTRHKYNFDNLGQALMSLFVLASKDGVVDIMYDGLDAVGVDQQPIMNHNPMWMLLY 1527

Db 1361 DKGYNWTAQINFHDVLSAYLALFQVATYKGMIDIMNNAIDSTEIGQQPSREENVIMYLF 1420

Qy 1528 FISFLIVAFVFLNMFVGVVVENFH--KCRQHQEEEEEARREERKRLRRLRLEKRRSKEKQM 1585

Db 1421 FVLFI VFCSPFTNLNFIGVNIENFNSQKKAGGSLEMFMTEDQKKYNAMKRMQSKSPQ- 1479

Qy 1586 AEAQCKPYSDYSRFRLLVHLCCTSHVLDLFTIGVIGLVNVTWAMEHYQQPQLDEALKI 1645

Db 1480 -KSI PRPKY---KLAGLIFDITTDQKFDIAIMVILMLTMMFEHHGMSAQMKNILGI 1534

Qy 1646 CNYIFTVIFVESVFKLVAFAPRRFFQDRWNQDLALVLLSIMGITLEEIEVNLSLPINP 1705

Db 1535 FNLIFITITAE CVLKLIGLRW-YFKIPWNVDFV VVVVLSILASSLSEFED--SFFISP 1591

Qy 1706 TIIRIMRVLRIARVLKLLKMAVGRALLHTVMQALPQVGNLGLLMLFFIFALGVLELF 1765

Db 1592 TLLRVIRVRGRVRLVKSAGKIRTLFMSAVSLPALFNIGLLGLIMFIYAIMGMNFF 1651

Qy 1766 GDLECDETHPEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDP SRDCDQESTCYNTV 1825

Db 1652 --MGAEQKY---GLDDAFNFDTLRSPILLFQMCTSA GSDVNLGLIARCAPEGTC KDYN 1706

Qy 1826 ISPIYFVSFVLTAQFVLVNVVIAVLMKHLSEESKEAEAELEAELEMLKTLSPQPHSP 1885

Db 1707 VATIYLATVLYVSVFLVNVNMYIAVILENFSQATED--EQQLTPD-DFDMMYKEWKYDP 1763

Qy 1886 LGSPFLWPGVEGVNSTDSPKPGAPHTTAHGAASGF--SLEHPTMVPHPE-----EVPVP 1938

Db 1764 KASKYI-----PLDQLSDFVDYLEEPLRLPKPNHFLVLDIP 1801

Qy 1939 LGP-----DLLTVRKSGVSRTHSLP 1958

Db 1802 ICENDRCYCRDILDALTGNFLGTGETSDIP 1831

RESULT 15

A37490

voltage-dependent calcium channel alpha 1B - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A37490

R:Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P. Science 260, 1133-1136, 1993

A>Title: Structure and functional expression of a member of the low voltage-activated calcium channel family

A:Reference number: A37490; MUID:93262464; PMID:8388125

A:Accession: A37490

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2222 <SOO>

A:Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083

A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBIP:132101)

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.6%; Score 1632.5; DB 2; Length 2222;

Best Local Similarity 23.6%; Pred. No. 3.3e-95;

Matches 587; Conservative 389; Mismatches 819; Indels 697; Gaps 81;

Qy 94 FYLSQDSRPRSWCLRTVCNWPFRVSMVLVILLNCVTLMFR--PCEDIA CDSQRCRILQA 151

Db 21 FIFGEDNIVRKYAKKLIDWPPFPEYMLATIIANCIIVLALEOHLPEDDKTPMSRR---LEK 77

Qy 152 FDDFIFAFFAVEMVVMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN--VSF 208

Db 78 TEPYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFNTHVDL 137

Qy 209 SAVRTVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFVFFIFGIVGVQLWAGL 268

Db 138 RTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLFFAILMFAIIGLEFYSGK 197

Qy 269 LNRNCFLENFSLPLSVLDLEPYQ TENEDESPFCISQPRENGMRSRCSVP TLRGEGGGSP 328

Db 198 LHRACFMNN-----SGILEGF-----DPPHPC-----GVQ 222

Qy 329 PCSLDYETYNSSNTTCVNNQYTNCSAGEHNPFPKGAINFDNIGYAWIAIFQVITLEGW 388

Db 223 GCPAGYE-----CKDW-----IGPNDGITQFDNILFAVLT V FQCITMEGW 262

Qy 389 VDIMYFVMDA-HSYNFYFIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREORVR 447

Db 263 TTVLYNTNDALGATWNWLYFIPLIIGSFVNLVNLVGLSGEFAKERERV-----ENRRA 317

Qy 448 FLSNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAI-GVRAGLLSSPVARSQ 506

Db 318 FMK-----LRRQQIIBRELNGYRAWIDKAEVMLAE 348

Qy 507 EPQPSGCTSRHRLSVHLLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLML 566

Db 349 ENKNSGTSALEVLRAT-----IKRSRTTEAMTRDSS----- 379

Qy 567 PPPSTPTPSGPPRGAESVHSFYHADCHLEPVRCQAPPPPCPSEASGRTVSGKVYPTVH 626

Db 380 ----- 379

Qy 627 TSPPEILKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLLETQSTGACHSSCKISSPC 686

Db 380 -----DEHCVDIS-----SVGTPL 393

Qy 687 SKADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYFTQDAQHSDLRDPHSRRRQ 746

Db 394 ARASIKSTKVDGASY-----FRHKE----- 413

Qy 747 RSLGPDABEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTN 806

Db 414 -----RLLRISIRHMVKSQVFWYIVLSVVALNTACVAIVHHNQPWLTW 457

Qy 807 ALEISNIVFTSLFALEMLLKVLYVGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGG 861

Db 458 LLYYAEFLGLFLLEMSLMKMGMPRLYFHSSFCNCFDEGVTVGSIFEVVWAI FRPGTSP 517

Qy 862 GLSVLRTRFLMRVLKVRFLPALQRLVVLMTMDNVATFCMLLMLFIFISILGMHLFG 921

Db 518 GISVLRALRLRIPKITYWASLRNLVSVLSMSSMKSIISLLFLFLFIVFVALLGMQLFG 577

Qy 922 CKFASERDGDTLPRKNFDSLLWAI VTFVFIQTQEDMNKVLNMG-----ASTSSWAALY 976

Db 578 GRF-NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMSAIFY 633

Qy 977 FIALMTFGNYVLFNLVAILVEGFQAEAGDATKSE-SEPDPFS----- 1017

Db 634 FIVLTFLFGNYVTLNVFLAIAVDNLANAQELTKDEQEEBEAFNQKHALQKAEVSPMSAPN 693

Qy 1018 -PSVDGDRKKRLAL-----VALGEHAELRKSL 1046

Db 694 MPSIERDRRRHHMSWEPSSHLRERRRRHHMSVWEQRTSQLRRHMOMSSQEA LNKEEA 753

Qy 1047 PPLIHTAATPMS-----HP---KSSSTGVGEALGSG-----SRRTSSSGSAE----- 1086

Db 754 PPMNPLNPLNPLNPLNPLNAHPSLYRRPRPIEGLALGLLEKCEEBRISRGSLKGDIGG 813

QY 1087 -----PGAHHKCPSPARSPPHSPW-----SAASSWTSRRS 1119  
Db 814 LTSVLNQSRPLSLGKREPPWLPSCRHG--NCDPTQQTGGGETVTFEDRARHRQSQR 871  
QY 1120 SRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEESSEEDRASACSDHRHRSGLEREA 1179  
Db 872 SRHRRVRTEGKESASASRSR-----SASQERSLDEGVSDIDGEKEHEPOSSHRSKPTIHEE 927  
QY 1180 KSSFDL--PDTLQVP--GL-----HRTASGRSSASEHQDCNGKASGRL 1219  
Db 928 ERTQDLRRTNSLMVPRGSLVGLGALDEAETPLVQPOPELEVKGDAALTEQEAEGSSEQALL 987  
QY 1220 A-----RTLRTDDPOL-----DG- 1232  
Db 988 ADVQLDVGRCISQSEPDLSCTMTNMDKATTESTSVTVAIPDVDPVLDSTVNVNISNKTGDE 1047  
QY 1233 -----DDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCH 1281  
Db 1048 ASPLKEAETKEEEEEVEKKKQKKEKRETG-KAMVPHS-----SMFIFSTNPIRKACH 1099  
QY 1282 RIITHKMFHVLVLIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKV 1341  
Db 1100 YIVNLRVYFEMCILLVIAASSIALAAEDPVLTNSEKRV-LRYFDYVFTGVFTFEMVIKMI 1158  
QY 1342 ALGWCFCGEQAYLRSSWNVLGGLVLISVIDI-LVSMVSDSGTKILGMLRVLRLTLRLPL 1400  
Db 1159 DQGLILQDGSFRDLWNILDFVVVVGALVAFALANALGNTNKGKRDIKTIKSLRVLRLPL 1218  
QY 1401 RVISRAQGLKVVTETLMSLSKPIGNIVVICAPFIIFGILGVQLFKGKFFVC--QGEDTR 1458  
Db 1219 KTIKRLPKLKA VDCVVTSLXNVENILIVYKLFEMFIFAVIAVOLFKGFFCYCTDSSKDE 1278  
QY 1459 N-----ITNKSDCAEASR-WVRHKYNFDNLGQALMSLFVLASKDGVWDIMYDGLDAVG 1511  
Db 1279 KECIGNYVDHEKNKMEVKGREWKREHFDYDNIWALLTLFTVSTGEGWPQVLOHSVDVTE 1338  
QY 1512 VDQOPIMHNPNMMLLYFISFLLI VAFVFLMVFVGVVVENFHKRQHOREEEEEARRREKRL 1571  
Db 1339 EDRGPSRSNRMEMSIFVYVFWFPFFVFVNIIFVALIITF-----QEQQDKMEE--- 1388  
QY 1572 RLEKKRSKEKQMAEAOCKPYYSYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTMA 1629  
Db 1389 CSLEKNERACIDFAISAKPLTRYMPQNRHTFPQYRVWHFVVSPEYTIMAMIALNTVVLM 1448  
QY 1630 MEHYQOQOILDEALKICNYIFTVIFVFESVFKLVAFARRFFODRWNLQDLAI VLLSIMG 1689  
Db 1449 MKYISAPWTYELALKYLNIAFTMVSLECVLKVIAFGLNYFRDTWNIFDITVIGSITE 1508  
QY 1690 ITLEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALPOVGNLGLL 1749  
Db 1509 IILTDSKLVNTSGFNMSFLKLFR-----ARLIKLRQGYTIRILLWTFVQSFKALPYVCLL 1565  
QY 1750 FMLLFFIFAALGVELFGDLECD-ETHPCGEGHGHATFRNFGMAFLTLFRVSTGDNWNGIM 1808  
Db 1566 IAMLFFIYAIIGMQVFGNIKLDDESH-----INRHNFRSFFGSLMLLFRSATGEAWOEIM 1621  
QY 1809 KD--PSRDCDQESTC-----YNTVISPIYFVSFVLTAQFVLNVVVI AVLMKHLEES 1857  
Db 1622 LSCIGKEGCEPDTTAPSGONESERCGTDLAYVYFVSFIFFCFSLMLNLFVAVIMDNFEYL 1681  
QY 1858 NKEAK-----EEAELEAELE-----LEMKTL-SPQPHSLG-----SPF 1890  
Db 1682 TRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMYLEMTLMSP-----PLGLGKRCPSKV 1737  
QY 1891 LWPGEVGNSTDSPKPGAPHTTAH-----IGAASG-----FSLEHPTM 1928  
Db 1738 AYKRLVLMN-----MPVAEDMTVHFTSTLMALIR TALDIKIAKGGADROQLDSELQKETL 1792  
QY 1929 V--PHPEE-----VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEBSLGHRCWG 1980  
Db 1793 AIWPHLSQKMLDLLVPMPKASD-LTVGKIYAA---MMIMDYKQSKVKKQKQQL----- 1842  
QY 1981 LPKAQSGSILSVHSQPAD-TSCILQPKDVHYLLQPHGAPTWGAIPKLP PPGRSPLAQR 2039

Db 1843 --EEQKNAPMFQRMESPSSLPQEIISNAKALPYLOQD---PVSGLSGRSGYPSPMSPLSPQE 1897  
QY 2040 LRRQAIRTDSL DVQGLSGREDLLSEVSGPSCPL-----TRSSSFW----- 2080  
Db 1898 IFQLACM--DPADDGQFQEQOQLV--VTDPSSMRRSFSTIRDKRSNSWLEEFMSERSSE 1953  
QY 2081 -----GGSSIQVQ-----QMSG-----IQSKVSKHIRLP--APC----- 2107  
Db 1954 NTKSRRRSYHSSRLSAHRLNSDSGHKSDTHRSGRGRGRSKERKHLSPDVSRCNSEE 2013  
QY 2108 PGLEPSW-----AKDPPETFRSSLELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVET 2160  
Db 2014 RGTQADWESPERRQSRSPSEGRSQTPNRQGTGSLSESSIPSIDTSTPRRRRQLPPVPP 2073  
QY 2161 QSCRRRPGFWLDEQRRHSIAVSCLDGSGOPRLCPSPSLGGQPLGGPGSRPKKK-LSPPS 2219  
Db 2074 ---KPRPLLSYSSLMRHTGGISPPPDGSE-----GGSPLASQALESNSACLTESS 2120  
QY 2220 ISIDPPESQGRPPP---CSPGVCLRRRAPASD 2248  
Db 2121 NSLHPQOQGHPSPOHYIYISEPYLALHEDSHASD 2152

Search completed: April 13, 2005, 19:11:27  
Job time : 123 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: April 13, 2005, 18:58:40 ; Search time 278 Seconds  
(without alignments)  
4212.680 Million cell updates/sec

Title: US-09-611-257A-24  
Perfect score: 12028  
Sequence: 1 MLPHRVPRVCVTPPLRGSAR.....KQDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11657	96.9	2254	1 CCAG_RAT	O54898 rattus norv
2	11532	95.9	2288	2 Q9WUB8	Q9wub8 rattus norv
3	11372.5	94.6	2295	2 Q9WUT2	Q9wut2 mus musculu
4	11263	93.6	2248	2 Q6PFV8	Q6pfv8 mus musculu
5	10732.5	89.2	2377	1 CCAG_HUMAN	O43497 homo sapien
6	6809.5	56.6	1389	2 Q6ZPX4	Q6zpx4 mus musculu
7	6226	51.8	2359	1 CCAH_RAT	Q9eq60 rattus norv
8	6222	51.7	2353	1 CCAH_HUMAN	O95180 homo sapien
9	6190	51.5	2365	1 CCAH_MOUSE	O88427 mus musculu
10	5418	45.0	2223	1 CCAI_HUMAN	Q9p0x4 homo sapien
11	5354	44.5	1835	1 CCAI_RAT	Q9z0y8 rattus norv
12	4750.5	39.5	1994	2 Q7Z6S8	Q7z6s8 homo sapien
13	4188.5	34.8	1762	2 Q7PQV4	Q7pqv4 anopheles g
14	4137.5	34.4	2893	2 Q9W433	Q9w433 drosophila
15	3856.5	32.1	1837	2 Q967R4	Q967r4 caenorhabdi
16	3849	32.0	1852	2 Q7Z002	Q7z002 caenorhabdi
17	3830	31.8	1844	2 Q7YZR6	Q7yze6 caenorhabdi
18	3824.5	31.8	1885	2 Q7Z003	Q7z003 caenorhabdi
19	3665	30.5	1460	2 Q80TJ2	Q80tj2 mus musculu
20	2941.5	24.5	1418	2 Q7JPB4	Q7jpb4 caenorhabdi
21	2813.5	23.4	1942	2 Q869H0	Q869h0 lymnaea sta
22	2098.5	17.4	1211	2 Q8MQ95	Q8mq95 caenorhabdi
23	1727	14.4	541	2 Q6PE92	Q6pe92 mus musculu
24	1720.5	14.3	1810	2 O44930	O44930 aiptasia pa
25	1678	14.0	2327	1 CCAB_MOUSE	O55017 mus musculu
26	1674	13.9	2339	1 CCAB_HUMAN	Q00975 homo sapien
27	1673	13.9	2331	2 Q9TTA4	Q9tta4 bos taurus
28	1666.5	13.9	1599	2 Q7PNK9	Q7pnk9 anopheles g
29	1665.5	13.8	2259	1 CCAE_RABIT	Q02343 oryctolagus
30	1661	13.8	2333	2 O89089	O89089 rattus norv
31	1660	13.8	2295	2 Q923K6	Q923k6 rattus norv

32	1656	13.8	2304	2 Q9BMO4	Q9bmq4 blattella g
33	1653.5	13.7	2272	1 CCAE_MOUSE	Q61290 mus musculu
34	1652.5	13.7	1891	2 O97017	O97017 stylophora
35	1650	13.7	2312	1 CCAE_HUMAN	Q15878 homo sapien
36	1649.5	13.7	1984	2 Q28644	Q28644 oryctolagus
37	1646.5	13.7	1847	2 Q6RKBO	Q6rkb0 brachydanio
38	1642.5	13.7	2336	1 CCAB_RAT	Q02294 rattus norv
39	1642.5	13.7	2357	2 Q9PUM6	Q9pum6 gallus gall
40	1642	13.7	1985	1 CCAE_MOUSE	Q9jis7 mus musculu
41	1642	13.7	2223	1 CCAE_DISOM	P56699 discopyge o
42	1639.5	13.6	1984	2 Q7TN13	Q7tni3 mus musculu
43	1636	13.6	1993	2 P90670	P90670 aplysia cal
44	1634.5	13.6	1984	2 O08562	O08562 rattus norv
45	1632.5	13.6	2222	1 CCAE_RAT	Q07652 rattus norv

ALIGNMENTS

RESULT 1  
CCAG\_RAT  
ID CCAG\_RAT STANDARD; PRT; 2254 AA.  
AC O54898;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1).  
DE Name=Cacnalg;  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=98154730; PubMed=9495342; DOI=10.1038/36110;  
RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J., Williamson M.P., Fox M., Rees M., Lee J.-H.;  
RT "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel.";  
RL Nature 391:896-900(1998).  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1G gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression in heart; low expression in placenta, kidney and lung.  
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; AF027984; AAC67372.1; -  
DR PIR; T09053; T09053.  
DR RGD; 68942; Cactnal9.  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCAlphal.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR01629; TVDCCALPHAL.  
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;  
KW Ionic channel; Multigene family; Phosphorylation; Repeat;  
KW Transmembrane; Voltage-gated channel.

FT REPEAT 68 398 I.  
FT REPEAT 730 968 II.  
FT REPEAT 1242 1519 III.  
FT REPEAT 1564 1822 IV.  
FT DOMAIN 1 80 Cytoplasmic (Potential).  
FT TRANSMEM 81 101 S1 of repeat I.  
FT DOMAIN 102 119 Extracellular (Potential).  
FT TRANSMEM 120 141 S2 of repeat I (Potential).  
FT DOMAIN 142 150 Cytoplasmic (Potential).  
FT TRANSMEM 151 170 S3 of repeat I.  
FT DOMAIN 171 175 Extracellular (Potential).  
FT TRANSMEM 176 193 S4 of repeat I.  
FT DOMAIN 194 213 Cytoplasmic (Potential).  
FT TRANSMEM 214 234 S5 of repeat I (Potential).  
FT DOMAIN 235 370 Extracellular (Potential).  
FT TRANSMEM 371 395 S6 of repeat I.  
FT DOMAIN 396 744 Cytoplasmic (Potential).  
FT TRANSMEM 745 765 S1 of repeat II (Potential).  
FT DOMAIN 766 778 Extracellular (Potential).  
FT TRANSMEM 779 800 S2 of repeat II (Potential).  
FT DOMAIN 801 806 Cytoplasmic (Potential).  
FT TRANSMEM 807 825 S3 of repeat II (Potential).  
FT DOMAIN 826 833 Extracellular (Potential).  
FT TRANSMEM 834 857 S4 of repeat II (Potential).  
FT DOMAIN 858 868 Cytoplasmic (Potential).  
FT TRANSMEM 869 889 S5 of repeat II (Potential).  
FT DOMAIN 890 940 Extracellular (Potential).  
FT TRANSMEM 941 965 S6 of repeat II (Potential).  
FT DOMAIN 966 1251 Cytoplasmic (Potential).  
FT TRANSMEM 1252 1274 S1 of repeat III (Potential).  
FT DOMAIN 1275 1292 Extracellular (Potential).  
FT TRANSMEM 1293 1313 S2 of repeat III (Potential).  
FT DOMAIN 1314 1323 Cytoplasmic (Potential).  
FT TRANSMEM 1324 1343 S3 of repeat III (Potential).  
FT DOMAIN 1344 1357 Extracellular (Potential).  
FT TRANSMEM 1358 1379 S4 of repeat III (Potential).  
FT DOMAIN 1380 1389 Cytoplasmic (Potential).  
FT TRANSMEM 1390 1413 S5 of repeat III (Potential).  
FT DOMAIN 1414 1490 Extracellular (Potential).  
FT TRANSMEM 1491 1516 S6 of repeat III (Potential).  
FT DOMAIN 1517 1578 Cytoplasmic (Potential).  
FT TRANSMEM 1579 1599 S1 of repeat IV (Potential).  
FT DOMAIN 1600 1613 Extracellular (Potential).  
FT TRANSMEM 1614 1635 S2 of repeat IV (Potential).  
FT DOMAIN 1636 1642 Cytoplasmic (Potential).  
FT TRANSMEM 1643 1661 S3 of repeat IV (Potential).  
FT DOMAIN 1662 1675 Extracellular (Potential).  
FT TRANSMEM 1676 1699 S4 of repeat IV (Potential).  
FT DOMAIN 1700 1713 Cytoplasmic (Potential).  
FT TRANSMEM 1714 1734 S5 of repeat IV (Potential).  
FT DOMAIN 1735 1794 Extracellular (Potential).  
FT TRANSMEM 1795 1822 S6 of repeat IV (Potential).  
FT DOMAIN 1823 2254 Cytoplasmic (Potential).  
FT DOMAIN 290 295 Poly-Gly.  
FT DOMAIN 496 506 Poly-His.

FT	DOMAIN	1527	1530	Poly-Glu.
FT	SITE	354	354	Calcium ion selectivity and permeability (By similarity).
FT	SITE	924	924	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1465	1465	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1770	1770	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	246	246	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	322	322	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1427	1427	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1430	1430	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1666	1666	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	2254 AA;	250405 MW;	697BHE06360CF0F6 CRC64;

Query Match 96.9%; Score 11657; DB 1; Length 2254;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	62	GAAGAGSTEKDPGSADSEAEGLYPALAPVVFYLSQDSRPSWCLRTVCNPFERSVMSL	121
Db	30	GRQPGSTEKDPGSADSEAEGLYPALAPVVFYLSQDSRPSWCLRTVCNPFERSVMSL	89
QY	122	VILLNCVTLMGFRPCEDIAQDSQRCRILQAFDDFIFAFAFVAVMVVWVVALGIFGKKCYLG	181
Db	90	VILLNCVTLMGFRPCEDIAQDSQRCRILQAFDDFIFAFAFVAVMVVWVVALGIFGKKCYLG	149
QY	182	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLTLLDTP	241
Db	150	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLTLLDTP	209
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLPENFSLPLSVLDLEPYQTENEDESPF	301
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLPENFSLPLSVLDLEPYQTENEDESPF	269
QY	302	ICSPRENGMRSCRSVPTLRGEGGGPPCSDLDETYSNNTTCVNNQYTYTNCAGEHN	361
Db	270	ICSPRENGMRSCRSVPTLRGEGGGPPCSDLDETYSNNTTCVNNQYTYTNCAGEHN	329
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMVFMVDAHSFYNFIFILLIIVGSFFMINL	421
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMVFMVDAHSFYNFIFILLIIVGSFFMINL	389
QY	422	CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLYILRKAAR	481
Db	390	CLVVIATQFSETKQRESQMLREQVRFLSNASTLASFSEPGSCYEELLYILRKAAR	449
QY	482	RLAQVSRAIGVRAGLLSSPVARSQEPQPSGCTSRSHRRLSVHHLVHHHHHHHHYHLGN	541
Db	450	RLAQVSRAIGVRAGLLSSPVARSQEPQPSGCTSRSHRRLSVHHLVHHHHHHHHYHLGN	509
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRQ	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRQ	569
QY	602	APPRCPSEASGRTVSGKVPYTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF	661
Db	570	APPRCPSEASGRTVSGKVPYTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF	629
QY	662	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGDPSCPYCARTGAGEPESADHVPDSD	721
Db	630	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGDPSCPYCARTGAGEPESADHVPDSD	689
QY	722	SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVLAFWRLICDTFRKIYDSKYFGRG	781
Db	690	SEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVLAFWRLICDTFRKIYDSKYFGRG	749
QY	782	IMIAILLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN	841

Db 750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYPPGYIKNPYN 809

Qy 842 IPDGIVIVISVWEIVGQGGSLVLRTRFRLMRVLKLVRFPLALQRLQVLVLMKTMNDNVATF 901

Db 810 IPDGIVIVISVWEIVGQGGSLVLRTRFRLMRVLKLVRFPLALQRLQVLVLMKTMNDNVATF 869

Qy 902 CMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIWTVFQILTQEDWNKV 961

Db 870 CMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIWTVFQILTQEDWNKV 929

Qy 962 LYNMGMASTSSWAALYFIALMTFGNYVLENNLVAILEVGFQAEQDATKSESEPDFFSVD 1021

Db 930 LYNMGMASTSSWAALYFIALMTFGNYVLENNLVAILEVGFQAEQDATKSESEPDFFSVD 989

Qy 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRTSS 1081

Db 990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRTSS 1049

Qy 1082 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSSRSNLSGRAPSLKRRSPSGERRS 1141

Db 1050 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSSRSNLSGRAPSLKRRSPSGERRS 1109

Qy 1142 LLSGEGQESQDEESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVGLHRTASGR 1201

Db 1110 LLSGEGQESQDEESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVGLHRTASGR 1169

Qy 1202 SSASEHQDCNGKSASGRLARTLRDTPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261

Db 1170 SSASEHQDCNGKSASGRLARTLRDTPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy 1322 TLSNYIFTAVFLAEMTVKVVALGWCFGQAYLRSSWNVLGGLVLISVIDILVSMVSDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVALGWCFGQAYLRSSWNVLGGLVLISVIDILVSMVSDSG 1349

Qy 1382 TKILGMLRVLRLRLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1441

Db 1350 TKILGMLRVLRLRLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1409

Qy 1442 VOLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGWVD 1501

Db 1410 VOLFKGKFFVCOGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGWVD 1469

Qy 1502 IMYDGLDAVGVDQOPIMHNPNWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHDEE 1561

Db 1470 IMYDGLDAVGVDQOPIMHNPNWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHDEE 1529

Qy 1562 EARRREEKRLRLEKKRRSKEQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTGVI 1621

Db 1530 EARRREEKRLRLEKKRRSKEQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTGVI 1589

Qy 1622 GLNVVTMAHEHYQOPQILDEALKICNVIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLA 1681

Db 1590 GLNVVTMAHEHYQOPQILDEALKICNVIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLA 1649

Qy 1682 IVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKQVGMRAALLHTVWQALP 1741

Db 1650 IVLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKQVGMRAALLHTVWQALP 1709

Qy 1742 QVGNLGLLFLMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1801

Db 1710 QVGNLGLLFLMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1769

Qy 1802 DNWNGIMKDPDRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861

Db 1770 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1829

Qy 1862 KEAELEAELELEMKTLSPOPHSPGLSPFWPVGVEGVNSTSPKPGAPHTTAHIGAASGF 1921

Db 1830 KEAELEAELELEMKTLSPOPHSPGLSPFWPVGVEGVNSTSPKPGAPHTTAHIGAASGF 1889

RESULT 2

Q9WUB8

ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.

AC Q9WUB8;

DT 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE T-type calcium channel isoform.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RX MEDLINE=20081696; PubMed=10615950;

RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,

RA Wu S., Berggren P.O., Li M.;

RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting

RT cells.";

RL Diabetes 49:59-64(2000).

CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits

CC family.

DR EMBL; AF125161; AAD26858.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR001682; Ca/Na\_pore.

DR InterPro; IPR002111; Cat\_channel\_TrpL.

DR InterPro; IPR002077; Ca\_channel\_alpha.

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR005820; M+channel\_nlg.

DR InterPro; IPR005445; TVDCCAlphal.

DR Pfam; PF00520; Ion\_trans; 4.

DR PRINTS; PR00167; CACHANNEL.

DR PRINTS; PR01629; TVDCCALPHA1.

KW Calcium; Calcium channel; Calcium transport; Calcium-binding;

KW Ion transport; Ionic channel; Transmembrane; Transport;

KW Voltage-gated channel.



SQ	SEQUENCE	2288 AA; 253476 MW; B89DBB5A1D81757F CRC64;	
	Query Match	95.9%; Score 11532; DB 2; Length 2288;	
	Best Local Similarity	97.7%; Pred. No. 0;	
	Matches 2206; Conservative	1; Mismatches 18; Indels 34; Gaps 2;	
QY	62	GAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSWCLRTVCNPNWFERVSM	121
DB	30	GRQPGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSWCLRTVCNPNWFERVSM	89
QY	122	VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIAPFAFVEMVVMKVALGIFGKCYLG	181
DB	90	VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIAPFAFVEMVVMKVALGIFGKCYLG	149
QY	182	DTWNRLDFFIVLAGMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVPSMRILVTLTLLD	241
DB	150	DTWNRLDFFIVLAGMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVPSMRILVTLTLLD	209
QY	242	MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPLSDLEPYQOTENEDESP	301
DB	210	MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPLSDLEPYQOTENEDESP	269
QY	302	ICSQPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYNTCSAGEHN	361
DB	270	ICSQPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYNTCSAGEHN	329
QY	362	PFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFNFIFILLIIVGSFFMINL	421
DB	330	PFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFNFIFILLIIVGSFFMINL	389
QY	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEBELLKYLVIILRKAAR	481
DB	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEBELLKYLVIILRKAAR	449
QY	482	RLAQVSRAGIVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN	541
DB	450	RLAQVSRAGIVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN	509
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPSPPTPPSGPPRGAESVHSFYHADCHLEPVR	601
DB	510	GTLRVPRASPEIQDRDANGSRRLMLPPSPPTPPSGPPRGAESVHSFYHADCHLEPVR	569
QY	602	APPRCPSEASGRTVSGKVYPTVHTSPPPPEILKDALVEAPSPGPPPTLTSFNIPPGPF	661
DB	570	APPRCPSEASGRTVSGKVYPTVHTSPPPPEILKDALVEAPSPGPPPTLTSFNIPPGPF	629
QY	662	SSMKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPEPESADHVM	721
DB	630	SSMKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPEPESADHVM	689
QY	722	SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDPAEPPSSVLAFWRLICDTFRKIVDSKYF	781
DB	690	SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDPAEPPSSVLAFWRLICDTFRKIVDSKYF	749
QY	782	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNP	841
DB	750	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNP	809
QY	842	IFDGVIVVSWWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF	901
DB	810	IFDGVIVVSWWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF	869
QY	902	CMLLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV	961
DB	870	CMLLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV	929
QY	962	LYNGMASTSSWAALFYIALMTFGNYVLFNLLVAILVEGFAE-----	1003
DB	930	LYNGMASTSSWAALFYIALMTFGNYVLFNLLVAILVEGFAEIGKREDASQLS	989
QY	1004	-----GDATKSESEPDFFSPSVDGDRKRLALVALGEHAELRKSLLPLIHTAATPM	1058
DB	990	VNSQGGDATKSESEPDFFSPSVDGDRKRLALVALGEHAELRKSLLPLIHTAATPM	1049

QY	1059	SHPKSSSTGVGEALGSGSRTSSSGSAEPGAHHEMKCPPSARSSSPHSPWSAASSWTSRR	1118
DB	1050	SLPKSSSTGVGEALGSGSRTSSSGSAEPGAHHEMKCPPSARSSSPHSPWSAASSWTSRR	1109
QY	1119	SSRNLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERE	1178
DB	1110	SSRNLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERE	1169
QY	1179	AKSSFDLPDTLQVPLGRLHTASGRSSASEHQDCNGKXASGRLARTLRTDDPQLDGGDDNDE	1238
DB	1170	AKSSFDLPDTLQVPLGRLHTASGRSSASEHQDCNGKXASGRLARTLRTDDPQLDGGDDNDE	1229
QY	1239	GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFEDHVVLIIF	1298
DB	1230	GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFEDHVVLIIF	1289
QY	1299	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN	1358
DB	1290	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN	1349
QY	1359	VLGGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLRPLRVISRAOGLKLVVETILMS	1418
DB	1350	VLGGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLRPLRVISRAOGLKLVVETILMS	1409
QY	1419	SLKPIGNIWVICCAFFIIFGILGVQLFKGFFVQCQGEDTRNITNKSDCAEASVWRVHKY	1478
DB	1410	SLKPIGNIWVICCAFFIIFGILGVQLFKGFFVQCQGEDTRNITNKSDCAEASVWRVHKY	1469
QY	1479	NFDNLQALMSLFLASKDGWVDIMYDGLDVGVDQQPIMNHNPMWLLLYFISFLLI	1538
DB	1470	NFDNLQALMSLFLASKDGWVDIMYDGLDVGVDQQPIMNHNPMWLLLYFISFLLI	1529
QY	1539	VLNMFVGVVVENFHKCRQHQEEEEARRRERKRLRLEKRR-----SKEKQMAE	1587
DB	1530	VLNMFVGVVVENFHKCRQHQEEEEARRRERKRLRLEKRRNMLDDVIASGSSASAASE	1589
QY	1588	AQCKPYSDYSRFRLLVHHLCTSHYLDLFTGVLGNVVTWAMEHYQQPQILDEALKICN	1647
DB	1590	AQCKPYSDYSRFRLLVHHLCTSHYLDLFTGVLGNVVTWAMEHYQQPQILDEALKICN	1649
QY	1648	YIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSLPINPTI	1707
DB	1650	YIFTVIFVFESVFKLVAFAPRRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSLPINPTI	1709
QY	1708	IRIMRVLRIARVLKLLKMAVGMALLHTVMQALPOVGNLGLLFFLFFIFAALGVLEFGD	1767
DB	1710	IRIMRVLRIARVLKLLKMAVGMALLHTVMQALPOVGNLGLLFFLFFIFAALGVLEFGD	1769
QY	1768	LECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPSCDCDOESTCYNTVIS	1827
DB	1770	LECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLDCDQESTCYNTVIS	1829
QY	1828	PIYFVSFVLTAQFVLNVVVIAMLMKHEESNKEAKEAELEAELEMKTLSPQPHSPLG	1887
DB	1830	PIYFVSFVLTAQFVLNVVVIAMLMKHEESNKEAKEAELEAELEMKTLSPQPHSPLG	1889
QY	1888	SPFLWPVGEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVR	1947
DB	1890	SPFLWPVGEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVR	1949
QY	1948	KSGVSRTHSLPNDSYMCRNGSTAEERSLGHARGWGLPKAQSGSILSVHSQPADTSCILQLPK	2007
DB	1950	KSGVSRTHSLPNDSYMCRNGSTAEERSLGHARGWGLPKAQSGSILSVHSQPADTSCILQLPK	2009
QY	2008	DVHYLLQPHGAPTGAIPKLPPPGSPPLAQRLRQRAIRTDSDLVQGLGSRDILLSEVS	2067
DB	2010	DVHYLLQPHGAPTGAIPKLPPPGSPPLAQRLRQRAIRTDSDLVQGLGSRDILLSEVS	2069
QY	2068	GPSCPLTRSSSWGGSSIOVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLLEL	2127
DB	2070	GPSCPLTRSSSWGGSSIOVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLLEL	2129

QY	2128	DTELSWISGDLPLSSQBEPLPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLD SG	218			
Db	2130	DTELSWISGDLPLSSQBEPLPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLD SG <td>2189</td>	2189			
QY	2188	SQRLCPSPSSSLGGQPLGGPSRPKKLSPPSISIDPPESQSGSRPPCSPGVCLRRAPAS	2247			
Db	2190	SQRLCPSPSSSLGGQPLGGPSRPKKLSPPSISIDPPESQSGSRPPCSPGVCLRRAPAS	2249			
QY	2248	DSKDPVSVPDSTAASPSPKKOTLSLSGLSSDPTDMDP	2286			
Db	2250	DSKDPVSVPDSTAASPSPKKOTLSLSGLSSDPTDMDP	2288			
RESULT 3						
Q9WUT2	ID	Q9WUT2	PRELIMINARY; PRT; 2295 AA.			
AC	Q9WUT2;					
DT	01-NOV-1999	(TREMBLrel. 12, Created)				
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)				
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)				
DE	Voltage-gated calcium channel, alpha-1-G subunit.					
GN	Name=Cacna1g;					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain;					
RX	MEDLINE=99189326; PubMed=10087148;					
RA	Klugbauer N.; Marais E.; Lacinova L.; Hofmann F.;					
RT	"A T-type calcium channel from mouse brain.";					
RL	Pflugers Arch. 437:710-715(1999).					
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).					
CC	-I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.					
DR	EMBL; AJ012569; CAB40793.1; -.					
DR	MGD; MGI:1201678; Cacna1g.					
DR	GO; GO:0016021; C:integral to membrane; TAS.					
DR	GO; GO:0005886; C:plasma membrane; IDA.					
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.					
DR	InterPro; IPR001682; Ca/Na_pore.					
DR	InterPro; IPR002111; Cat_channel_TrpL.					
DR	InterPro; IPR002077; Ca_channel_alpha.					
DR	InterPro; IPR005821; Ion_trans.					
DR	InterPro; IPR005820; M+channel_nlg.					
DR	InterPro; IPR005445; TVDCCalpal.					
DR	Pfam; PF00520; Ion_trans; 4.					
DR	PRINTS; PR00167; CACHANNEL.					
DR	PRINTS; PR01629; TVDCCALPAL.					
KW	Calcium; Calcium channel; Calcium transport; Calcium-binding;					
KW	Ion transport; Ionic channel; Transmembrane; Transport;					
KW	Voltage-gated channel.					
SQ	SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;					
Query Match 94.6%; Score 11372.5; DB 2; Length 2295;						
Best Local Similarity 96.1%; Pred. No. 0;						
Matches 2178; Conservative 12; Mismatches 34; Indels 43; Gaps 4;						
QY	62	GAAGAGSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPSWCLRTVCNPFERSML	121			
Db	30	GRQPGSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPSWCLRTVCNPFERSML	89			
QY	122	VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	181			
Db	90	VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	149			
QY	182	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLP	241			
Db	150	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLP	209			
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLPENFSLPSVDLEPYQOTENEDESPF	301			

DE	Cacnalg protein.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6; TISSUE=Brain;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6; TISSUE=Brain;	
RA	Strausberg R.;	
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC057399; AAH57399.1; -.	
DR	GO; GO:0016021; C:integral to membrane; TAS.	
DR	GO; GO:0005886; C:plasma membrane; IDA.	
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.	
DR	InterPro; IPR001682; Ca/Na pore.	
DR	InterPro; IPR002111; Cat_channel_TripL.	
DR	InterPro; IPR005821; Ion trans.	
DR	InterPro; IPR005820; M+channel_nlg.	
DR	InterPro; IPR005445; TVDCCalphal.	
DR	Pfam; PF00520; Ion trans; 4.	
DR	PRINTS; PR01629; TVDCCALPHAL.	
KW	Ion transport; Ionic channel; Transmembrane; Transport.	
SQ	SEQUENCE 2248 AA; 248888 MW; 332C5A8D9115A64F CRC64;	
Query Match 93.6%; Score 11263; DB 2; Length 2248;		
Best local similarity 96.3%; Pred. No. 0;		
Matches 2155; Conservative 12; Mismatches 40; Indels 30; Gaps 4;		
QY	62 GAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSWCLRTVCNPFERVSM	121
Db	30 GROGPGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPSWCLRTVCNPFERVSM	89
QY	122 VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIPAFFAVEMVVMKVALGFGKKCYLG	181
Db	90 VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIPAFFAVEMVVMKVALGFGKKCYLG	149
QY	182 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	241
Db	150 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	209
QY	242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDLEPYQOTENEDESPF	301
Db	210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDLEPYQOTENEDESPF	269
QY	302 ICSPRENGMRSRCSVPTLRGEGGGPPCSDLDETYSNNTTCVNNQYTTNCAGEHN	361
Db	270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDYEAYNNTTCVNNQYTTNCAGEHN	329
QY	362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYFIYFILLIIVGSFFMINL	421

RESULT 4

Q6PFV8  
ID Q6PFV8  
AC Q6PFV8;  
DT 05-JUL-2004 (TremBLrel. 27, Created)  
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)

Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLII----- 380  
QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYBELLKYLVIYLKRAAR 481  
Db 381 -----FSETKQRESQLMREQVRFLSNASTLASFSEPGSCYBELLKYLVIYLKRAAR 432  
QY 482 RLAQVSRAGVRAGLSSPVARSQEQPQSGSCSTRSHRRRLSVHHLVHHHHHHHHYHLGN 541  
Db 433 RLAQVSRAGVRAGLSSPVVRGGQEQPQSGSCSRSHRRRLSVHHLVHHHHHHHHYHLGN 492  
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTSPGGPPRGAEVSHSFYHADCHLEPVRQ 601  
Db 493 GTLRVPRASPEIQDRDANGSRWLMLPPSTPTSPGGPPRGAEVSHSFYHADCHLEPVRQ 552  
QY 602 APPPRCPSEASGRVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPGPF 661  
Db 553 APPPRSPSEASGRVSGKVYPTVHTSPPEMLKDKALVEVAPSPGPTLTSTFNIPGPF 612  
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD 721  
Db 613 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD 672  
QY 722 SEAVYEFTQAOHSDLRDPHSRRRQRLSGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781  
Db 673 SEAVYEFTQAOHSDLRDPH-RRRRPSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 731  
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALNISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 841  
Db 732 IMIAILVNTLSMGIEYHEQPEELTNALNISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 791  
QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFPLALQRLVLMKTMNDNVATF 901  
Db 792 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFPLALQRLVLMKTMNDNVATF 851  
QY 902 CMLLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 961  
Db 852 CMLLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 911  
QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSVD 1021  
Db 912 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFFSVD 971  
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSPKSSSTGVGEALGSGSRTSS 1081  
Db 972 GDGDRKKRLALVALGEHSELRSLLPPLIIHTAATPMSPKSSSTGVGEALGSGSRTSS 1031  
QY 1082 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSSRRSSRLGRAPSLKRRSPSGERRS 1141  
Db 1032 SGSAEPGTAHHEMKPPSARSSPHSPWSAASSWTSSRRSSRLGRAPSLKRRSPSGERRS 1091  
QY 1142 LLSGEGQESQDEESSEEDRASPAQSDHHRGSLEREAKSSFDLPDTLQVGLHRTASGR 1201  
Db 1092 LLSGEGQESQDEESSEEDRASPAQSDHHRGSLEREAKSSFDLPDTLQVGLHRTASGR 1151  
QY 1202 SSASEHQDCNGKSASGRILARTLRDTPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE 1261  
Db 1152 SSASEHQDCNGKSASGRILARTLRADDPPLDGGDDNDEGNLSKGERLRAWVRARLPACCRE 1211  
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321  
Db 1212 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1271  
QY 1322 TLSNYIFTAVFLAEMTVKVALGWCFGEOAYLRSSWNVLGDLVLISVIDILVSMVSDSG 1381  
Db 1272 TLSNYIFTAVFLAEMTVKVALGWCFGEOAYLRSSWNVLGDLVLISVIDILVSMVSDSG 1331  
QY 1382 TKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1441  
Db 1332 TKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1391  
QY 1442 VOLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFDNLQALMSLFLVASKDGWVD 1501

Db 1392 VOLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFDNLQALMSLFLVASKDGWVD 1451  
QY 1502 IMYDGLDAVGVDQQPIMNHNPMWLLYPIFSLLIVAFFVLNMFVGVVVENFHKCRQHQQEE 1561  
Db 1452 IMYDGLDAVGVDQQPIMNHNPMWLLYPIFSLLIVAFFVLNMFVGVVVENFHKCRQHQQEE 1511  
QY 1562 EARRREKRLRLERLEKRR-----SKEQMAEAAQCKPYSDYSRFRLLVHHLCTS 1610  
Db 1512 EARRREKRLRLERLEKRRNMLDDVIASSSSASAASEAQCKPYSDYSRFRLLVHHLCTS 1571  
QY 1611 HYLDLFTITGIVGLNVVTMAMEHYQQPILDEALKICNYIFTVIFVFEVFKLVAFARFRF 1670  
Db 1572 HYLDLFTITGIVGLNVVTMAMEHYQQPILDEALKICNYIFTVIFVFEVFKLVAFARFRF 1631  
QY 1671 FQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730  
Db 1632 FQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1691  
QY 1731 ALLHTVMQALPQVGNLGLLFMLFFIPAALGVLELFGDLECDETHPCCEGLGRHATFRNFGM 1790  
Db 1692 ALLDTVMQALPQVGNLGLLFMLFFIPAALGVLELFGDLECDETHPCCEGLGRHATFRNFGM 1751  
QY 1791 AFLTLFRVSTGDNWNGIMKOPSRDCDQESTCYNTVISPIYFVSFVLTQAQFVLNVVIAVL 1850  
Db 1752 AFLTLFRVSTGDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTQAQFVLNVVIAVL 1811  
QY 1851 MKHLEESNKEAKEAELEAELEEMKTLSPQHSPLGSPFLWPGVGVNSTDSPKPGAPH 1910  
Db 1812 MKHLEESNKEAKEAELEAELEEMKTLSPQHSPLGSPFLWPGVGVNSTDSPKPGAPH 1871  
QY 1911 TTAHIGAA-SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST 1969  
Db 1872 TTAHIGAASSGFSLEHPTMVPHTEEGVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST 1931  
QY 1970 AERSLGHGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHLLQPHGAPTWGAIPKLPP 2029  
Db 1932 AERSLGHGWGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTWGAIPKLPP 1991  
QY 2030 PGRSPLAQRLRRQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQ 2089  
Db 1992 PGRSPLAQRLRRQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQ 2051  
QY 2090 RSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQEEPLFP 2149  
Db 2052 RSGSQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQEEPLFP 2111  
QY 2150 RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVCLDSCSQPRLCPSPSLGGQPLGGPGS 2209  
Db 2112 RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVCLDSCSQPRLCPSPSLGGQPLGGPGS 2171  
QY 2210 RPKKLSPPSISIDPPESQSGRRPPCPGVCLRRRAPASDKDPSSVSSPLDSTAASPSPKK 2269  
Db 2172 RPKKLSPPSISIDPPESQSGRRPPCPGVCLRRRAPASDKDPSSVSSPLDSTAASPSPKK 2231  
QY 2270 DTLSLGLSSDPTDMDP 2286  
Db 2232 DALSLGLSSDPTDLDP 2248

RESULT 5

CCAG\_HUMAN

ID CCAG HUMAN STANDARD; PRT; 2377 AA.

AC O43497; O43498; O94770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;

AC Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;

AC Q9Y5T3;

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-

DE gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).

GN Name=CACNA1G; Synonyms=KIAA1123;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CC NCBI\_TaxID=9606;  
CC [1]  
CC SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).  
CC TISSUE=Brain;  
CC MEDLINE=20014446; PubMed=10548410; DOI=10.1016/S0304-3940(99)00716-8;  
CC Mittman S., Guo J., Agnew W.S.;  
CC "Structure and alternative splicing of the gene encoding alpha1G, a  
CC human brain T calcium channel alpha1 subunit.";  
CC Neurosci. Lett. 274:143-146(1999).  
CC [2]  
CC SEQUENCE FROM N.A. (ISOFORM 1).  
CC TISSUE=Brain;  
CC MEDLINE=20115462; PubMed=10648811; DOI=10.1016/S0014-5793(99)01756-1;  
CC Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;  
CC "Molecular cloning and functional expression of ca(v)3.1c, a T-type  
CC calcium channel from human brain.";  
CC FEBS Lett. 466:54-58(2000).  
CC [3]  
CC SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).  
CC TISSUE=Brain;  
CC MEDLINE=20158909; PubMed=10692398; DOI=10.1074/jbc.275.9.6090;  
CC Montell A., Chemin J., Bourinet E., Mennessier G., Lory P.,  
CC Nargeot J.;  
CC "Molecular and functional properties of the human alpha1G subunit that  
CC forms T-type calcium channels.";  
CC J. Biol. Chem. 275:6090-6100(2000).  
CC [4]  
CC SEQUENCE FROM N.A. (ISOFORM 14).  
CC Kishi F.;  
CC Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC [5]  
CC SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).  
CC TISSUE=Brain;  
CC MEDLINE=22158633; PubMed=12168954;  
CC Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
CC "Construction of expression-ready cDNA clones for KIAA genes: manual  
CC curation of 330 KIAA cDNA clones.";  
CC DNA Res. 9:99-106(2002).  
CC [6]  
CC SEQUENCE OF 750-2377 FROM N.A. (ISOFORM 13).  
CC TISSUE=Brain;  
CC MEDLINE=20039618; PubMed=10574461;  
CC Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,  
CC Ohara O.;  
CC "Characterization of cDNA clones selected by the GeneMark analysis  
CC from size-fractionated cDNA libraries from human brain.";  
CC DNA Res. 6:329-336(1999).  
CC [7]  
CC SEQUENCE FROM N.A. (ISOFORM 3), AND GENE STRUCTURE.  
CC TISSUE=Prostatic carcinoma;  
CC MEDLINE=99421245; PubMed=10493502;  
CC Toyota M., Ho C., Ohe-Toyota M., Baylin S.B., Issa J.-P.J.;  
CC "Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant  
CC methylation of its 5' CpG island in human tumors.";  
CC Cancer Res. 59:4535-4541(1999).  
CC [8]  
CC SEQUENCE OF 1126-1444; 1778-1927 AND 2021-2312 FROM N.A.  
CC TISSUE=Brain;  
CC MEDLINE=98154730; PubMed=9495342; DOI=10.1038/36110;  
CC Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,  
CC Williamson M.P., Fox M., Rees M., Lee J.-H.;  
CC "Molecular characterization of a neuronal low-voltage-activated T-type  
CC calcium channel.";  
CC Nature 391:896-900(1998).  
CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the  
CC entry of calcium ions into excitable cells and are also involved  
CC in a variety of calcium-dependent processes, including muscle  
CC contraction, hormone or neurotransmitter release, gene expression,  
CC cell motility, cell division and cell death. The isoform alpha-1G  
CC gives rise to T-type calcium currents. T-type calcium channels  
CC belong to the "low-voltage activated (LVA)" group and are strongly  
CC blocked by mibefradil. A particularity of this type of channels is

CC an opening at quite negative potentials and a voltage-dependent  
CC inactivation. T-type channels serve pacemaking functions in both  
CC central neurons and cardiac nodal cells and support calcium  
CC signaling in secretory cells and vascular smooth muscle. They may  
CC also be involved in the modulation of firing patterns of neurons  
CC which is important for information processing as well as in cell  
CC growth processes.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=14;  
CC Comment=Additional isoforms seem to exist;  
CC Name=5;  
CC IsoId=O43497-1; Sequence=Displayed;  
CC Name=1;  
CC IsoId=O43497-2; Sequence=VSP\_000940, VSP\_000943, VSP\_000946;  
CC Name=2;  
CC IsoId=O43497-3; Sequence=VSP\_000940, VSP\_000944, VSP\_000946;  
CC Name=3;  
CC IsoId=O43497-4; Sequence=VSP\_000940;  
CC Name=4;  
CC IsoId=O43497-5; Sequence=VSP\_000940, VSP\_000943, VSP\_000946,  
CC VSP\_000948;  
CC Name=6;  
CC IsoId=O43497-6; Sequence=VSP\_000943, VSP\_000946;  
CC Name=7;  
CC IsoId=O43497-7; Sequence=VSP\_000943, VSP\_000947;  
CC Name=8;  
CC IsoId=O43497-8; Sequence=VSP\_000940, VSP\_000943, VSP\_000947;  
CC Name=9;  
CC IsoId=O43497-9; Sequence=VSP\_000940, VSP\_000946;  
CC Name=10;  
CC IsoId=O43497-10; Sequence=VSP\_000940, VSP\_000945;  
CC Name=11;  
CC IsoId=O43497-11; Sequence=VSP\_000946;  
CC Name=12;  
CC IsoId=O43497-12; Sequence=VSP\_000947;  
CC Name=13;  
CC IsoId=O43497-13; Sequence=VSP\_000944, VSP\_000946;  
CC Name=14;  
CC IsoId=O43497-14; Sequence=VSP\_000941, VSP\_000942;  
CC -1- TISSUE SPECIFICITY: Highly expressed in brain, in particular in  
CC the amygdala, subthalamic nuclei, cerebellum and thalamus.  
CC Moderate expression in heart; low expression in placenta, kidney  
CC and lung. Also expressed in colon and bone marrow and in tumoral  
CC cells to a lesser extent. Highly expressed in fetal brain, but  
CC also in peripheral fetal tissues as heart, kidney and lung,  
CC suggesting a developmentally regulated expression.  
CC -1- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one  
CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -1- DOMAIN: The linker region between repeat III and IV probably play  
CC a role in the inactivation of the channel. The C-terminal part may  
CC be implicated in the anchoring of the protein to the membrane,  
CC this by interfering/restricting its lateral diffusion.  
CC -1- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II.  
CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AF134986; AAF19347.1; --  
CC EMBL; AF134985; AAF19346.1; --  
CC EMBL; AF227744; AAF37689.1; --  
CC EMBL; AF227745; AAF37690.1; --





QY	1539	VLMFVGVVVENFHKCRQHOEEAEARRRERKRLRLEKKRR-----SKEQMAE	1587
Db	1528	VLMFVGVVVENFHKCRQHOEEAEARRRERKRLRLEKKRNLMLDDVTASGSSASAASE	1587
QY	1588	AQCKPYSDYSRFRLLVHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKICN	1647
Db	1588	AQCKPYSDYSRFRLLVHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKICN	1647
QY	1648	YIFTVIFVESVFKLVAFARFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTI	1707
Db	1648	YIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTI	1707
QY	1708	IRIMRVLRIRARVLKLLKMAVGMRAILLHTVMQALPQVGNLGLLFMLFFIFAALGVELEFGD	1767
Db	1708	IRIMRVLRIRARVLKLLKMAVGMRAILLDTVMQALPQVGNLGLLFMLFFIFAALGVELEFGD	1767
QY	1768	LECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOPSRDCDOESTCYNTVIS	1827
Db	1768	LECDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDOESTCYNTVIS	1827
QY	1828	PIYFVSFVLTAQFVLNVNVIIVLMKHLEESNKEAELEAELEAELEMTLSPQPHSPLG	1887
Db	1828	PIYFVSFVLTAQFVLNVNVIIVLMKHLEESNKEAELEAELEAELEMTLSPQPHSPLG	1887
QY	1888	SPFLWPGVEGVNSTDSPKPGAPHTTAHIGAAAGFSLEHPT-----	1927
Db	1888	SPFLWPGVEGVNSTDSPKPGALHPAAHARSASHFSLEHPTDRQLFDTISLLIQGSLEWEL	1947
QY	1928	-----	1927
Db	1948	KLMDELAGPGGQPSAPPSAPSLGGSDPQIPLAEMEALSLTSEIVSEPSCSLALTDSDLPD	2007
QY	1928	-----MVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL	1974
Db	2008	DMHTLLLSALESNNQPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPL	2064
QY	1975	GHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHCAPTWGAI PKLPPGRSP	2034
Db	2065	GHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLQLPHSAPTWTGTIPKLPPGRSP	2124
QY	2035	LAQRPLRRQAAIRTDSDLVQGLGSRDILLSEVSGPSCPLTRSSSFVGGSSIQVQQRSGIQ	2094
Db	2125	LAQRPLRRQAAIRTDSDLVQGLGSRDILLAEVSGPSPPLARAYFWGQSSTQAQQHSRSH	2184
QY	2095	SKVSKHIRLPAPCPGLEPSWAKOPPETRSSLELDTLSWISGDLL- PSSQEEPLFRDLK	2153
Db	2185	SKISKHMTPPAPCPGPEPNWGKPPETRSSLELDTLSWISGDLLPPPGQEEPPSPRDLK	2244
QY	2154	KCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSSSLGGQPLGGPGRPKK	2213
Db	2245	KCYVEAQSCQRRPTSPWLDQRRHSIAVSCLDGSGQPHLGTDPNLGGQPLGGPGRPKK	2304
QY	2214	KLSPPSISIDPPESQSGRPPCPSPGVCLRRRAPASDKDPSVSSPLDSTAASPPKKDTLS	2273
Db	2305	KLSPPSITIDPPESQSGRTPPSPGICLRRRAPSSDKDPLASGPPDSMAASPPKKDVL	2364
QY	2274	LSGLSSDPTDMDP	2286
Db	2365	LSGLSSDPADLDP	2377
RESULT 6			
Q6ZPX4			
ID	Q6ZPX4	PRELIMINARY;	PRT; 1389 AA.
AC	Q6ZPX4;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	MKIAA1123	protein (Fragment).	
GN	Name=mKIAA1123;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	PubMed=14621295;
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA	Saga Y., Nagase T., Ohara O., Koga H.;
RT	"Prediction of the coding sequences of mouse homologues of KIAA gene:
RT	III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT	cDNAs identified by screening of terminal sequences of cDNA clones
RT	randomly sampled from size-fractionated libraries.";
RL	DNA Res. 10:167-180(2003).
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC	-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC	family.
DR	EMBL; AK129294; BAC98104.1; -.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0005886; C:plasma membrane; IDA.
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR	InterPro; IPR001682; Ca/Na_pore.
DR	InterPro; IPR002111; Cat_channel_TrpL.
DR	InterPro; IPR002077; Ca_channel_alpha.
DR	InterPro; IPR005821; Ion_trans.
DR	InterPro; IPR005820; M_channel_nlg.
DR	Pfam; PF00520; Ion_trans; 3.
DR	PRINTS; PR00167; CACHANNEL.
KW	Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW	Ion transport; Ionic channel; Transmembrane; Transport;
KW	Voltage-gated channel.
FT	NON TER 1
SQ	SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;
Query Match 56.6%; Score 6809.5; DB 2; Length 1389;	
Best Local Similarity 94.8%; Pred. No. 0;	
Matches 1317; Conservative 8; Mismatches 29; Indels 35; Gaps 3;	
QY	933 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 992
Db	1 LPDRKNFDSLLWAIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 60
QY	993 VAILVEGFQAE-----GDATKSESEPDFSPSVDGDGDRKKR 1029
Db	61 VAILVEGFQAEIGKREDTSGQLSCIQLPVNSQGGDATKSESEPDFSPSVDGDGDRKKR 120
QY	1030 LALVALGEHAELRKSLLPPLIIHTAATPMSPKSSSTGVGEALGSGRRRTSSSGSAEPGA 1089
Db	121 LALVALGEHSELKSLPPLIIHTAATPMSPKSSSTGVGEALGSGRRRTSSSGSAEPGT 180
QY	1090 AHHEMKPPSARSSPHSPWSAASSWTSRRSSRNISGRAPSLKRRSPSGERRSLLSGEQE 1149
Db	181 AHHEMKSPPSARSSPHSPWSAASSWTSRRSSRNISGRAPSLKRRSPSGERRSLLSGEQE 240
QY	1150 SQDEEESSEEDRASPGSDHRRGSLEREAKSSFDPDLPTLQVPLHRTASGRSSASEHQD 1209
Db	241 SQDEEESSEEDRASPGSDHRRGSLEREAKSSFDPDLPTLQVPLHRTASGRSSASEHQD 300
QY	1210 CNGKSASGRLLARTLRDTPDQLDGGDDNDEGNLSKGERIQAWRSRLPACCRERDSWSAYI 1269
Db	301 CNGKSASGRLLARTLRADDPPLDGGDDGDDNDEGNLSKGERLAWVRARLPACCRERDSWSAYI 360
QY	1270 FPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITTIAMERP KIDPHSAERIFLTLSNYIFT 1329
Db	361 FPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITTIAMERP KIDPHSAERIFLTLSNYIFT 420
QY	1330 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLGGLVLSVIDILVSMVSDSGTKILGMLR 1389
Db	421 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLGGLVLSVIDILVSMVSDSGTKILGMLR 480
QY	1390 VLRLRLTLRLRVLVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLPKGKF 1449
Db	481 VLRLRLTLRLRVLVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLPKGKF 540

QY 1450 FVCQGEDTRNITNKSDCAEASRVRHRYKYNFDNLGQALMSFLVASKDGVWDIMYDGLDA 1509  
DB 541 FVCQGEDTRNITNKSDCAEASRVRHRYKYNFDNLGQALMSFLVASKDGVWDIMYDGLDA 600  
QY 1510 VGVDQOPIMNHPWMLLYFISFLLIIVAFVNLNMFVGVVVENFHKCRQHQQEERREBEK 1569  
DB 601 VGVDQOPIMNHPWMLLYFISFLLIIVAFVNLNMFVGVVVENFHKCRQHQQEERREBEK 660  
QY 1570 RLRLLEKKRR-----SKEKQMAEBAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 1618  
DB 661 RLRLLEKKRRNMLDDVIASGSSASAASEAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 720  
QY 1619 GVIGLNVVTVMAEHYQOQILDEALKICNYIFTVIFVFSVFKLVAPAPRRFFQDRWNQL 1678  
DB 721 GVIGLNVVTVMAEHYQOQILDEALKICNYIFTVIFVFSVFKLVAFGRFFQDRWNQL 780  
QY 1679 DLAIVLLSIMGITLEEIEVNLNLPINPTIIRIMRVLRARVLLKLMKAVGMRLHTVMQ 1738  
DB 781 DLAIVLLSIMGITLEEIEVNLNLPINPTIIRIMRVLRARVLLKLMKAVGMRLHTVMQ 840  
QY 1739 ALPQVGNLGLFMLFFIFAALGVLFGLDECEHPCEGLGRHATFRNFGMAFLTLFRV 1798  
DB 841 ALPQVGNLGLFMLFFIFAALGVLFGLDECEHPCEGLGRHATFRNFGMAFLTLFRV 900  
QY 1799 STGDNWNGIMKDPDRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMKHLSESN 1858  
DB 901 STGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMKHLSESN 960  
QY 1859 KEAKEEALEAELEEMKTLSPQPHSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAA 1918  
DB 961 KEAKEEALEAELEEMKTLSPQPHSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAA 1020  
QY 1919 -SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1977  
DB 1021 SSGFSLEHPTMVPHTEEGVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1080  
QY 1978 GWGLPKAQSGSILSVHSQPADTSCILQPLPKDVHYLLQPHGAPTWGAIPKLP PPGSRPLAQ 2037  
DB 1081 GWGLPKAQSGSILSVHSQPADTSCILQPLPKDAHYLLQPHGAPTWGAIPKLP PPGSRPLAQ 1140  
QY 2038 RPLRRQAAIRTDSDVQGLGSRREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQRSGIQSKV 2097  
DB 1141 RPLRRQAAIRTDSDVQGLGSRREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQRSGIQSKV 1200  
QY 2098 SKHIRLPAPCGLEPSWAKDPPETRSLSLELDTLSWISGDLPLPSSQEEPLFPRLDKKCY 2157  
DB 1201 SKHIRLPAPCGLEPSWAKDQETRSLSLELDTLSWISGDLPLPSSQEEPLSPRLDKKCY 1260  
QY 2158 VETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRCLPSPSSLGQPLGGPGSRPKKLSP 2217  
DB 1261 VEAQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRCLPSPSSLGQPLGGPGSRPKKLSP 1320  
QY 2218 PSISIDPPESQSRPPCPSPGVCLRRRAPASDKSPSVSSPLDSTAASPKKDTLSLSGL 2277  
DB 1321 PSISIDPPESQSRPPCPSPGVCLRRRAPASDKSPSASSPLDSTAASPKKDALSLSG 1380  
QY 2278 SSDPTDMDP 2286  
DB 1381 SSDPTDLDP 1389

RESULT 7  
CCAH\_RAT STANDARD; PRT; 2359 AA.  
ID\_CCAH\_RAT  
AC Q9EQ60;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).  
DE Name=Cacnalh;  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]\_SEQUENCE FROM N.A.  
TISSUE=Brain;  
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;  
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G., Baillie D.L., Stea A., Snutch T.P.;  
RT "Molecular and functional characterization of a family of rat brain T-type calcium channels";  
RL J. Biol. Chem. 276:3999-4011(2001).  
CC -I- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -I- TISSUE SPECIFICITY: Expressed in brain.  
CC -I- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.  
CC -I- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.  
CC -I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.  
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EMBL; AF290213; AAC35187.1; --  
RGD; 68943; Cacnalh.  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_TpL.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCALPHA1.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR01629; TVDCCALPHA1.  
KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;  
KW Multigene family; Phosphorylation; Repeat; Transmembrane;  
KW Voltage-gated channel.  
FT REPEAT 87 422 I.  
FT REPEAT 776 1015 II.  
FT REPEAT 1292 1569 III.  
FT REPEAT 1607 1868 IV.  
FT DOMAIN 1 100 Cytoplasmic (Potential).  
FT TRANSMEM 101 119 S1 of repeat I (Potential).  
FT DOMAIN 120 139 Extracellular (Potential).  
FT TRANSMEM 140 160 S2 of repeat I (Potential).  
FT DOMAIN 161 169 Cytoplasmic (Potential).  
FT TRANSMEM 170 184 S3 of repeat I (Potential).  
FT DOMAIN 185 193 Extracellular (Potential).  
FT TRANSMEM 194 212 S4 of repeat I (Potential).  
FT DOMAIN 213 232 Cytoplasmic (Potential).  
FT TRANSMEM 233 253 S5 of repeat I (Potential).  
FT DOMAIN 254 394 Extracellular (Potential).





Db 1290 PNRRLRVSQKVI AHKMFHDVVLVFI FLNCITIALERPDIDPGSTERAFLSVSNYIFTAI 1349  
QY 1332 FLAEMTVKVVALGWC FGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1391  
Db 1350 FVEMVMKVVALG LLLWGEHAYLQSSWNVDGLLVLSVDIIVAMASAGGAKILGVLRVW 1409  
QY 1392 RLLRTLRLPLRVISRAQGLKLVVETLMSILKPIGNIVVICCAFFIIFGILGVQLFKGFV 1451  
Db 1410 RLLRTLRLPLRVISRAPGLKLVVETLSSILRPIGNIVLICCAFFIIFGILGVQLFKGFY 1469  
QY 1452 CQGEDTRNITNKSDCAEASRWRHKNFDFNLGQALMSFLVLSKDGWVDIMYDGLDAVG 1511  
Db 1470 CEGTDTRNITTKAECHAAHYRWRRKYNFDFNLGQALMSFLVLSKDGWVNIMYDGLDAVG 1529  
QY 1512 VDQOPIMNHNPMMLLYFISFLLI VAFVLMFVGVVVENFHKRQHQBEEARRREKRL 1571  
Db 1530 IDQOPVQNHNPWMLLYFISFLLI VSFVLMFVGVVVENFHKRQHQBEEARRREKRL 1589  
QY 1572 RRLEKKRRSKEQMAEAOCKPYYSRFRLLVHHLCTSHYLDLPITGVIGLNVVTNAME 1631  
Db 1590 RRLERRR-----KAQRRPYADYSHTRRSIHSLCTSHYLDLPITFIICLNVTMSME 1642  
QY 1632 HYQPOILDEALKICNYIFTVIFVFSVKLVAFARRFFQDRWNQLDLAI VLLSINGIT 1691  
Db 1643 HYNQPKSLDEALKYCNVFTIVFVEAALKLVAFGFRFFQDRWNQLDLAI VLLSINGIA 1702  
QY 1692 LEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALPOVGNLGLLFM 1751  
Db 1703 LEEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATGMRALDVTVQALPOVGNLGLLFM 1762  
QY 1752 LFFFIYAALGVLEFGDLECEDETHPCEGILGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDP 1811  
Db 1763 LFFFIYAALGVLEFGRLCESDNPNCEGLSRHATFTNFGMAFLTLFRVSTGDNWNGIMKDT 1822  
QY 1812 SRDC---DQESTCYNVTISP IYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELE 1868  
Db 1823 LRECTREDKHLSYLPALSPVYFVT FMLVAQFVLNVVIAVLMKHLEESNKEAREDAEMD 1882  
QY 1869 AELELEMKTLSPQHSPLGSPFLWPVGEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTM 1928  
Db 1883 AEIELEM-----AQGSTAQPPTAQES----- 1904  
QY 1929 VPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRWGMLP----- 1982  
Db 1905 -----QGTQDTPNLLVWRKVSVRMLSLPNDSYMFRPVAPAAAPHSH-----PLQEVEM 1954  
QY 1983 KAQGSILSVHSQPADTSCILQLP-----KDVHYLLQHPGAPTGAIPKLPPPGRS 2033  
Db 1955 ETYTGPVTSAPHPLEPRASFQVPSAASSPARVSDPLCALSRGTP-----RS 2002  
QY 2034 PLAQRPLRRQAI RTDSDL--VQGLSREDLLSEVSGPSCPLTRSSFWG----- 2082  
Db 2003 LSLSRILCRQEAHSESLEGGKVDVVG--DSIPDYTEPAENNMSTSQASTGAPRSPPCSPR 2060  
QY 2083 -SSIQVQORSIGTSKVKHIRLPAPCGLEPWSWAKOPPETRSSLELDTELSWISGDL LPS 2141  
Db 2061 PASVTRTKHTFGQRCISSR----PPTLGGDEAEAADP-----ADEEVSHITSSAHPW 2108  
QY 2142 SQEPLFP-----RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAV---- 2181  
Db 2109 PATEPHSPEASPTASPVKGTMGSGRDRPRFCSVDAQSF LDKPG-RPDAQRWSSVELDNGE 2167  
QY 2182 SCLDSGS-----QPRLCPSSSLGGQPLGGPSRKKLSPPSISIDPP--ESQGSR 2231  
Db 2168 SHLESGEVRGRASLEPAL-----GSRKKKMSPPCISIEPTTKDEGSSR 2212  
QY 2232 PPCSPG--VCLRRRAPADS---KDPVSSSLPLDSTAASP-----SPKKDTLSLSG 2276  
Db 2213 PPAEAGGNTTLRRRTPSCEAALHRDCPEPTGPGTGGDPVAKGERWGQASCR AEHLTVPN 2272  
QY 2277 LSSDPTDM 2284  
: : | |

Db 2273 FAFEPLDM 2280  
RESULT 8  
CCAH\_HUMAN  
ID CCAH\_HUMAN STANDARD; Q96QI6; Q96RZ9; Q9NYY4; Q9NYY5;  
AC O95180; O95802; Q8WWI6; Q96QI6; Q96RZ9; Q9NYY4; Q9NYY5;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated calcium channel alpha 3.2 subunit).  
DE Name=CACNA1H;  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Heart;  
RX MEDLINE=98333998; PubMed=9670923;  
RA Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N., Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.;  
RT "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family.";  
RL Circ. Res. 83:103-109(1998).  
RN [2]  
RP REVISIONS.  
RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Thyroid carcinoma;  
RX MEDLINE=99127945; PubMed=9930755;  
RA Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F., Prodanovich P., Harpold M.M., Stauderman K.A.;  
RT "Structure and functional characterization of a novel human low-voltage activated calcium channel.";  
RL J. Neurochem. 72:791-799(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;  
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.;  
RT "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";  
RL Hum. Mol. Genet. 10:339-352(2001).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Testis;  
RX MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200;  
RA Jagannathan S., Punt E.L., Gu Y., Arnoult C., Sakka S., Barratt C.L., Publicover S.J.;  
RT "Identification and localization of T-type voltage-operated calcium channel subunits in human male germ cells. Expression of multiple isoforms.";  
RL J. Biol. Chem. 277:8449-8456(2002).  
RN [6]  
RP SEQUENCE OF 86-817 FROM N.A.  
RA Cobley V.E.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).  
RA Mittman S., Agnew W.S.;  
RT "Organization and alternative splicing of CACNA1H.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H



CC gives rise to T-type calcium currents. T-type calcium channels  
CC belong to the "low-voltage activated (LVA)" group and are strongly  
CC blocked by nickel and mibefradil. A particularity of this type of  
CC channels is an opening at quite negative potentials, and a  
CC voltage-dependent inactivation. T-type channels serve pacemaking  
CC functions in both central neurons and cardiac nodal cells and  
CC support calcium signaling in secretory cells and vascular smooth  
CC muscle. They may also be involved in the modulation of firing  
CC patterns of neurons which is important for information processing  
CC as well as in cell growth processes.  
CC  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=AlH-a;  
CC IsoId=O95180-1; Sequence=Displayed;  
CC Name=2; Synonyms=AlH-b;  
CC IsoId=O95180-2; Sequence=VSP\_000949;  
CC TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.  
CC  
CC -!- Isoform 2 seems to be testis-specific.  
CC  
CC -!- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one  
CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC  
CC -!- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II.  
CC  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
CC  
CC -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown  
CC in this entry. The additional 20 amino acids found in the Ref.4  
CC and Ref.6 sequences are due to a misunderstanding of the real type  
CC of splicing mechanism involved.  
CC  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; AF051946; AAC67239.3; -  
CC EMBL; AF073931; AAD17668.1; -  
CC EMBL; AE006466; AAK61268.1; ALT\_SEQ.  
CC EMBL; AJ420779; CAD12646.1; -  
CC EMBL; AL031703; CAC42094.1; ALT\_SEQ.  
CC EMBL; AF223562; AAF60162.1; -  
CC EMBL; AF223563; AAF60163.1; -  
CC Genbank; HGNC:1395; CACNA1H.  
CC  
CC MIM; 607904; -  
CC DR GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.  
CC DR GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.  
CC DR GO; GO:0006936; P:muscle contraction; TAS.  
CC DR GO; GO:0007520; P:myoblast fusion; TAS.  
CC DR GO; GO:0008016; P:regulation of heart rate; TAS.  
CC DR GO; GO:0006810; P:transport; TAS.  
CC DR InterPro; IPR001682; Ca/Na\_pore.  
CD InterPro; IPR002111; Cat\_channel\_TrpL.  
CD InterPro; IPR005821; Ion\_trans.  
CD InterPro; IPR005820; M+channel\_nlg.  
CD InterPro; IPR005445; TVDCCAlphal.  
CD Pfam; PF00520; Ion\_trans; 4.  
CD PRINTS; PR01629; TVDCCAlphAl.  
KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;  
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;  
KW Repeat; Transmembrane; Voltage-gated channel.  
FT REPEAT 87 422 I.  
FT REPEAT 779 1018 II.  
FT REPEAT 1281 1558 III.  
FT REPEAT 1602 1863 IV.  
FT DOMAIN 1 100 Cytoplasmic (Potential).  
FT TRANSMEM 101 119 S1 of repeat I (Potential).  
FT DOMAIN 120 139 Extracellular (Potential).

FT	TRANSMEM	140	160	S2 of repeat I (Potential).
FT	DOMAIN	161	169	Cytoplasmic (Potential).
FT	TRANSMEM	170	184	S3 of repeat I (Potential).
FT	DOMAIN	185	193	Extracellular (Potential).
FT	TRANSMEM	194	212	S4 of repeat I (Potential).
FT	DOMAIN	213	232	Cytoplasmic (Potential).
FT	TRANSMEM	233	253	S5 of repeat I (Potential).
FT	DOMAIN	254	394	Extracellular (Potential).
FT	TRANSMEM	395	419	S6 of repeat I (Potential).
FT	DOMAIN	420	793	Cytoplasmic (Potential).
FT	TRANSMEM	794	814	S1 of repeat II (Potential).
FT	DOMAIN	815	827	Extracellular (Potential).
FT	TRANSMEM	828	849	S2 of repeat II (Potential).
FT	DOMAIN	850	855	Cytoplasmic (Potential).
FT	TRANSMEM	856	874	S3 of repeat II (Potential).
FT	DOMAIN	875	882	Extracellular (Potential).
FT	TRANSMEM	883	906	S4 of repeat II (Potential).
FT	DOMAIN	907	917	Cytoplasmic (Potential).
FT	TRANSMEM	918	938	S5 of repeat II (Potential).
FT	DOMAIN	939	990	Extracellular (Potential).
FT	TRANSMEM	991	1015	S6 of repeat II (Potential).
FT	DOMAIN	1016	1290	Cytoplasmic (Potential).
FT	TRANSMEM	1291	1313	S1 of repeat III (Potential).
FT	DOMAIN	1314	1331	Extracellular (Potential).
FT	TRANSMEM	1332	1352	S2 of repeat III (Potential).
FT	DOMAIN	1353	1362	Cytoplasmic (Potential).
FT	TRANSMEM	1363	1382	S3 of repeat III (Potential).
FT	DOMAIN	1383	1396	Extracellular (Potential).
FT	TRANSMEM	1397	1418	S4 of repeat III (Potential).
FT	DOMAIN	1419	1428	Cytoplasmic (Potential).
FT	TRANSMEM	1429	1452	S5 of repeat III (Potential).
FT	DOMAIN	1453	1529	Extracellular (Potential).
FT	TRANSMEM	1530	1555	S6 of repeat III (Potential).
FT	DOMAIN	1556	1616	Cytoplasmic (Potential).
FT	TRANSMEM	1617	1637	S1 of repeat IV (Potential).
FT	DOMAIN	1638	1651	Extracellular (Potential).
FT	TRANSMEM	1652	1673	S2 of repeat IV (Potential).
FT	DOMAIN	1674	1680	Cytoplasmic (Potential).
FT	TRANSMEM	1681	1699	S3 of repeat IV (Potential).
FT	DOMAIN	1700	1713	Extracellular (Potential).
FT	TRANSMEM	1714	1737	S4 of repeat IV (Potential).
FT	DOMAIN	1738	1751	Cytoplasmic (Potential).
FT	TRANSMEM	1752	1772	S5 of repeat IV (Potential).
FT	DOMAIN	1773	1835	Extracellular (Potential).
FT	TRANSMEM	1836	1863	S6 of repeat IV (Potential).
FT	DOMAIN	1864	2353	Cytoplasmic (Potential).
FT	DOMAIN	520	530	Poly-His.
FT	DOMAIN	1107	1110	Poly-Ser.
FT	DOMAIN	1583	1586	Poly-Arg.
FT	SITE	378	378	Calcium ion selectivity and permeability (By similarity).
FT	SITE	974	974	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1504	1504	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1808	1808	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).
Query Match 51.7%; Score 6222; DB 1; Length 2353;				
Best Local Similarity 56.7%; Pred. No. 5.5e-296;				
Matches 1370; Conservative 208; Mismatches 529; Indels 310; Gaps 62;				
Qy	25	PPGPRLARGWTRRRMERAPRSRDS-	--VASRSSTTCPPGPGGAAGAGSTKDPGSADSEAE	82
Db	19	PPGPAALVG-----ASPE	PGAPGREARGSELGVSPE	69
Qy	83	LPYPALAPVVFYLSQDSRPR	SWCLRTVCNPNWFERVSMVL	142
Db	70	VPYPALAAATVFFCLGQTTR	PRSWCLRLVCNPNWFEHVS	129
Qy	143	SQRCRILQAFDDFI	PAFFAVEMVVVMVALGIFG	202

Db 130 SERCNILEAFDAFIAFAVEMVIMKVALGLFGOKCYLGDWNRDLDFIIVAGMMEYSLD 189  
QY 203 LQNVFSAVRTVRVLRPLRAINRVPMSRILVTLTLLDTPMLGNVLLCCFFVFFIFGIVGV 262  
Db 190 GHNVSLSAIRTVRVRPLRAINRVPMSRILVTLTLLDTPMLGNVLLCCFFVFFIFGIVGV 249  
QY 263 QLWAGLLNRNRCFLPENFSLPLSVD-LEPYQOTENEDESPPFICSQPRENGMRSCRSVPTLR 321  
Db 250 QLWAGLLNRNRCFLDSAFVRNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHIP--- 306  
QY 322 GEGGGPPCSDLVETYN-----SSSNTTCVNWNQYTYNCSAGEHNPFKGAINFDNIGY 374  
Db 307 GRRELMPCTLGWEAYTQPAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGY 366  
QY 375 AWIAIFQVITLEGWVIMYFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETK 434  
Db 367 AWIAIFQVITLEGWVIMYVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETK 426  
QY 435 QRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAGVRA 494  
Db 427 QRESQLMREQVARHLSNDSTLASFSEPGSCYEELLKYVGHIFRKYVRRSLRLYARWQSRW 486  
QY 495 GLLSSPVARSQGPSPSGSCTRSHR-----LSVHLV-HHHHHHHHHYHLNGTLRV 546  
Db 487 RKKVDPASVQGP-----GHRQRRAGRHTASVHLVYHHHHHHHHYHFGSGSPRR 538  
QY 547 PRASPEIQDRDANGSRRML-PPPSPTPPSGGPPRGAESVHSFYHADCHLE--PVRQA 602  
Db 539 PGPEPGACD-----TRLVRAGAPSPSPSGRGP-DAESVHSIYHADCHIEGPQERARV 591  
QY 603 PPRPCPSEASGR-TVGSGKV-YPTV-----HTSPPPPEILKDKALVEVAPSP---- 646  
Db 592 AHAATAAASRLATGLTMNYPTILPSGVSGKSTSPGK-----GKWAGGPPGTG 644  
QY 647 --GPPTLTSFNTPPGPFSSMHKLLTQSTGAC--HSS-----CKISSPCSKADSGACGPD 697  
Db 645 GHGPLSLNS-----PDYKIPHVVGHEGLGQAPCHLSGLSVPCPLSP--PAGTLTCELK 698  
QY 698 SCPYCART-GACEPESADHVPDSDSEAYVEFTQDAQHSDLRDP----- 740  
Db 699 SCPYCTRALEDEGELSGSESGSDGRGYEFTQDVRHGDRWDTPRPRATDTPGPGGS 758  
QY 741 HSRRRQSLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQ 800  
Db 759 PORRAQQAAP-GEPGWGRLVWTFSGKLRRIVDSKYFSRGIMAILVNTLSMGVEYHEQ 817  
QY 801 PEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQOG 860  
Db 818 PEELTNALEISNIVFTSMFALEMLKLLACGPLGYIRNPYNIFDGIIVVISWEIVGQAD 877  
QY 861 GGLSVLRTFRLMRVLKLVFLPALQRLVVLMTMDNVATFCMLMLFIFIFSILGMHLF 920  
Db 878 GGLSVLRTFRLRLVLKLVFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLF 937  
QY 921 GCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIA 979  
Db 938 GCKFSLKTDGTVPDRKNFDSLLWAIVTVFQILTQEDWNVLYNGMASTSSWAALYFVA 997  
QY 980 LMTFGNYVLFNLLVAILVEGFAEGDAFKSESEPDFFSPSVDGDGRKKRLALVAL---- 1035  
Db 998 LMTFGNYVLFNLLVAILVEGFAEGDANRSDTDEKTSVHFEBDFHKLRELQTELKMC 1057  
QY 1036 ----GEHAELRKSLLPPLIIHTAATPMSHPKSSS-TGVGEALGSGSRRTSSSGSAEPGA 1089  
Db 1058 LAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGSSSSGDDPLG- 1116  
QY 1090 AHHEMKPPSARSPSPSWSAASSWTSSRRSNLSGRAPSLKRRSPSGERRSLLSGEGQE 1149  
Db 1117 ---DQKPPASLRSSPCAPWGPSPGAWSSRRSSWSSLSGRAPSLKRRGQCGERESLLSGEGKG 1173  
QY 1150 SQDEEESSEEDRASPA--GSDHRHRGSLEREAKSFDLPDTL-----QVPLGH-----R 1196

Db 1174 STDDE--AEDGRAAPGPRATPLRRRAESLDRPLRPAALPPTKCRDRDQVVALPSDFFLR 1231  
QY 1197 TASGRSSASEHQCNGKSASGRLARLTRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLP 1256  
Db 1232 IDSHREDAAEELDDSDSCCLRLHKVLEPYKQ-----W----- 1265  
QY 1257 ACCRERDSWAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSA 1316  
Db 1266 --CRSREAWALYLFSPQNRFRVSCQVITHKMFHDHVLVFIFLNCVTIALERPDIDPGST 1323  
QY 1317 ERIFLTLSNYIFTAVFLAEMTVKVVALGCWCFGEQAYLRSSWNVDGLLVLISVIDILVSM 1376  
Db 1324 ERVFLSVSNYIFTAIFVAEMVMKVVALGGLLSGEHAYLQSSWNLLDGLLVLVSLVDIVVAM 1383  
QY 1377 VSDSGTKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFII 1436  
Db 1384 ASAGGAKILGLVLRVLRLLRLTLRPLRVISRAPGLKLVVETLISLRLPIGNIVLICCAFFII 1443  
QY 1437 FGILGVQLFKGPFVCOGEDTRNITNKSDCAEASYRWVRHKYNFNDNLGOALMSLFLVASK 1496  
Db 1444 FGILGVQLFKGPFYCEGPDTRNISTKAQCAAHYRWVRKYNFNDNLGOALMSLFLVSSK 1503  
QY 1497 DGWVDIMYDGLDVGVDQOQIMNHNPMWMLLYFISFLLIYAFVFLNMFGVVVENFHKCRQ 1556  
Db 1504 DGWVNIMYDGLDVGVDQOQVQNHNPWMLLYFISFLLIYFVFLNMFGVVVENFHKCRQ 1563  
QY 1557 HOEEEEARRREKRLRREKRRSKEKQMAEAOCKPYSDYSRFRLLVHHLCTSHYLDLF 1616  
Db 1564 HQEABEARREKRLRRLRRRRRSTFPS-PEAQRPPYADYSPTRRSIHSLSCTSHYLDLF 1622  
QY 1617 ITGVIGLNVVTMAMEHYQOQOILDEALKICNYIFTVIFVESVFKLVAFARFRFFQDRWN 1676  
Db 1623 ITFIIICNVITMSMEHYNQPKSLDEALKYCNVFTIVFVEAALKLVAFGFRFRFFQDRWN 1682  
QY 1677 QLDLAILVLSIMGITLEEIEVNLSLPINPTIIRIMRVLIARVLLKLMKAVGMRLHHTV 1736  
Db 1683 QLDLAILVLSIMGITLEEIEMSAALPINPTIIRIMRVLIARVLLKLMKATGMRLALDTV 1742  
QY 1737 MQALPQVGNLGLLMLLFFIFAALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLF 1796  
Db 1743 VQALPQVGNLGLLMLLFFIYAALGVELFGRLECEDNCPCELSRHATFSNFGMAFLTLF 1802  
QY 1797 RVSTGDNWNGIMKDPDRDC--DOESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKH 1853  
Db 1803 RVSTGDNWNGIMKDTLRECSREDXCHLSYLPALSPVYFTFVLVAQFVLNVNVIIVLMKH 1862  
QY 1854 LEESNKEAKEAEAELEAELEEMKTLSPQSPHSPGLSPFLWPGVEGVNSTDSPKPGAPHTTA 1913  
Db 1863 LEESNKEAREDAELDAEIELEMA-----QGPASRRVADARP----- 1899  
QY 1914 HIGAAAGSFSLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--- 1970  
Db 1900 -----PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP 1943  
QY 1971 -----ERSLHGRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVH-----YLLQP 2015  
Db 1944 HPRPLQEVEMETYGAGTP--LGSVASVHSPPAESCASLQIPLAVSSPARSGEPLHALSP 2000  
QY 2016 HGAPTWGAIPKLPPPGRSPLAQRPLRQAAIRTDLSLDVQGLGSRDILLSEV----SGPSC 2071  
Db 2001 RGT-----ARSPLSRLLCRQEAHVHTDSLEGK-IDSPRDTLDPAEPEGKTPVR 2047  
QY 2072 PLTRSSFWGGSSIQVQORSIGIQSKV--SKH-----IRLPAPCPGLEPSWAKDPPETRS 2123  
Db 2048 PVTQ-----GGSLSQSPRSPRPAVTRKHTFGQRCVSSRPAAPGGEAEASDP----- 2096  
QY 2124 SLELDELISWISGDLLP-SSQEEPLFP-----RDLKKYCVETQSCRRRRPGFWLDE 2173  
Db 2097 ---ADEEVSHITSSACPWQPTAEPHGPEASPVAGGERDLRLYSDAQGLDKPG-RADE 2152  
QY 2174 QRRHSIAVSCLDGSGQRLCPSPSISLGGQPLGGP--GSRPKKLSPPSISIDPP-ESQGS 2230  
Db 2153 QWRPSAE---LGSGE-----PGEAKAWG-PEAEPALGARKKKMSPPCISVEPPAEDEGS 2203

QY 2231 -RPKSPG-VCLRRAPA-----SDSKDPSVSPDSTAAS-----PSPKOTLSL 2274

Db 2204 ARPSAEGGSTTLRRTPSCBTPHRDLSLEPTGSCAGGDPAAKGERWGQASCRAEHLTV 2263

QY 2275 SGLSSDPTDM-----DP 2286

Db 2264 PSFAFEPLDLGVPSGDP 2280

RESULT 9

CCAH\_MOUSE

ID\_CCAH\_MOUSE STANDARD; PRT; 2365 AA.

AC O88427; Q9JKU5;

DT 15-JUL-1999 (Rel. 38, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).

GN Names=Cacnalh;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RA Mitterman S.;

RT "Exon organization of mouse Cacnalh.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1823-1952 FROM N.A.

RC STRAIN=C57BL/6J;

RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.

CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by Cam-kinase II.

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

CC -----

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CC -----

CC EMBL; AF226868; AAK21607.2; --

DR EMBL; AY026385; AAK21607.2; JOINED.

DR EMBL; AF051947; AAC67240.1; --

DR MGD; MGI:1928842; Cacnalh.

DR InterPro; IPR001682; Ca/Na\_pore.

DR InterPro; IPR002111; Cat\_channel\_TripL.

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR005820; M+channel\_nlg.

DR InterPro; IPR005445; TVDCCALphal.

DR Pfam; PF00520; Ion\_trans; 4.

DR PRINTS; PR01629; TVDCCALPHAL.

KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;

KW Multigene family; Phosphorylation; Repeat; Transmembrane;

KW Voltage-gated channel.

FT REPEAT 87 422 I.

FT REPEAT 776 1015 II.

FT REPEAT 1292 1569 III.

FT REPEAT 1613 1874 IV.

FT DOMAIN 1 100 Cytoplasmic (Potential).

FT TRANSMEM 101 119 S1 of repeat I (Potential).

FT DOMAIN 120 139 Extracellular (Potential).

FT TRANSMEM 140 160 S2 of repeat I (Potential).

FT DOMAIN 161 169 Cytoplasmic (Potential).

FT TRANSMEM 170 184 S3 of repeat I (Potential).

FT DOMAIN 185 193 Extracellular (Potential).

FT TRANSMEM 194 212 S4 of repeat I (Potential).

FT DOMAIN 213 232 Cytoplasmic (Potential).

FT TRANSMEM 233 253 S5 of repeat I (Potential).

FT DOMAIN 254 394 Extracellular (Potential).

FT TRANSMEM 395 419 S6 of repeat I (Potential).

FT DOMAIN 420 790 Cytoplasmic (Potential).

FT TRANSMEM 791 811 S1 of repeat II (Potential).

FT DOMAIN 812 824 Extracellular (Potential).

FT TRANSMEM 825 846 S2 of repeat II (Potential).

FT DOMAIN 847 852 Cytoplasmic (Potential).

FT TRANSMEM 853 871 S3 of repeat II (Potential).

FT DOMAIN 872 879 Extracellular (Potential).

FT TRANSMEM 880 903 S4 of repeat II (Potential).

FT DOMAIN 904 914 Cytoplasmic (Potential).

FT TRANSMEM 915 935 S5 of repeat II (Potential).

FT DOMAIN 936 987 Extracellular (Potential).

FT TRANSMEM 988 1012 S6 of repeat II (Potential).

FT DOMAIN 1013 1301 Cytoplasmic (Potential).

FT TRANSMEM 1302 1324 S1 of repeat III (Potential).

FT DOMAIN 1325 1342 Extracellular (Potential).

FT TRANSMEM 1343 1363 S2 of repeat III (Potential).

FT DOMAIN 1364 1373 Cytoplasmic (Potential).

FT TRANSMEM 1374 1393 S3 of repeat III (Potential).

FT DOMAIN 1394 1407 Extracellular (Potential).

FT TRANSMEM 1408 1429 S4 of repeat III (Potential).

FT DOMAIN 1430 1439 Cytoplasmic (Potential).

FT TRANSMEM 1440 1463 S5 of repeat III (Potential).

FT DOMAIN 1464 1540 Extracellular (Potential).

FT TRANSMEM 1541 1566 S6 of repeat III (Potential).

FT DOMAIN 1567 1627 Cytoplasmic (Potential).

FT TRANSMEM 1628 1648 S1 of repeat IV (Potential).

FT DOMAIN 1649 1662 Extracellular (Potential).

FT TRANSMEM 1663 1684 S2 of repeat IV (Potential).

FT DOMAIN 1685 1691 Cytoplasmic (Potential).

FT TRANSMEM 1692 1710 S3 of repeat IV (Potential).

FT DOMAIN 1711 1724 Extracellular (Potential).

FT TRANSMEM 1725 1748 S4 of repeat IV (Potential).

FT DOMAIN 1749 1762 Cytoplasmic (Potential).

FT TRANSMEM 1763 1783 S5 of repeat IV (Potential).

FT DOMAIN 1784 1846 Extracellular (Potential).

FT TRANSMEM 1847 1874 S6 of repeat IV (Potential).

FT DOMAIN 1875 2365 Cytoplasmic (Potential).

FT TRANSMEM 521 531 Poly-His.

FT DOMAIN 1594 1597 Poly-Arg.

FT SITE 378 Calcium ion selectivity and permeability (By similarity).

FT SITE 971 Calcium ion selectivity and permeability (By similarity).

FT SITE 1515 Calcium ion selectivity and permeability (By similarity).

FT SITE 1819 Calcium ion selectivity and permeability (By similarity).

FT FT

FT	CARBOHYD	192	192	N-linked (GlcNAc. .) (Potential).		
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).		
FT	CARBOHYD	1477	1477	N-linked (GlcNAc. .) (Potential).		
FT	CONFLICT	1823	1825	GIM -> ARG (in Ref. 2).		
FT	CONFLICT	1914	1914	D -> E (in Ref. 2).		
FT	CONFLICT	1945	1947	APA -> LLQ (in Ref. 2).		
FT	CONFLICT	1952	1952	S -> A (in Ref. 2).		
FT	CONFLICT	1953	2351	Missing (in Ref. 2).		
SQ	SEQUENCE	2365	AA; 261944 MW; 9A8A17570C210596 CRC64;			
Query Match						
Best Local Similarity 51.5%; Score 6190; DB 1; Length 2365;						
Matches 1356; Conservative 249; Mismatches 511; Indels 304; Gaps 61;						
Qy	30	LARGWTRRRMERAPRRSDSPVASRSSTTCPG-PG----	AAGAGST----	EKDPGS----	AD--	77
Db	6	LAADDEVRLGASPSAAPV--RASPASPGVGREEQ	RGS	SVLAPESPGTECGADLG		63
Qy	78	-SEAEGLPYPALAPVVFYLSQDSRPRSCLRTVCNPWF	ERVSMLVILLNCVTILGMFRPC			136
Db	64	ADEEQVPYPALAAATVFFCLGQTTTPRSWCLRLVCNPWF	EHISMLVIMLNCVTILGMFRPC			123
Qy	137	EDIACDSQRCRILOAFDDFIFAFFAVEMVVMVALGIFG	KCKCYLGDGTWNLDDFFIVIAGM			196
Db	124	EDVECRSERCISLEAFDDFIFAFFAVEMVVMVALGLF	GQCKCYLGDGTWNLDDFFIVMAGM			183
Qy	197	LEYSLDLQNVFSAVRTVRVLRPLRAINRVPSMRILVT	LLDTPMLGNVLLLCFFVFFI			256
Db	184	MEYSLDGHNVLSAIRTVRVLRLRAINRVPSMRILVT	LLDTPMLGNVLLLCFFVFFI			243
Qy	257	FGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LEPYQ	TENEDESPFICSQPRENGMRSCR			315
Db	244	FGIVGVQLWAGLLRNRCFLDSAFVRNNNLTLFLRPYQ	TEEGEENPFICSSRRDNGMQKCS			303
Qy	316	SVPT---LRGEGGGPPCSDLDETY-----	NSSNTTCVNNWQYTYTNC	SAGEHNPFKG		365
Db	304	HIPSRRELVRQ-----CTLGWEAYGQPAEDGG	AGRNACINWQYNNVCRSGEFNPHNG			357
Qy	366	AINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFY	NIYFIYFILLIIVGSFFMINCLVV			425
Db	358	AINFDNIGYAWIAIFQVITLEGWVDIMYVMDAHSFY	NIYFIYFILLIIVGSFFMINCLVV			417
Qy	426	IATQFSETKQRESQLMREQRVRLFNASTLASFSEPG	SCYEELLKYLVYLKAAARLQAQ			485
Db	418	IATQFSETKQRENQLMREQRARYLSNDSTLASFSEPG	SCYEELLKYVGHIFRKVKRRSLR			477
Qy	486	VSRAIGVRAGLLSSPVARSGQEPQPSGSC-----	TRSHRR-LSVHHLV-HHHHHH			534
Db	478	-----LYARWQSRWRKKVDPSTLHGQGP	RRRRPRRAGRRTASVHHLVYHHHHH			527
Qy	535	HHYHLNGTLVRPRASPEIQDRDANGSRRLM--	LPPSTPTPSGGPPRGAESVHSFYHAD			592
Db	528	HHYHSHGGPR--RPSPE---PGAGDTRLVRA	CVPPSPPGHGP-DSESVHSIYHAD			580
Qy	593	CHLEPVRCAQPPRCPCSEASGRITVSG--	KVYPTV-----HTSPPEILKDKAL			639
Db	581	CHVEGPQERARVAHTIATAASLKASGLGTWNYPTIL	PSGAVNSKGSTSSRPKGLRS---			637
Qy	640	VEVAPSPGPPTLTSFNI-PPGPFSSMHKLLETQ	STGACHSSCK-ISSPC---SKADSGA			693
Db	638	---AGTPGATAHSPSLGSPSPYEKIQHVVGEOGL	GRASSHLSGLSVPCPLPSPQAGTLT			694
Qy	694	CGPDCPYCARTGAGEP--ESADHVMPDSDSEAVYEFT	QDAQHSDLRDP-----			740
Db	695	CELKSCPICA-SALEDPFEFSGSESGSDAHGVYEFT	QDVRHGDRCRDPVQQPHEGGTPG			753
Qy	741	HSRRQR-SLGPDAEPSSVLAFWRLICDTRFKIVDSKY	FGRGIMAILVNTLSMGIEYHE			799
Db	754	HGNERWRPPLRTASQPGGLGRLWASFSSKLRRIVDSKY	FNRGIMAILVNTLSMGVEYHE			813
Qy	800	QPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYI	KNPYNIFDGVIVISVWEIVGQQ			859
Db	814	QPELTNALEISNIVFTSMFALEMLLKLACGELGIYR	NPYNIFDGVIVVVISVWEIVGQA			873

QY	860	GGGLSVLRTFRLMRVLKLVRELPALORQLVVL	MKTMDNVATFCMLLMFLFIFISILGMHL			919
Db	874	DGGLSVLRTFRLRLRVLKLVRFLPALRQLVVL	MRTMDNVATFCMLLMFLFIFISILGMHL			933
QY	920	FGCKFASERD-GDTLPDRKNFDSLWAIWTVFQ	ILTQEDWNKVLYNGMASTSSWAALFYI			978
Db	934	FGCKFSLKTDSDGTVPDRKNFDSLWAIWTVFQ	ILTQEDWNVLYNGMASTSSWAALFYV			993
QY	979	ALMTFGNYVLPNLLVAILVEGFAEGDATKSESE	PDFSPSVDGDRKK-----			1028
Db	994	ALMTFGNYVLPNLLVAILVEGFAEGDATRSDT	DEKDTSTHLEEDFDKLRDVRATEMKMY			1053
QY	1029	RLALVALGEHAELRKSLLPPLIHTAATPM	SHPKSS-STGVGEALGSGSRRTSSSGSAEP			1087
Db	1054	SLAVTPNG-HLEGRGSLPPPLITHAATPM	TPKSSPHLDMATL-LDSRR-SSSGSVDP			1110
QY	1088	GAAHHEMKCPPSARSSPHSPWSAASSWT	RRSSRNSLGRAPSLKRSPSGERRSLLSCEG			1147
Db	1111	QLG--DQKSLASLRSSPCAPWGPNSAG	SSRNSLGRAPSLKRSPSGERRSLLSCEG			1168
QY	1148	QESQDEE-ESSEEDRASPGSDHHRGSL	EREA-----KSSFDL-----			1197
Db	1169	KGSTDDEADSRPNSGTHPGASPGPRAT	PLRRAESLGHIRSTMDLCPPRPATL-LP			1222
QY	1198	ASGRSSASEHQDCNGKSAASRLARTLRTD	DDPQLDGGDDNDEGNLSKGERIQAWVRSLPA			1257
Db	1223	-----TKPRDCNGQVALPSEFFLRID	SHKEDAAEFDDIEDSCCFLRHKVLPEYAPQ			1275
QY	1258	CCRERDSNAYIFPPQSRFRLLCHRIITHK	MFHDHVLVLIIFLNCITIAMERP	KIDPHSAE		1317
Db	1276	WCSSRESWALYLFPPQNLRVSCQVIAH	KMFHDHVLVLIIFLNCITIALERP	DPIDPGSTE		1335
QY	1318	RIFLTLSNYIFTAVFLAEMTVKVVALG	WCFCGEQAYLRSSWNVDGLLVLSVIDILVSMV			1377
Db	1336	RAFLSVSNYIFTAFVEMVMKVVALGL	LNGEHAYLQSSWNVDGLLVLSLVDIIIVA			1395
QY	1378	SDSGTKILGMLRVLLRLRLRPLRVISRA	QGLKLVETLMSLSLPIGNIVVICCAFFIIF			1437
Db	1396	SAGGAKILGVLRLVLLRLRLRPLRVISRA	PGLKLVETLISLRPIGNIVLICCAFFIIF			1455
QY	1438	GILGVQLFKGKFFVCQGEDTRNITN	KSDCAEASRWRHVKYNFNDNLGQALMSLFLVASKD			1497
Db	1456	GILGVQLFKGKFFYCEGTDTRNITTKA	ECHAAHYRWRVKYNFNDNLGQALMSLFLVSSKD			1515
QY	1498	GWVDIMYDGLDVGVDQOPIMNHN	PWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQH			1557
Db	1516	GWVNIMYDGLDVGIDQOPVQNHNP	WMLLYFISFLLIIVSFFVLNMFVGVVVENFHKCRQH			1575
QY	1558	QEEEEARRREKRLRLEKKRRSKE	QMAEAQCKPYYSYDSRFRLLVHHLCTSHYLDLFI			1617
Db	1576	QEAEEARRREKRLRRLERRRRSTFPN-PEA	ORRPPYADYSHTRRSIHSLSCTSHYLDLFI			1634
QY	1618	TGVIGLNVVTMAHEHYQQOILDEAL	KICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQ			1677
Db	1635	TFIICLVNITMSMEHYNQPKSDEAL	KYCNYVFTIVVFPAALKLVAFGFRFFKDRWNQ			1694
QY	1678	LDLAILLSIMGITLEEIEVNL	SLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALHTVM			1737
Db	1695	LDLAILLSIMGIALEEIEENAL	PINPTIIRIMRVLRIRARVLKLLKMATGMRALDVTV			1754
QY	1738	QALPQVGNLGLLMLFFIFAALGV	ELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFR			1797
Db	1755	QALPQVGNLGLLMLFFIYAALGV	ELFGLECEDNCPCEGLSRHATFTNFGMAFLTFR			1814
QY	1798	VSTGDNWNGIMKDP	SRDC--DQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHL			1854
Db	1815	VSTGDNWNGIMKDTRECTRED	KHCLSYLPALSPYFVFTFVLVAQFVLNVVIAVLMKHL			1874
QY	1855	EESNKEAKEAEAELEAELE	EMKTLSPQSPHSLGSPFLWPGEVGNSTDSPKPGAPHTAH			1914
Db	1875	EESNKEAREDAEMDAEIE	LEI-----			1895



QY 1915 IGAAGSFSLHPTWPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESRL 1974  
Db 1896 ---AQGSTAQFPSTAQESQGT-DPTPNLLVVRKVSVRMLSLPNDSYMFRPVAPAAAPH 1951  
QY 1975 GHRGWGLP-----KAQSGSILSVHSQPADTSCILQLP-----KDVHLLQPHGAP 2019  
Db 1952 SH-----PLQEVEMETYTGPVTSASHPSLEPRTSFQVFAASSPARASDPLCALSPRDT 2006  
QY 2020 TWGAIPKLPFPGRSPLAQRPLRQAARTDLSLVQGLSREDLLSEVSGPSCPLTRSSSF 2079  
Db 2007 -----RSLSLRILYQEAHVAESLEGQIDDAAGEDGIPDYTEPAENISMSSQAP 2054  
QY 2080 WG-----GSSIQVQQRSGIQSKVSKHRLPAPCPGLEPSWAKDPPETRSSLELDT 2129  
Db 2055 LGTLRSPPCSPRPASVTRKHTFGHCISR-----PPTLGDDDAEADP-----ADE 2102  
QY 2130 ELSWISGDLPLSSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDE 2173  
Db 2103 EVSHITSSAHPWPATEPHSPASPTASPAKGTGVSGRDPHRFCSVDAQSFDPKGR-RPDA 2161  
QY 2174 QRRHSIAV-----SCLDSGS-----QRLCPSPSSSLGGQPLGGPSRPPKKLSPPSIS 2221  
Db 2162 QRWSSVELDNGDGHLESGEVRARASELEPAL-----GARRKKMSPPCIS 2206  
QY 2222 IDPP-ESQG-SRPPCSPG---VCLRRRAPASDS---KDPVSSSPLDSTAASP----- 2265  
Db 2207 IDPPTDEGSSRPFAEGGNTTLRRTPSCAALHRDCPESTEGTGTPGDPVAKGRWGQ 2266  
QY 2266 -SPKDTLSLSGLSSDPTDM 2284  
Db 2267 ASCRAEHLTVNFAFEPLDM 2286

RESULT 10

CCAI HUMAN  
ID CCAI HUMAN STANDARD; PRT; 2223 AA.  
AC Q9P0X4; Q95504; Q7Z6S9; Q8NFX6; Q9NZC8; Q9UH15; Q9UH30; Q9ULU9;  
AC Q9UNE6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).  
DE Name=CACNA1I; Synonyms=KIAA1120;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=99381950; PubMed=10454147; DOI=10.1016/S0304-3940(99)00319-5; Mittman S., Guo J., Emerick M.C., Agnew W.S.;  
RT "Structure and alternative splicing of the gene encoding alpha1I, a human brain T calcium channel alpha subunit."  
RL Neurosci. Lett. 269:121-124(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Brain;  
RX MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200; Monteil A., Chemin J., Leuranguer V., Altier C., Mennessier G., Bourinet E., Lory P., Nargeot J.;  
RT "Specific properties of T-type calcium channels generated by the human alpha1I subunit."  
RL J. Biol. Chem. 275:16530-16535(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.  
RC TISSUE=Brain;  
RX MEDLINE=22074770; PubMed=12080115; Gomora J.C., Murbartian J., Arias J.M., Lee J.-H., Perez-Reyes E.;  
RT "Cloning and expression of the human T-type channel Ca(v)3.3: insights into prepulse facilitation."  
RL Biophys. J. 83:229-241(2002).

RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031; Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dharni P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T., McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L., Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfsing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.;  
RT "The DNA sequence of human chromosome 22."  
RL Nature 402:489-495(1999).  
RN [5]  
RP SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=20039618; PubMed=10574461; Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N., Ohara O.;  
RT "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain."  
RL DNA Res. 6:329-336(1999).  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. Isoform alpha-1I gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes. Gates in voltage ranges similar to, but higher than alpha 1G or alpha 1H (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=Delta36b;  
CC IsoId=Q9P0X4-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9P0X4-2; Sequence=VSP\_000951;  
CC Name=3; Synonyms=Alpha1-a;  
CC IsoId=Q9P0X4-3; Sequence=VSP\_000950, VSP\_000951;  
CC Name=4;  
CC IsoId=Q9P0X4-4; Sequence=VSP\_000950;  
CC TISSUE SPECIFICITY: Brain specific.  
CC -!- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one  
CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II (By similarity).  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
CC -!- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to  
CC erroneous gene model prediction.  
CC -----  
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CC -----  
DR EMBL; AF129133; AAD45251.1; -.  
DR EMBL; AF142567; AAF25722.1; -.  
DR EMBL; AF211189; AAF44626.1; -.  
DR EMBL; AF393329; AAM67414.1; -.  
DR EMBL; AL008716; CAA15494.1; -.  
DR EMBL; AL022312; CAB62988.1; -.  
DR EMBL; AL022319; CAB62996.1; ALT\_SEQ.  
DR EMBL; AL022319; CAD92536.1; -.  
DR EMBL; AB032946; BAA86434.1; -.  
DR Genew; HGNC:1396; CACNA1I.  
DR MIM; 608230; -.  
DR GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.  
DR GO; GO:0008332; F:low voltage-gated calcium channel activity; NAS.  
DR GO; GO:0006816; P:calcium ion transport; NAS.  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_trpl.  
DR InterPro; IPR002077; Ca\_channel\_alpha.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCALPHA1.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR00167; CCHANNEL.  
DR PRINTS; PR01629; TVDCCALPHA1.  
KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;  
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;  
KW Polymorphism; Repeat; Transmembrane; Voltage-gated channel.  
FT REPEAT 66 401 I.  
FT REPEAT 626 865 II.  
FT REPEAT 1157 1434 III.  
FT REPEAT 1472 1733 IV.  
FT DOMAIN 1 78 Cytoplasmic (Potential).  
FT TRANSMEM 79 99 S1 of repeat I (Potential).  
FT DOMAIN 100 120 Extracellular (Potential).  
FT TRANSMEM 121 141 S2 of repeat I (Potential).  
FT DOMAIN 142 148 Cytoplasmic (Potential).  
FT TRANSMEM 149 168 S3 of repeat I (Potential).  
FT DOMAIN 169 173 Extracellular (Potential).  
FT TRANSMEM 174 191 S4 of repeat I (Potential).  
FT DOMAIN 192 211 Cytoplasmic (Potential).  
FT TRANSMEM 212 232 S5 of repeat I (Potential).  
FT DOMAIN 233 377 Extracellular (Potential).  
FT TRANSMEM 378 398 S6 of repeat I (Potential).  
FT DOMAIN 399 640 Cytoplasmic (Potential).

FT	TRANSMEM	641	661	S1 of repeat II (Potential).
FT	DOMAIN	662	676	Extracellular (Potential).
FT	TRANSMEM	677	697	S2 of repeat II (Potential).
FT	DOMAIN	698	702	Cytoplasmic (Potential).
FT	TRANSMEM	703	721	S3 of repeat II (Potential).
FT	DOMAIN	722	729	Extracellular (Potential).
FT	TRANSMEM	730	753	S4 of repeat II (Potential).
FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).

Query Match 45.0%; Score 5418; DB 1; Length 2223;  
Best Local Similarity 49.9%; Pred. No. 1.2e-256;  
Matches 1235; Conservative 243; Mismatches 533; Indels 462; Gaps 68;

Qy	12	TPPLRGSRPSSDP-----PGRLARGWTRRRMERAPRRSDPVSARSSTTCGPGGAAG	65
Db	6	SPPSSSAAAPAAEPGVTTTEQGPGR-----SPPSSPPGLEPLDGA--	45
Qy	66	AGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRRPRSWCLRTVCNPFVRSMLVLIL	125
Db	46	-----DP-----HVPHPDLAPIAFFCLRTQTSRPNWCINKVCPNPFECVSMVLILL	91
Qy	126	NCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFEAVEMVMVALGIFGKCYLGDWTN	185
Db	92	NCVTGLMGYQCDMDCLSDRCKILQVDFDFIFFFAMEMVMKVALGIFGKCYLGDWTN	151
Qy	186	RLDFFIVIAGMLEYSLDLQNVFSVAVTVRVLRLPLRAINRVPSMRILVTLTLLDTPMLGN	245
Db	152	RLDFFIVMAGWVEYSLDLQNLNLSAIRTVRLPLKAINRVPSMRILVTLTLLDTPMLGN	211
Qy	246	VLLLCFFVFFIFGIVGVQLWAGLLNRNCFLPENFSLPLSVDLBPPYQTENEDESPFICSQ	305
Db	212	VLLLCFFVFFIFGIIGVQLWAGLLNRNCFLEENFTIQGDVALPPYQPEEDEMPPFICSL	271
Qy	306	PRENGMRSCTSVPTLRGEGGGPPCSL-----DYETYNSSNTT--CVNWNQYTNCSA	357
Db	272	SGDNGIMGCHIEIPLKEQ---GRECCLSKDDVDYDFGAGRQDLNASGLCVNWNRYNVVCR	328
Qy	358	GEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFF	417
Db	329	GSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVYMDAHSFYNFYIFILLIIVGSFF	388
Qy	418	MINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFEPGSCYEELLKYLVIYLR	477
Db	389	MINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASVAFPGDCYEEIFQYVCHILR	447
Qy	478	KAARRLAQVSRAGVIRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHHLVHHHHHHHY	537
Db	448	KAKRRALGLYQALQSRRLQAL-GPEAPAPAKPGP-----HAKPRHY	487
Qy	538	H---LGNGTLRVPRASPEIQDRDAN-GSRRRLM-LPPPSTPTSPGGPPRGAESVHSFYHAD	592
Db	488	HGKTKGQG-----DEGRHLGSRHCQTLHGPAASP-----GNDHSGRE-----	523
Qy	593	CHLEPVRQAPPPRCPCSEASGRITVSGKVPYTVHTSPPEILKDKALVEVAPSPGPTILT	652
Db	524	-----LC---PQHSPLDA-----TPHT-----LVQ---PIPATLA	547
Qy	653	SFNIPPGPFSSMHKLLLETQSTGAC-HSSCKISSPCSKADSGACGPDSCPCYARTGAGEPE	711
Db	548	S-----DPASCPCQCHEDGRRPSGLGSTDGSGSGS-----GSSAGGEDE	588
Qy	712	SADHVMPDSDSEAVYEFTQDAHQHSLDRDPHSRRRRQRRSLGPDAPPSVLA--FWRLICDTF	769
Db	589	A-----DGDGA---RSSEGDGASSELGKEEEEEEQ-----ADGAVWLCGDVWRETRAKL	633



CC TISSUE=Brain;  
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;  
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,  
RA Baillie D.L., Stea A., Snutch T.P.;  
RT "Molecular and functional characterization of a family of rat brain T-  
RL type calcium channels.";  
J. Biol. Chem. 276:3999-4011(2001).  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the  
CC entry of calcium ions into excitable cells and are also involved  
CC in a variety of calcium-dependent processes, including muscle  
CC contraction, hormone or neurotransmitter release, gene expression,  
CC cell motility, cell division and cell death. Isoform alpha-11  
CC gives rise to T-type calcium currents. T-type calcium channels  
CC belong to the "low-voltage activated (LVA)" group and are strongly  
CC blocked by nickel and mibefradil. A particularity of this type of  
CC channels is an opening at quite negative potentials, and a  
CC voltage-dependent inactivation. T-type channels serve pacemaking  
CC functions in both central neurons and cardiac nodal cells and  
CC support calcium signaling in secretory cells and vascular smooth  
CC muscle. They may also be involved in the modulation of firing  
CC patterns of neurons which is important for information processing  
CC as well as in cell growth processes. Gates in voltage ranges  
CC similar to, but higher than alpha 1G or alpha 1H.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Brain.  
CC -!- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one  
CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II (By similarity).  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
-----  
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DR EMBL; AF086827; AAD17796.2; -.  
DR EMBL; AF290214; AAG35188.1; -.  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR002077; Ca\_channel\_alpha.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCALPHAL.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR00167; CACHANNEL.  
DR PRINTS; PR01629; TVDCCALPHAL.  
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;  
KW Ionic channel; Multigene family; Phosphorylation; Repeat;  
KW Transmembrane; Voltage-gated channel.  
FT REPEAT 64 399 I.  
FT REPEAT 584 823 II.  
FT REPEAT 1116 1393 III.  
FT REPEAT 1431 1692 IV.  
FT DOMAIN 1 76 Cytoplasmic (Potential).  
FT TRANSMEM 77 97 S1 of repeat I (Potential).  
FT DOMAIN 98 115 Extracellular (Potential).  
FT TRANSMEM 116 137 S2 of repeat I (Potential).  
FT DOMAIN 138 146 Cytoplasmic (Potential).  
FT TRANSMEM 147 166 S3 of repeat I (Potential).  
FT DOMAIN 167 171 Extracellular (Potential).  
FT TRANSMEM 172 189 S4 of repeat I (Potential).  
FT DOMAIN 190 209 Cytoplasmic (Potential).  
FT TRANSMEM 210 230 S5 of repeat I (Potential).  
FT DOMAIN 231 371 Extracellular (Potential).  
FT TRANSMEM 372 396 S6 of repeat I (Potential).

FT DOMAIN 397 598 Cytoplasmic (Potential).  
FT TRANSMEM 599 619 S1 of repeat II (Potential).  
FT DOMAIN 620 632 Extracellular (Potential).  
FT TRANSMEM 633 654 S2 of repeat II (Potential).  
FT DOMAIN 655 660 Cytoplasmic (Potential).  
FT TRANSMEM 661 679 S3 of repeat II (Potential).  
FT DOMAIN 680 687 Extracellular (Potential).  
FT TRANSMEM 688 711 S4 of repeat II (Potential).  
FT DOMAIN 712 722 Cytoplasmic (Potential).  
FT TRANSMEM 723 743 S5 of repeat II (Potential).  
FT DOMAIN 744 795 Extracellular (Potential).  
FT TRANSMEM 796 820 S6 of repeat II (Potential).  
FT DOMAIN 821 1125 Cytoplasmic (Potential).  
FT TRANSMEM 1126 1148 S1 of repeat III (Potential).  
FT DOMAIN 1149 1166 Extracellular (Potential).  
FT TRANSMEM 1167 1187 S2 of repeat III (Potential).  
FT DOMAIN 1188 1197 Cytoplasmic (Potential).  
FT TRANSMEM 1198 1217 S3 of repeat III (Potential).  
FT DOMAIN 1218 1231 Extracellular (Potential).  
FT TRANSMEM 1232 1253 S4 of repeat III (Potential).  
FT DOMAIN 1254 1264 Cytoplasmic (Potential).  
FT TRANSMEM 1264 1287 S5 of repeat III (Potential).  
FT DOMAIN 1288 1364 Extracellular (Potential).  
FT TRANSMEM 1365 1390 S6 of repeat III (Potential).  
FT DOMAIN 1391 1445 Cytoplasmic (Potential).  
FT TRANSMEM 1446 1466 S1 of repeat IV (Potential).  
FT DOMAIN 1467 1480 Extracellular (Potential).  
FT TRANSMEM 1481 1502 S2 of repeat IV (Potential).  
FT DOMAIN 1503 1509 Cytoplasmic (Potential).  
FT TRANSMEM 1510 1528 S3 of repeat IV (Potential).  
FT DOMAIN 1529 1542 Extracellular (Potential).  
FT TRANSMEM 1543 1566 S4 of repeat IV (Potential).  
FT DOMAIN 1567 1580 Cytoplasmic (Potential).  
FT TRANSMEM 1581 1601 S5 of repeat IV (Potential).  
FT DOMAIN 1602 1664 Extracellular (Potential).  
FT TRANSMEM 1665 1692 S6 of repeat IV (Potential).  
FT DOMAIN 1693 1835 Cytoplasmic (Potential).  
FT SITE 355 Calcium ion selectivity and permeability  
FT SITE 779 (By similarity).  
FT SITE 1339 Calcium ion selectivity and permeability  
FT SITE 1637 Calcium ion selectivity and permeability  
FT CARBOHYD 171 (By similarity).  
FT CARBOHYD 242 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 309 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 1301 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 1304 N-linked (GlcNAc. .) (Potential).  
FT CONFLICT 193 M -> L (in Ref. 3).  
FT CONFLICT 291 C -> V (in Ref. 3).  
FT CONFLICT 394 V -> L (in Ref. 3).  
FT CONFLICT 406 E -> N (in Ref. 3).  
FT CONFLICT 485 C -> S (in Ref. 3).  
FT CONFLICT 512 D -> Y (in Ref. 3).  
FT CONFLICT 558 S -> R (in Ref. 3).  
FT CONFLICT 683 G -> S (in Ref. 3).  
FT CONFLICT 691 F -> S (in Ref. 3).  
FT CONFLICT 739 MH -> ID (in Ref. 3).  
FT CONFLICT 833 C -> Y (in Ref. 3).  
FT CONFLICT 846 F -> L (in Ref. 3).  
FT CONFLICT 856 S -> R (in Ref. 3).  
FT CONFLICT 905 L -> R (in Ref. 3).  
FT CONFLICT 913 M -> YW (in Ref. 3).  
FT CONFLICT 936 W -> G (in Ref. 3).  
FT CONFLICT 996 A -> R (in Ref. 3).  
FT CONFLICT 1060 I -> M (in Ref. 3).  
FT CONFLICT 1094 D -> CC (in Ref. 3).  
FT CONFLICT 1197 SS -> TD (in Ref. 3).  
FT CONFLICT 1229 Missing (in Ref. 3).  
FT CONFLICT 1422 K -> Y (in Ref. 3).  
FT CONFLICT 1623 FGM -> SAR (in Ref. 3).





Db	1802	SGSVFHHYASPDG	1814	
RESULT 12				
Q7Z6S8				
AC	Q7Z6S8	PRELIMINARY;	PRT;	1994 AA.
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	DJ172B20.1	(Calcium channel, voltage-dependent, alpha 1I subunit) (Fragment).		
DE				
GN	Name=CACNA1I;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Phillips S.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL022319; CAD92537.1; --			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005261; F:cation channel activity; IEA.			
DR	GO; GO:0006812; P:cation transport; IEA.			
DR	InterPro; IPR001682; Ca/Na pore.			
DR	InterPro; IPR002111; Cat channel TrpL.			
DR	InterPro; IPR000345; CytC heme BS.			
DR	InterPro; IPR005821; Ion trans.			
DR	InterPro; IPR005820; M+channel_nlg.			
DR	Pfam; PF00520; Ion trans; 4.			
DR	PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.			
KW	Ion transport; Ionic channel; Transmembrane; Transport.			
FT	NON_TER	1		
SQ	SEQUENCE	1994 AA; 220004 MW; A5EPAE5FA32DCF76 CRC64;		
Query Match 39.5%; Score 4750.5; DB 2; Length 1994;				
Best Local Similarity 49.0%; Pred. No. 5.1e-224;				
Matches 1099; Conservative 214; Mismatches 485; Indels 447; Gaps 61;				
Qy	229	MRILVTLTLLDTPMLGNVLLLCFFVFFIFIGVQVQLWAGLLRNRCFLPENFSLPLSDLE	288	
Db	1	MRILVNLTLTLPMLGNVLLLCFFVFFIFIGVQVQLWAGLLRNRCFLEENFTIQGDVALP	60	
Qy	289	PYYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSL-----DYETNSSN	342	
Db	61	PYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECLSKDDVYDFGAGRQDLN	117	
Qy	343	TT--CVNWNQYVNCISAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHS	400	
Db	118	ASGLCVNWNRYNVCRTGSANPHKGAINFNDNIGYAWIVIFQVITLEGWVEIMYVYVMDAHS	177	
Qy	401	FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASPSE	460	
Db	178	FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAE	236	
Qy	461	PGSCYEELKLVYILRKAARRLAQVSRAGVRAGLLSSPVARSQEPQPSGSCTRSHRR	520	
Db	237	PGDCYEEIFQYVCHILRKAKR-----RALGLYQALQS-----RR	270	
Qy	521	LSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGPPR	580	
Db	271	QAL-----GPE-----APAPAKGP-----	285	
Qy	581	GAESVHSFYHADCHLEPVRQAPPRCFSEASGRVTGSGKVYPTVHTSPPEILKDHALV	640	
Db	286	-----HAK---EPRHYQLCPQHSPLDA-----TPHT-----LV	310	
Qy	641	EVAPSPGPPTLTSFNIPPGPFSSMHKLLTQSTGAC-HSSCKISSPCSKADSGACGPDSC	699	
Db	311	Q----PIPATLAS-----DPASCPCQCHEDGRRPSSGLGSTDSGQEGSGS-	350	
Qy	700	PYCARTGAGEPESADHVMPSDSEAVYEFQTQDAQHSDLRDPHSRRRQRLSLGPAERSSVL	759	
Db	351	---GSSAGGEDEA-----DGDGA---RSSDGGASSELGKEEEEQ-----ADGAVWL	392	
Qy	760	A--FWRLICDTPFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTS	817	
Db	393	CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS	452	
Qy	818	LFALEMLLKLIVYGPFGYIKNPYNIPFDGVIWISVWEIVGQGGSLVLRTRFLMRVLKL	877	
Db	453	MFALEMILKLAAGFLDYLRNPYNIPFDSIIWISWEIVGQADGGLSVLRTRFLRLRVKL	512	
Qy	878	VRFLPALQRLVVLMTMDNVATFCMLLMFIFISILGMHLFGCKFASERD-GDTLPDR	936	
Db	513	VRFPALRRQLVVLMTMDNVATFCMLLMFIFISILGMHLFGCKFSLRTDGTVPDR	572	
Qy	937	KNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAAALYFIALMTFGNYVLFNLLVAIL	996	
Db	573	KNFDSLWAIWTVFQILTQEDWNVVLNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL	632	
Qy	997	VEGFAEGDATKSESEPDFFSPV-----DGDGDRKRLALVALGEHAELRKSL	1046	
Db	633	VEGFAEGDANRSYDEDDQSSSNIEEFDKLGLEDSSGDPK--LCPIMPTPNGHLDPSL-	689	
Qy	1047	PPLIIHT---AATPMHPKSSSTGVGEALGSGRRRTSSGSABPAAHHEMKCPPSARS	1102	
Db	690	-PLGGHLGPAGAAGPA--PRLSLQDPMLVALGSRKSSVMSL---GRMSYDQSRSLSSRS	743	
Qy	1103	SPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE--GESQDEEESSE--	1159	
Db	744	SYGPGWGRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGARVCEVADEGP	797	
Qy	1160	DRASPAGSDH-----RHRGSLEREAKSSFDPDLPDTPQLVPLHRTASGRSS-	1203	
Db	798	PRAAPLHTPHAHIHGHPLAHRHRHRTLSLDNRDSVDLAELVPAGVAPRAAWRAAG	857	
Qy	1204	-ASEHQDCNGKSASGRRLARTLD-DPQLDGGDDNDENGLSKGERIQAWRSRLPACCRE	1261	
Db	858	PAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEIDYTLCFRVRKMDIVYKPDWCEV	915	
Qy	1262	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERP KIDPHSAERIFL	1321	
Db	916	REDWSVYLFSPENRFRVLCQTIIAHKLFYVVLAFIFLNCITIALERPQIEAGSTERIFL	975	
Qy	1322	TLSNYIFTAVFLAEMTVKVALGCFGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDG	1381	
Db	976	TVSNYIFTAIFVGEMTLKVSLGLYFGEQAYLRSSWNVDGLFVFSIIDIVVSLASAGG	1035	
Qy	1382	TKILGMLRVLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGLG	1441	
Db	1036	AKILGVLRLRLTLRLPLRVISRAPGLKLVVETLISLKPIGNIVVICCAFFIIFGLG	1095	
Qy	1442	VQLFKGKFFVCOGEDTRNITNKSDEASRWRHKNYFNFNLGQALMSLFLVASKDGWVD	1501	
Db	1096	VQLFKGKFYHCLGVDRNITNRSDCMAANRWRVHHKNYFNFNLGQALMSLFLVASKDGWVN	1155	
Qy	1502	IMYDGLDAVGVDQQPIMNHNPMMLLYFISFLLIIVAFFVLNMVGVVVENFHKCRHQEEE	1561	
Db	1156	IMYNGLDAVAVDQQPVTNHNPMMLLYFISFLLIIVSFFVLNMVGVVVENFHKCRHQEAE	1215	
Qy	1562	EARRREEKRLRLEKRRSKEKQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITVI	1621	
Db	1216	EARRREEKRLRLEKRR-----KAQRLPYATYCHTRLLIHSMTCTSHYLDIFITFI	1268	
Qy	1622	GLNVVTMAHEHYQQPQILDEALKICNVIFTVIFVFESVFKLVAFARFRFFQDRWNQLDLA	1681	
Db	1269	CLNVVTMSLEHYNQPTSLTALKYCNYMFTTVFVLEAVLKVAFGLRRFFKDRWNQLDLA	1328	
Qy	1682	IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHHTVMQALP	1741	
Db	1329	IVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIRARVLKLLKMATGMRLHHTVMQALP	1388	
Qy	1742	QVGNLGLLEMLLFFIFAALGVLEFGDLECDETHPCBGLGRHATFRNFGMAFLTFLFRVSTG	1801	

Db 1389 QVGNLGLLFFIYAAALVELFGKLVNDENPCGMSRHATFENFGMAFLTTLFQVSTG 1448

QY 1802 DNWNGIMKDPSPDC-DQESTCVNTV--ISPIYFVSFVLTAQFVLNVVIAVLMKHEESN 1858

Db 1449 DNWNGIMKDTLRDCTHDSRCLSSLOFVSPLYFVSFVLTAQFVLNVVIAVLMKHLDDSN 1508

QY 1859 KEAKEEAELEAELELEM-KTISLPQPHSPLGSP-----1889

Db 1509 KEAQEDAEMDAELEMAHGLGPGPRLPTGSPGAPGRGPGGAGGGDTGGLCRRRCYSPA 1568

QY 1890 --FLW-----PGVEG-VNSTDSPKPGAPHTTAHIGAASG-----1920

Db 1569 QENLWLDVSLLIKDSLEGELTIIDNLSGSIFH---HYSSPAGCKKCHHDKQEVQLAETE 1625

QY 1921 -----FSLEHPTMVP-----HPEEVPV-PLGPDLLTVRKSGV 1951

Db 1626 AFSLNSDRSSILLGDDLSLEDPACPPGRKDSKGELDPPEPMRVGDLGECFFPLSSTAV 1685

QY 1952 SRTHSLPN-DSYMCNRNGSTAERSLGHGWLPLKPAQSGSILSVHSQPADTSCILQLPKDVH 2010

Db 1686 S-----PDPENFLCEMEEI PFNPV--RSW--LKHDSSQAPPSPFSPDASSPLLPMPAEFF 1736

QY 2011 Y-----LLQHCAPTWGAIPKLPPG-----RSPLAQRLRRQAAI RTDSL DVQGLSR 2059

Db 1737 HPAVASQKGEKGTGTGLPKIALQGSWASLRSRVNCTLLRQATGSDTSLDAS-----1791

QY 2060 EDLLSEVSGPCLTRSSSFWGGSSIQVQORSIGIQSVKXHIRLPAPCPGLEPSWAKDPP 2119

Db 1792 -----PSSAGSLQTTLEDLSLTSDSPRALGPPAPAG-----1825

QY 2120 ETRSSLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSI 2179

Db 1826 -----PRAGLSPAARRL-----SLRGRGLFSLRGLRAHOR 1856

QY 2180 AVSCLDSGQPRCLPSPSSL-----GGQPLGGPSRPRKKLSPPSIS---IDPPESQ 2228

Db 1857 SHS--SGGSTSPGCTHDSMDPSDEGRGAGGGAGSEHSETLSLSLTSLFCPPP---1911

QY 2229 GSRPPCSPGVCLRR-----RAP-----ASDSKDPSSVSPLDST 2261

Db 1912 ---PPPAPGLTPARKFSSSTSSLAAPGRPHAAALAHGLARSPSWAADRSKDPGPGRAPLPMG 1968

QY 2262 AASPSPKKDTLSLGLSDPTDMDP 2286

Db 1969 LGPLAPPQPL-----PGELEP 1985

RESULT 13

Q7PQV4 PRELIMINARY; PRT; 1762 AA.

AC Q7PQV4;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE ENSANGP0000003024 (Fragment).

GN Name=ENSANGS0000002480;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

OX NCBI\_TaxID=180454;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PEST;

RA Anopheles Genome Sequencing Consortium;

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AAB01008859; EAA08229.2; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR001682; Ca/Na\_pore.

DR InterPro; IPR002111; Cat\_channel\_TrpL.

DR InterPro; IPR005821; Ion\_channel.

DR InterPro; IPR005820; M+channel\_nlg.

DR InterPro; IPR005445; TVDCCALphal.

DR Pfam; PF00520; Ion\_trans; 4.

DR PRINTS; PR01629; TVDCCALPHAL.

KW Ion transport; Ionic channel; Transmembrane; Transport.

FT NON\_TER 1

FT NON\_TER 1762

SQ SEQUENCE 1762 AA; 199928 MW; AF70F5349068EDE2 CRC64;

Query Match 34.8%; Score 4188.5; DB 2; Length 1762;

Best Local Similarity 48.9%; Pred. No. 1.4e-196;

Matches 918; Conservative 270; Mismatches 457; Indels 231; Gaps 49;

QY 114 WFERVSMVLVLLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGI 173

Db 2 WFERISMLVLLNCVTLMGYQPCVDDACVTNRCKILQIFDDIIFAFFSLEMTIKIVAMGA 61

QY 174 FGKCYLGDWTNRLDFFIVIAGMLEYSLDLQNVFSAVRTVRVLRPLRAINRVPSMRILV 233

Db 62 WKGTYLADSWNRLDFFIVLAGALEYCLQVENLNTAIRTVLRPLRAINRIPSRLV 121

QY 234 TLLDLTLPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNRCF--LPENFSLPLSVDLEPY 291

Db 122 MLLDLTLPMLGNVLLCFFVFFIFGIVGVQLWEGILRQRCVIKLPDNVS-PPSYLVSFY 180

QY 292 QTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGP----PCSLDYETYNSSNTTCVN 347

Db 181 EFSKEQD--YICSKPEDSGMHLCONLPPYR----IGPLLNCDSALPY-SENEPTATACVN 233

QY 348 WNOYITNCISAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNIYF 407

Db 234 WNOYITNCTQLGNNPFGTISFDNIGLAWAIFLVISLEGWTDIMYVYQDAHSFWDWIYF 293

QY 408 ILLIVGSFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNASTLASF---SEPGSC 464

Db 294 VLLIVGSFFMINCLVVIATQFSETKKREMRMRQERARFTS--SSILASSTNNSEPTTC 352

QY 465 YEELKYLVIILRKAARLAQVSRAGIVRAGLLSSPVARSQEQPQSGSCTSRSHRRLSVH 524

Db 353 YAEIVKYIGHLYRRFRRLIK-----KLRLYKYHMQKKEGLIPTPETITLSPNKIKAH 407

QY 525 H-----LVHHH-----HHHHYHLGNGTIRVPRASPEIQDRDANGSRRLMLPPPS 570

Db 408 HPKCPRMGALLQQQHASITNLQQQKNKHDLOSSLINRTGVTLNH-----PEPG 456

QY 571 TPTPSG---GPPRGAESV-----HSFYHADCHLEPVRCQAPPPRCSE--ASGRTVG 617

Db 457 TIVPSADNQVSSPEVSEIVSLENIKNNALNNSTTYLNEDRQKVLKLNEDQSGNGQVRG 516

QY 618 SGKVYPTV-----HTSP-----PPEILKDKALV---EVAPSPGPPT 650

Db 517 MGWLGMVWEGRSTFEGSSLSLAPQDHHCMPSLLSPPSAGRRRSSVMFNEYVVLHTPPT 576

QY 651 LTSFNIPPGPFSSMHKLLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEP 710

Db 577 ITE---PPQDKNYY--CLEKMTQAAANPATSRRAPAST----RCRPASTTSTWRS-----622

QY 711 ESADHVMPSDSEAVYEFTQDAQHSDLRDPHSRRRRQRSLGPDAPESPSSVLAFWRLICDTFR 770

Db 623 -----LP-----AATSTTKTRWRRRRSDRSAPSARGSSRWRCFRRTCHLTR 663

QY 771 -----KIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISINIVFTSLFALEMLLK 826

Db 664 VLVKCLVDHKYFQQGILLAILNITLSMGIEYHDQPAELTAIVETSINIVFSAIFAVERMILK 723

QY 827 LLVYGPFGYIKNPYNIFDGVIVVIVSWEI-----VGQQGGSLSVLRTFLRMRLKLVRF 880

Db 724 VIAEGPFYRYVANGFNVDGVIVILSVVVLGQSYLGEGQSSGLSVLRTFLRLILKLVRF 783







Db 1417 PPSPVLSHKPLNINLASQLVG--MGGVVPSTAGSSSMHSLVIDDISKSSSTAAATPI 1474  
QY 1088 -----GAAHEMKCPPSARSSP-----HSPWSAASSWTSRR----- 1118  
Db 1475 YVPTISSTADAQSQSHSLN-DVSVGSPGGEIPATGMSRNPANTGASTGSSSERLPLAP 1533  
QY 1119 -----SSRNSLGRAPSLKRRSPS-----GERRSLSGEQESQDEEE----- 1155  
Db 1534 PPQGSFKQLRRGSSKRRASALATDDNPARRTLDNQARRTQDEEEEQQLNNGDN 1593  
QY 1156 -----SSEEDRASPAGSDHRRGSL-----ERAKS-----SFDLPD 1187  
Db 1594 SCLLRNSNAVVGSSSGTKETNRLSPQNSIRRLSNTLSIGSPVGSRRASACIFNSQVYQ 1653  
QY 1188 TLQVPLGHRASGRS-----SASEHQDCNGKSAAGRLARTLRTDDPQLDGDNDDE 1238  
Db 1654 NLNQPPKLRPGSGQRRMSSIELAFSKTSHLNHLNLEAN---RKSLSYTNKMDLDKWNKS 1710  
QY 1239 -GNLSKGER-IQAWVRSR----- 1254  
Db 1711 YGNLNEPDNMLQQYMEARDKRKNSISHYNLKKRLEEKELQQLHQQQLLQQRQDSFSS 1770  
QY 1255 -----LPA-----CCREDSWSA 1267  
Db 1771 TTQQQQQLQOHLRLSKOQQQLAMQPHSMVPGGGERYSKLMKMLIEQLTPKHFTTEREDYSL 1830  
QY 1268 YIFPPQSRFLLCHRIITHKMFHDHVLVLIIFLNCITIAMERP KIDPHSAERIFLTLSNYI 1327  
Db 1831 YIFPEDNRFQICTWFVNQKWFEDNVLLFIALNCITLAMERNPIPPSSTERLFLATANYV 1890  
QY 1328 FTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLVLSVIDILVSMVSDSGTKILGM 1387  
Db 1891 FTVVFTVEMFIKVATGMFYGHDAYFTSGWNIMDGLSVTISIIDLMSLISESSRIFGI 1950  
QY 1388 LRVLRLLRLRPLRVISRAOGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKG 1447  
Db 1951 LRVFRLRLRPLRVINRAPGLKLVVQTLSSLRPIGNIVLICCTFFIIFGILGVQLFKG 2010  
QY 1448 KFFVCOGEDTRNITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFVLASKDGVIMYDG 1506  
Db 2011 TFYCEGENIKGVRNADECRRIPGNVWNTNRKYNFDDLGKALMSLFVLSRRDGNWIMYTG 2070  
QY 1507 LDAGVDDQDIPMHNPNWMLLYFISFLLIYAFVFLNMFVGVVVENFHKCRHQHEEEARR 1566  
Db 2071 LDAGVDDQDIPVYNWRLLYFIAPILLVGFVFLNMFVGVVVENFHCREEQKEKIRR 2130  
QY 1567 EEKRLRLLEKRRSKEKQMAEAQCKPYSDYSRFRLLVHLCTSHYLDLFTIGVLNVV 1626  
Db 2131 AAKRALQMEKKRR---RMHE---PPYNTNYSPTRMFVHNVTYSKYFDLAIAAVIGLNVV 2183  
QY 1627 TMAMEHYQOPQILDEALKICNYIFTVIFVFESVFKLVAFAFRFFQDRWNQDLAIVLLS 1686  
Db 2184 TMAMEYYKMPGLKYALKIFNYFFTAFFILEANMKLVAGWKLYLKDRWNQDLVGVILL 2243  
QY 1687 IMGITLEEIEVNLS--LPINPTIIRMRVLRIRARVLKLLKMAVGMRALLTVMQALPQVG 1744  
Db 2244 IVGIVLEELTNTHQIIPINPTIIRMRVLRIRARVLKLLKMAVGMRALLTVMQALPQVG 2303  
QY 1745 NLGLLFFMLFFIFAALGVVELFGDCEDETHPCEGLRHATFRNFGMAFLTFRVSTGDNW 1804  
Db 2304 NLGLLFFLLFFIFAALGVVELFGRLECSDEIPCOQLGEHAHPANFGMAFLTFRVATGDNW 2363  
QY 1805 NGIMKOPSRD-CDQ-----ESTCVNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEESN 1858  
Db 2364 NGIMKDTLRNCDDAADCVRNCCVSSVIAPIFFVIFVLMAQFVLNVVIAVLMKHEESH 2423  
QY 1859 KEAKEEAEEAELEALEM-----KTLSPQPHSPL-----G 1887  
Db 2424 KOMEDELMEVELERELVREQEFAQEQKLCQQLAEAQSKAAAPPRPLAKVKSLEPKNFIYS 2483  
QY 1888 SPFL---WPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEVPVPLGPDLL 1944

Db 2484 TPSLDKKFPFAVGVNPSLTSSAATNLNQVATAGSGAA-----PGAVPAGSGAG-- 2533  
QY 1945 TVRKSQSVSRTHSLPNDSYMCRNGSTAERSLGRGWLKPAQSGSILSVHSQPADTSCILQ 2004  
Db 2534 -PRROTVOYFQPP-----QSMLG-----GLSLAEMGTLTPQALGA----- 2569  
QY 2005 LPKDVHYLLQPHGAPTGAIPKLPPGRSPLAQRLRRQAARTD-SLDVQGLGSRDILL 2063  
Db 2570 -----RLGEFFGG---GGNKGSPRRQSYQWQINPIKRGVLSKERSLDEQAIRRNLEA 2620  
QY 2064 SEVSGPSCPLTRSSSFVGGSSIQVQORS-----GIQSKVSKHI 2101  
Db 2621 KRTSCDSL-----WGGDALDCRRGTIFESLESDDGGVGGGGGGGGVSYDL 2673  
QY 2102 RLPAPCPGLEPSWAKDPPETRSLELDTELSWISG-----DLLPSSQEE 2145  
Db 2674 RS-----VRSADVGHSEMDGDVSLSVSALVPSVTTPLPPLSLPIVTTSTPT 2722  
QY 2146 PL---FPRDLKKCYSETQSCRRAPGFWLDEQRRHSIAVCLDSG---SQPRLCPSPSSL 2199  
Db 2723 PLQLPMPMPMAHPPP-----RRPFGW-----SQSVDOGLRSLNLLSVPRSMPPRSRS 2772  
QY 2200 GG-----QPL-----GGPSRPPKKLSPPSISIDPPESQGSRRPCCSP 2236  
Db 2773 GSTKQLFKQALDEADMDENSLLLPTAAGGSGPGSVAVIASSSLDLPDQSGSSKQILP 2832  
QY 2237 GVCL-----RRAPASDSKDP 2252  
Db 2833 DIALGVSKSDSSDILRIISERRRMDQREOREP 2864

RESULT 15

Q967R4  
ID Q967R4 PRELIMINARY; PRT; 1837 AA.  
AC Q967R4;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Voltage-dependent calcium channel alpha13 subunit (T-type calcium channel alpha subunit isoform A) (Calcium channel, alpha subunit protein 1, isoform a).  
DE GN Name=cca-1; ORFNames=C54D2.5;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mittman S.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Steger K.A., Thacker C., Snutch T.P., Avery L.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Minx M.;  
RT "The sequence of C. elegans cosmid C54D2.";  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

[6]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Wilson R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL
RN
[7]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Wilson R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL
RN
[8]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC WormBase Consortium;
RG Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
CC
DR EMBL; AF368920; AAK53427.1; -.
DR EMBL; AY313898; AAP79881.1; -.
DR EMBL; U37548; AAM51534.1; -.
DR WormBase; WBGene0000367; cca-1.
DR WormPep; C54D2.5a; CE30919.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005891; C: voltage-gated calcium channel complex; IEA.
DR GO; GO:0005261; F: cation channel activity; IEA.
DR GO; GO:0005245; F: voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P: calcium ion transport; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR001682; Ca/Na\_pore.
DR InterPro; IPR002111; Cat\_channel\_TrpL.
DR InterPro; IPR002077; Ca\_channel\_alpha.
DR InterPro; IPR005821; Ion\_trans.
DR InterPro; IPR005820; M+channel\_nlg.
DR InterPro; IPR005445; TVDCCalpal.
DR Pfam; PF00520; Ion\_trans\_4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPAL.
DR KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
SQ SEQUENCE 1837 AA; 210160 MW; 113367B5298AA49B5 CRC64;

Query Match 32.1%; Score 3856.5; DB 2; Length 1837;
Best Local Similarity 42.8%; Pred. No. 2.7e-180;
Matches 891; Conservative 273; Mismatches 577; Indels 339; Gaps 49;

QY 13 PPLRGSRPSSDPPGRLARG-----WTRRRMERAPRSRD-----SPVASRSSTTCPG 60
DB 7 PELRSFQSLSKYAGGPRSVLGRRTSAITVNRQSQSTRRHEDVEALGIEGSKETLQLSE 66
QY 61 PGAAGAGSTEKDRG-----SADSEAEGLPYPALAPVFFVLSQDSRPRSWCL 107
DB 67 HGRL-ASSSEASPSRWEGRQIEWGNEEQIEESE-LPYPGFAEPALRCFYQARPPRKWAL 124
QY 108 RTVCNPFERVSMLVILLNCVTLGMFRPCED-IACDSQRCRILQAFDDFIFAFFAVEMVV 166
DB 125 QMVMSPFDRITMAVIMINCVTLGMFRPCEDGPDCTVRCQILDIIIDNCIFVYFAFEMVI 184
QY 167 KVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQ---NVFSAVRTVRLRPLRAI 223
DB 185 KIMALGYGPAAYMSDTNRLDFFIVMAGIAEFVLHGLGNLNTAIRTVRLRPLRAV 244
QY 224 NRVPMSRILVTLTLLDTPMLGNVLLCFFVFFIFGIVGVOLWAGLLNRNCF--LPENFS- 280
DB 245 NRIPMSRILVNLTLTLPMLGNVLLCFFVFFIFGIVGVOLWAGLLNRNRCVNLPKTISE 304
QY 281 ----LPLSVDLEPYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSLDYET 336
DB 305 NOSALFNKLTFRFYIPE-DTSLEYICSPDANGLHTCSNLPYPTVD---GVKCNLTLD 360
QY 337 YNSSSNTTCVNWNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVM 396

Db 361 YDKVTNDSINWNIYNECQMQRNPFQGSVSDNIGFAWVAIFLVISLEGWTDIMYVQ 420
QY 397 DAHSFNFYIFILLIIVGSFFMINCLVVIATQPSQKQRESQLMRQVRFLSNASTLA 456
DB 421 DAHSFNNWYIFVLLIVIGAFFMINCLVVIATQPAETKRRETERMQERKMLNDRDISC 480
QY 457 SFSEPG-----SCYEELLKYLVIILKRAARLAQVSRAGVRAGLLSSPVARSQOE 507
DB 481 TGSEIGGASSKEEGDTVYAAAFVRFIGHTFRTRKRAAKKYTAY-----MEE 526
QY 508 POPSGSCTRSRRRLSVHHLVHHHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRMLP 567
DB 527 RAERKSSERQQRKSKL-----DDMATLSRIEKAEDDE----- 560
QY 568 PPSTPTPGPGPPRGAESVHSFYHADCHLEPVRCOAPPRCPSEASGRTVSGKVPVHT 627
DB 561 DETTITRENGDDQIEQN-----GDGVRIRKRVKI 588
QY 628 SPPPEILKDKALVEVAPSPGPPTILTSFNIPPGPFSSMHKLLTQSTGACHSSCKISSPCS 687
DB 589 EEPKI----- 594
QY 688 KADSGACGPDSCPYCARTGAGEPESADHVMPSDSDSEAVYFTQDAQHSDLRPHSRRQR 747
DB 595 -----KIGNGNSNGPHYKHSSSDEES-----DEDGEEDQVYDGEAKKK- 633
QY 748 SLGPDAPSSVLAFWRLLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNA 807
DB 634 -----STPSKL--WW--FREKIQKVICDHFTRGILVAILVNTLSMGVEYHQPEILTVI 684
QY 808 LEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLR 867
DB 685 LEYSNLFFTALFALEMLLKIIASGLFGYLAGDNFLFDGGIVALSVLFLFQEGKGLSVLR 744
QY 868 TFRLMRVLKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKFASE 927
DB 745 TFRLLRLKLVRFPALRYQLVVMRLTMDNVTVFFGLLVLFIFISILGMNLFQCKCKV 804
QY 928 RD--GDTLP--DRKNFDSLLWAIIVTVFQILTQEDWNKVLVNGMASTSSWAALYFIALMT 982
DB 805 EEFGLGGLAKKCKERNFTLLWALITVQILTQEDWNMVLVFNMAQTNPWAALYFVALMT 864
QY 983 FGNYVLNLLVAILVEGFAEGDATKSEEDFFSPVDGDKRKLALVALGEHAELR 1042
DB 865 FGNYVLNLLVAILVEGFAEGDEEKQLEEDARKQAVEEEDERKELELII----- 916
QY 1043 KSLPLPLIHTAATPMShPKSSSTGVGEALGSGSRRTSSSGSAEPGAHHMKC--PPSA 1100
DB 917 -----AKTTPAFNNGVAPAECTCQRPSSP 941
QY 1101 RSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLLSGEGQESQDEE 1155
DB 942 EESP-SPRLLSANY-----HPSPERKHSANLDAIIDKRLVL-----RN 978
QY 1156 SSEEDRASPADSDHRRGSLEREAKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSA 1215
DB 979 SAPFDR-SPV-SEGRDDSLNRHA--SLVLPVANGVYRRQRVHWSGLCHHFNPCPVH 1034
QY 1216 SGRLARTLRTDDPQLDGGDDNDDEGNLSKGERIQA---WVRSRL-PACCRERDSWAYIF 1270
DB 1035 GRRALIETVAREKFLASQELKQALAEKNEAKQNTFVRKLLKTKTCLHNRTEFSFLM 1094
QY 1271 PQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1330
DB 1095 GPKNPLRIKLOTTQKKWFDYTVLFFIGINCITLAMERPSIPDSEFERQFLHSYIFTV 1154
QY 1331 VFLAEMTVKVVVALGWCFCGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSGT-KILGMLR 1389
DB 1155 IFTGEMMKVIANGCFIGQAAAYFKDGNILDGILVVISLINIAFELLATGDSPKIFGVR 1214
QY 1390 VRLRLTLRLPLRVTSRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGF 1449
DB 1215 VRLRLRLRLRLRVINRAPGVKLVVMTLISLSKPIGNIVLICCTFFIIFGILGVQLFKGM 1274





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:00:31 ; Search time 243 Seconds  
(without alignments)  
3606.580 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKDVLISLSSDPADLDP 2266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11862.5	99.7	2273	4 AAE01019	Aae01019 Human T-t
2	11815.5	99.3	2377	8 ADQ89064	Adq89064 Human uro
3	11758.5	98.8	2243	2 AAY14589	Aay14589 Human T-t
4	11758.5	98.8	2243	7 ADJ68819	Adj68819 Human hea
5	11741	98.6	2250	2 AAY14586	Aay14586 Human T-t
6	11735.5	98.6	2261	2 AAY14587	Aay14587 Human T-t
7	11727	98.5	2268	2 AAY14588	Aay14588 Human T-t
8	11653	97.9	2266	4 AAB66481	Aab66481 Human alp
9	11111	93.3	2428	3 AAY70720	Aay70720 Rat pancr
10	10962.5	92.1	2247	2 AAY14593	Aay14593 Rat T-typ
11	10945	91.9	2254	2 AAY14590	Aay14590 Rat T-typ
12	10939.5	91.9	2265	2 AAY14591	Aay14591 Rat T-typ
13	10925	91.8	2272	2 AAY14592	Aay14592 Rat T-typ
14	10774	90.5	2287	4 AAB66475	Aab66475 Rat alpha
15	6315.5	53.1	1207	4 AAU00474	Aau00474 Human T-t
16	6218	52.2	2359	4 AAB66476	Aab66476 Rat alpha
17	6212	52.2	2353	2 AAY06299	Aay06299 Human act
18	6212	52.2	2353	6 ABP72254	Abp72254 Human T-t
19	6212	52.2	2353	7 ADJ69322	Adj69322 Human hea
20	6211	52.2	2353	2 AAY06298	Aay06298 Human act
21	6178	51.9	2353	5 ABG30840	Abg30840 Human vol
22	5855.5	49.2	2038	2 AAY14595	Aay14595 Human T-t
23	5845.5	49.1	2044	2 AAY14594	Aay14594 Human T-t
24	5709.5	48.0	2034	2 AAY06300	Aay06300 Human act
25	5492.5	46.1	2175	5 AAU10535	Aau10535 Human T-t

26	5492.5	46.1	2175	6 ABU08511	Abu08511 Human T-t
27	5492.5	46.1	2175	8 ADH69265	Adh69265 Human TCC
28	5484	46.1	2188	5 AAU10536	Aau10536 Human T-t
29	5484	46.1	2188	6 ABU08512	Abu08512 Human T-t
30	5484	46.1	2188	8 ADH69267	Adh69267 Human TCC
31	5366	45.1	1835	2 AAY14597	Aay14597 Rat T-typ
32	5366	45.1	1835	8 ADH69268	Adh69268 Rat T-typ
33	5361.5	45.0	1823	2 AAY14596	Aay14596 Human T-t
34	5198.5	43.7	1792	4 AAB66477	Aab66477 Rat brain
35	5043.5	42.4	982	4 AAM23743	Aam23743 Human EST
36	3959.5	33.3	1854	2 AAW79161	Aaw79161 Human cal
37	3959.5	33.3	1854	4 AAB66472	Aab66472 Protein e
38	3564.5	29.9	1657	8 ADN24183	Adn24183 Bacterial
39	3442	28.9	2435	4 ABB60448	Abb60448 Drosophil
40	3427	28.8	644	4 AAB66478	Aab66478 Human alp
41	3020.5	25.4	1859	4 ABG10954	Abg10954 Novel hum
42	1960	16.5	853	4 AAM93437	Aam93437 Human pol
43	1960	16.5	853	8 ADL31041	Adl31041 Human pro
44	1753	14.7	2264	8 ADM31026	Adm31026 Human cal
45	1752.5	14.7	2339	2 AAR33549	Aar33549 Sequence

ALIGNMENTS

RESULT 1  
AAE01019  
ID AAE01019 standard; protein; 2273 AA.  
XX

AC AAE01019;

XX  
DT 17-JUL-2001 (first entry)

XX  
DE Human T-type low voltage activated calcium channel alpha1G-c protein.

KW Human T-type low voltage activated calcium channel alpha1G-c; stress;  
KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;  
KW endocrine disorder; respiratory disorder; peripheral muscle disorder;  
KW muscle excitability; fertilisation; contraception; hypertension;  
KW neuronal firing regulation; cardiovascular disorder; gene therapy;  
KW forensic analysis; epidemiological study; neuroleptic.

XX Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 1138 /note= "Encoded by GAG"  
FT Misc-difference 1142 /note= "Encoded by GAA"  
FT Misc-difference 1680 /note= "Encoded by ACG"  
FT Misc-difference 1683 /note= "Encoded by GAA"

XX WO200130844-A1.

XX 03-MAY-2001.

XX 06-OCT-2000; 2000WO-US027761.

XX 26-OCT-1999; 99US-00426998.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Dublin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;

XX WPI; 2001-300486/31.

XX N-PSDB; AAD04756.

XX New nucleic acid encoding human calcium channel protein, useful for  
PT identifying specific modulators and potential pharmaceuticals for  
PT treating e.g. epilepsy.



QY 1794 LRDCDQESTCYNVTISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAEL 1853  
Db 1801 LRDCDQESTCYNVTISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAEL 1860  
QY 1854 ELEMKTLSQPSPHPLGSPFLWPVGVEGSDSPDKPGALHPAAHARSASHFSLEHPTMQPH 1913  
Db 1861 ELEMKTLSQPSPHPLGSPFLWPVGVEGSDSPDKPGALHPAAHARSASHFSLEHPTMQPH 1920  
QY 1914 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLHGRGWGLPKAQSGSVLSVHS 1973  
Db 1921 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLHGRGWGLPKAQSGSVLSVHS 1980  
QY 1974 QPADTSYIQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRLRRQAAIRTDSDVQ 2033  
Db 1981 QPADTSYIQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRLRRQAAIRTDSDVQ 2040  
QY 2034 GLGSREDLLAEVSGSPPLARAYSFWGSSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNW 2093  
Db 2041 GLGSREDLLAEVSGSPPLARAYSFWGSSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNW 2100  
QY 2094 GKGPPESTRSSLELDTLSWISGDLPLPGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2153  
Db 2101 GKGPPESTRSSLELDTLSWISGDLPLPGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDE 2160  
QY 2154 QRRHSIAVCLDSGSPHLGTDPSNLGGQPLGGGSRPKKLSPPSITIDPPESQGRPTP 2213  
Db 2161 QRRHSIAVCLDSGSPHLGTDPSNLGGQPLGGGSRPKKLSPPSITIDPPESQGRPTP 2220  
QY 2214 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKOVLSSLSSDPADLDP 2266  
Db 2221 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKOVLSSLSSDPADLDP 2273

RESULT 2

ADQ89064 ID ADQ89064 standard; protein; 2377 AA.  
XX AC ADQ89064;  
XX DT 21-OCT-2004 (first entry)  
XX DE Human urological disorder related protein 4421 SEQ.16.  
XX KW urological disorder; uropathic; cytostatic; urinary incontinence;  
XX KW benign prostatic hyperplasia; human.  
XX OS Homo sapiens.  
XX PN WO2004065576-A2.  
XX PD 05-AUG-2004.  
XX PF 14-JAN-2004; 2004WO-US0000750.  
XX PR 15-JAN-2003; 2003US-0440318P.  
PR 04-FEB-2003; 2003US-0444783P.  
PR 27-MAR-2003; 2003US-0457901P.  
PR 08-MAY-2003; 2003US-0468775P.  
PR 19-MAY-2003; 2003US-0471614P.  
PR 16-JUN-2003; 2003US-0478742P.  
PR 18-JUL-2003; 2003US-0488529P.  
PR 30-JUL-2003; 2003US-0491156P.  
PR 02-SEP-2003; 2003US-0499594P.  
PR 26-SEP-2003; 2003US-0506332P.  
XX (MILL-) MILLENNIUM PHARM INC.  
PA Karicheti V, Silos-Santiago I, Eliasof SD;  
XX PI  
XX WPI; 2004-562167/54.  
DR N-PSDB; ADQ89063.  
XX

PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,  
PT 211 or for identifying a compound capable of treating a urological  
PT disorder or identifying and treating a subject having a urological  
PT disorder.  
XX  
PS Claim 1; SEQ ID NO 16; 542pp; English.  
XX  
CC The present invention describes the use of polypeptides related to  
CC urological disorders for identifying a compound capable of treating a  
CC urological disorder, identifying a subject having a urological disorder,  
CC or treating a subject having a urological disorder. Also described: (1) a  
CC method for identifying a compound capable of treating a urological  
CC disorder; (2) a method for identifying a subject having a urological  
CC disorder; and (3) a method for treating a subject having a urological  
CC disorder. The compound has uropathic and cytostatic activities. The  
CC polypeptides related to urological disorders are useful for identifying a  
CC compound capable of treating a urological disorder, identifying a subject  
CC having a urological disorder, or treating a subject having a urological  
CC disorder. Disorders include urinary incontinence and benign prostatic  
CC hyperplasia. The present sequence represents a human urological disorder  
CC related protein, which is used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 2377 AA;

Query Match 99.3%; Score 11815.5; DB 8; Length 2377;  
Best Local Similarity 95.2%; Pred. No. 0;  
Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;  
QY 1 MDEEDGAGAEESGQPRSFMRNLDSGAGRPGGSAEKDPSADSEAEGLYPALAPV 60  
Db 1 MDEEDGAGAEESGQPRSFMRNLDSGAGRPGGSAEKDPSADSEAEGLYPALAPV 60  
QY 61 FFYLSQDSRPRSWCLRTVCNPWFERRISMLVILLNCVTLMRPPCEDIACDSQRCRILQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNPWFERRISMLVILLNCVTLMRPPCEDIACDSQRCRILQAF 120  
QY 121 DDFIFAFFAVEMVMVMVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSFSAVR 180  
Db 121 DDFIFAFFAVEMVMVMVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSFSAVR 180  
QY 181 TVRVLRLRAINRVPSMRILVLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240  
Db 181 TVRVLRLRAINRVPSMRILVLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240  
QY 241 CFLPENFSLPSVDLERYYYOTENEDESFFICSQPRENGMRSCRSVPTLRDGGGGPPCGL 300  
Db 241 CFLPENFSLPSVDLERYYYOTENEDESFFICSQPRENGMRSCRSVPTLRDGGGGPPCGL 300  
QY 301 DYEAYNSSNTTCVNNQYTYNCSSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEAYNSSNTTCVNNQYTYNCSSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYEELLYVILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPS 480  
Db 421 STLASFSEPGSCYEELLYVILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPS 480  
QY 481 SCSRSRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPTP 540  
Db 481 SCSRSRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPTP 540  
QY 541 ALSGAPPGAEESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVPTVHTSPPE 600  
Db 541 ALSGAPPGAEESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660  
Db 601 TLKEKALVEVAASSGPPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660



QY 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAYVEFTQDAQHSDLRDPHSRRQRSLGPD 720  
Db 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAYVEFTQDAQHSDLRDPHSRRQRSLGPD 720  
QY 721 EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780  
Db 721 EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR 840  
Db 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR 840  
QY 841 VLKLVFLPALQRQLVVLMTMDNVATFCMLLMFLFIPIFISILGMHLFGCKFASERDGDTL 900  
Db 841 VLKLVFLPALQRQLVVLMTMDNVATFCMLLMFLFIPIFISILGMHLFGCKFASERDGDTL 900  
QY 901 PDRKNFDSLWAIWTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVVLENLV 960  
Db 901 PDRKNFDSLWAIWTVFQIILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVVLENLV 960  
QY 961 AILVEGFOAEIISKREDASGOLSCIQLPVDVSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020  
Db 961 AILVEGFOAEIISKREDASGOLSCIQLPVDVSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020  
QY 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAA 1080  
Db 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAA 1080  
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1140  
Db 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1140  
QY 1141 DEESSEERASAPGSDHRHRSGLEREAKSFDLPDTLQVPLGHRASGRGSASEHQDCN 1200  
Db 1141 DEESSEERASAPGSDHRHRSGLEREAKSFDLPDTLQVPLGHRASGRGSASEHQDCN 1200  
QY 1201 GKSASGLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACLERDSWSAYIFP 1260  
Db 1201 GKSASGLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACLERDSWSAYIFP 1260  
QY 1261 PQSRFLLCHRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
Db 1261 PQSRFLLCHRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
QY 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLVLISVIDILVSMVSDSGTKILGMLRVL 1380  
Db 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLVLISVIDILVSMVSDSGTKILGMLRVL 1380  
QY 1381 RLLRTLRLPVRISRAOGLKVVEITLMSLLKPIGNIWVICCAFFIIFGILGVQLFKGKFFV 1440  
Db 1381 RLLRTLRLPVRISRAOGLKVVEITLMSLLKPIGNIWVICCAFFIIFGILGVQLFKGKFFV 1440  
QY 1441 CQGEDTRNITNKSDCAEASRWRHKYNFDNLGQALMSLFLVASKDGVWDIMYDGLDAVG 1500  
Db 1441 CQGEDTRNITNKSDCAEASRWRHKYNFDNLGQALMSLFLVASKDGVWDIMYDGLDAVG 1500  
QY 1501 VDQQPIMNHNPMWMLLYFISFLLIVAFVFLNMFVGVVVENFHKCRHQHEEEARRREEKRL 1560  
Db 1501 VDQQPIMNHNPMWMLLYFISFLLIVAFVFLNMFVGVVVENFHKCRHQHEEEARRREEKRL 1560  
QY 1561 RRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHVLDLFTIGV 1602  
Db 1561 RRLEKKRRNMLDDVIASSGSSASAASEAQCKPYSDYSRFRLLVHHLCTSHVLDLFTIGV 1620  
QY 1603 IGLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDL 1662  
Db 1621 IGLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDL 1680  
QY 1663 AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLVAGVMRALLDTVMQAL 1722  
Db 1681 AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLVAGVMRALLDTVMQAL 1740  
QY 1723 PQVGNLGLLFMLLFFIFAALGVLEFGDLECDTHPC EGLGRHATFRNFGMAFLTILFRVST 1782

Db 1741 PQVGNLGLLFMLLFFIFAALGVLEFGDLECDTHPC EGLGRHATFRNFGMAFLTILFRVST 1800  
QY 1783 GDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKE 1842  
Db 1801 GDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKE 1860  
QY 1843 AKEEAELEAELEEMKTLSPQPHSPGLSPFLWPVEGPDSPSPKPGALHPAAHARSASH 1902  
Db 1861 AKEEAELEAELEEMKTLSPQPHSPGLSPFLWPVEGPDSPSPKPGALHPAAHARSASH 1920  
QY 1903 FSLEHPT----- 1909  
Db 1921 FSLEHPTDRQLFDTISLLIQGSLEWELKLMDELACGCGQPSAFPSAPSLGSGSDPQIPLAE 1980  
QY 1910 -----MQPHPTELPGPDILLTVRKSG 1929  
Db 1981 MEALSLTSEIVSEPCSLALTDSDLPDDMHTLLLSALESNMQPHPTELPGPDILLTVRKSG 2040  
QY 1930 VSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSOPADTSYILQLPKDAP 1989  
Db 2041 VSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSOPADTSYILQLPKDAP 2100  
QY 1990 HLLQPHSAPTWTGTPKLP PPGRSPLAQRPLRRQAAIRTDSDLVQGLGSRREDLLAEVSGPS 2049  
Db 2101 HLLQPHSAPTWTGTPKLP PPGRSPLAQRPLRRQAAIRTDSDLVQGLGSRREDLLAEVSGPS 2160  
QY 2050 PPLARAYSFWGQSSTQAQHSRSHSKISKHMTTPPAPCPGPEENWKGPPETRRSSLELDTE 2109  
Db 2161 PPLARAYSFWGQSSTQAQHSRSHSKISKHMTTPPAPCPGPEENWKGPPETRRSSLELDTE 2220  
QY 2110 LSWISGDLPPGGQEEPPSPRDLKKCYSVEAQSCORRPTSMWDEQRRHSIAVSCLDGSGSQ 2169  
Db 2221 LSWISGDLPPGGQEEPPSPRDLKKCYSVEAQSCORRPTSMWDEQRRHSIAVSCLDGSGSQ 2280  
QY 2170 PHLGTDPSNLGGQPLGGPSRPPKLSPPSITIDPPESQGPRTPSPGICLRRRAPSSDS 2229  
Db 2281 PHLGTDPSNLGGQPLGGPSRPPKLSPPSITIDPPESQGPRTPSPGICLRRRAPSSDS 2340  
QY 2230 KDPLASGPPDMSMAASPSPKDVLSLGSLSSDPADLDP 2266  
Db 2341 KDPLASGPPDMSMAASPSPKDVLSLGSLSSDPADLDP 2377  
  
RESULT 3  
AA14589  
ID AA14589 standard; protein; 2243 AA.  
XX  
AC AA14589;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavTld).  
XX  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX  
OS Homo sapiens.  
XX  
PN WO929847-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
DR N-PSDB; AAX83484.

XX New T-type voltage-gated calcium channels.  
PT Disclosure; Page 58-67; 138pp; English.  
XX  
PS  
XX  
CC This sequence represents a human T-type voltage-gated calcium (Ca)  
CC channel alpha-1-G designated hCavTid. Voltage gated channels are membrane  
CC bound glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2243 AA;

Query Match 98.8%; Score 11758.5; DB 2; Length 2243;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

QY 1 MDEEEDGAGAEESQPRSMRLNDLSGAGRPGPSAEKDPGSADSEAEGLYPALAPVV 60  
DB 1 MDEEEDGAGAEESQPRSMRLNDLSGAGRPGPSAEKDPGSADSEAEGLYPALAPVV 60  
QY 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLMGFRPCEDIAQSQRILQAF 120  
DB 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLMGFRPCEDIAQSQRILQAF 120  
QY 121 DDFIFAFFAVEMVVMKVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180  
DB 121 DDFIFAFFAVEMVVMKVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180  
QY 181 TVRVLRLPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLNRN 240  
DB 181 TVRVLRLPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLNRN 240  
QY 241 CFLPENFSLPLSDLERYQYQTENEDESPFICSQPRENGMRSCRSVPTRLRGDGGGPPCGL 300  
DB 241 CFLPENFSLPLSDLERYQYQTENEDESPFICSQPRENGMRSCRSVPTRLRGDGGGPPCGL 300  
QY 301 DYEAYNSSNTTCVNWQYTYNCSAGHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIM 360  
DB 301 DYEAYNSSNTTCVNWQYTYNCSAGHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
DB 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480  
DB 421 STLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480  
QY 481 SCSRSRRRLSVHLLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
DB 481 SCSRSRRRLSVHLLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKYPTVHTSPPE 600  
DB 541 ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKYPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLLETSQSTGACQSSCKISSPCLKADSG 660  
DB 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLLETSQSTGACQSSCKISSPCLKADSG 660

QY 661 ACPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720  
DB 661 ACPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720  
QY 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
DB 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVIVISVWEIVGQGGGLSVLRTFRLMR 840  
DB 781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVIVISVWEIVGQGGGLSVLRTFRLMR 840  
QY 841 VLKLVRELPALQRLVVLKMTMDNVATFCMLLMFLFIFISILGMHLFGCKFASERDGD 900  
DB 841 VLKLVRELPALQRLVVLKMTMDNVATFCMLLMFLFIFISILGMHLFGCKFASERDGD 900  
QY 901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLNMGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
DB 901 PDRKNFDSLLWAIVTVFQILTQEDWNKVLNMGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
QY 961 AILVEGFAEEISKREDASQLSQILPVDVSQGGDANKSESEPDFFPSLDGDGDRKKCL 1020  
DB 961 AILVEGFAE-----GDANKSESEPDFFPSLDGDGDRKKCL 997  
QY 1021 ALVSLGEHPPELKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080  
DB 998 ALVSLGEHPPELKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057  
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140  
DB 1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117  
QY 1141 DEESSEERASPDGSHRHRGSLERAKSSFDPDLPTLQVPLHRTASGRGSASEHQDCN 1200  
DB 1118 DEESSEERASPDGSHRHRGSLERAKSSFDPDLPTLQVPLHRTASGRGSASEHQDCN 1177  
QY 1201 GKSASGRALARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260  
DB 1178 GKSASGRALARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP 1237  
QY 1261 PQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
DB 1238 PQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297  
QY 1321 FLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1380  
DB 1298 FLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1357  
QY 1381 RLLRTLRLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440  
DB 1358 RLLRTLRLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1417  
QY 1441 COGEDTRNITNKSDCAEASRVRWRHKYNFNDLQALMSLFVLASKDGVVDIMYDGLDAVG 1500  
DB 1418 COGEDTRNITNKSDCAEASRVRWRHKYNFNDLQALMSLFVLASKDGVVDIMYDGLDAVG 1477  
QY 1501 VDQOPIMHNPMWMLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEARRREKRL 1560  
DB 1478 VDQOPIMHNPMWMLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEARRREKRL 1537  
QY 1561 RRLEKKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTMAMEHYQQPQI 1620  
DB 1538 RRLEKKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTMAMEHYQQPQI 1597  
QY 1621 LDEALKICNYIFTVIFVLESVFKLVAFGFRFRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1680  
DB 1598 LDEALKICNYIFTVIFVLESVFKLVAFGFRFRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1657  
QY 1681 ASLPINPTIIRIMRVLRARVLKLLKMAVGMRRALLDTVMQALPOVGNLGLLFFMFFIFA 1740  
DB 1658 ASLPINPTIIRIMRVLRARVLKLLKMAVGMRRALLDTVMQALPOVGNLGLLFFMFFIFA 1717  
QY 1741 ALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFLRVSTGDNWNGIMKDTLRDCDQE 1800

Db 1718 ALGVFLPGDLECDETHPCCEGLGRHATERNFMAFLTLFRVSTGDNWNGIMKDTLRDCDQE 1777

QY 1801 STCVNTVISPIYFVSFVLTAFVLVNVVIAVMKHLSESNKEAKEEAELEAEMKTL 1860

Db 1778 STCVNTVISPIYFVSFVLTAFVLVNVVIAVMKHLSESNKEAKEEAELEAEMKTL 1837

QY 1861 SPQHPSLGSPFLWPVGEGPSPDSPKPGALHPAAHARSASHFSLEHPTMQPHTLP 1920

Db 1838 SPQHPSLGSPFLWPVGEGPSPDSPKPGALHPAAHARSASHFSLEHPTMQPHTLP 1897

QY 1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWLKPAQSGSVLSVHSPADTSY 1980

Db 1898 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWLKPAQSGSVLSVHSPADTSY 1957

QY 1981 ILQLPKDAPHLLQPHSAPTWTGTPKLPPLPPGRSPLAQRLRRQAAIRTDSDLVQGLGSRD 2040

Db 1958 ILQLPKDAPHLLQPHSAPTWTGTPKLPPLPPGRSPLAQRLRRQAAIRTDSDLVQGLGSRD 2017

QY 2041 LLAEVSGPSPPLARAYSFWGQSSSTQAQHSRSHSKISHMTPPAPCPGPEPNWGKGPET 2100

Db 2018 LLAEVSGPSPPLARAYSFWGQSSSTQAQHSRSHSKISHMTPPAPCPGPEPNWGKGPET 2077

QY 2101 RSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVRAQSCQRRPTSWLDBQRRHSIA 2160

Db 2078 RSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVRAQSCQRRPTSWLDBQRRHSIA 2137

QY 2161 VSCLDGSGQPHLGTDPNLGGQPLGGPGRPKKLSPPSITIDPPESQGRPTPSPGICL 2220

Db 2138 VSCLDGSGQPHLGTDPNLGGQPLGGPGRPKKLSPPSITIDPPESQGRPTPSPGICL 2197

QY 2221 RRRAPSSDSKOPLASGPPDPSMAASPSPKKDVLSLGLSSDPADLDP 2266

Db 2198 RRRAPSSDSKOPLASGPPDPSMAASPSPKKDVLSLGLSSDPADLDP 2243

RESULT 4

ADJ68819

ID ADJ68819 standard; protein; 2243 AA.

XX AC ADJ68819;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID625.

XX KW mitochondrial; human; screening assay; diabetes mellitus;

XX KW Huntington's disease; osteoarthritis;

XX KW Leber's hereditary optic neuropathy; LHON;

XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;

XX KW osteopathic; ophthalmological; cytostatic.

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

XX PI Warnock DE;

XX XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX Claim 1; SEQ ID NO 625; 180pp; English.

PS

XX This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, neurotropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytotostatic activities. This polypeptide sequence is a human heart

CC mitochondrial protein of the invention.

XX SQ Sequence 2243 AA;

Query Match 98.8%; Score 11758.5; DB 7; Length 2243;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

QY 1 MDEEDGAGAEESGQPSRSMRLNLSGAGRPGPGSAEKDPGADSEAEGLPYPALAPVV 60

Db 1 MDEEDGAGAEESGQPSRSMRLNLSGAGRPGPGSAEKDPGADSEAEGLPYPALAPVV 60

QY 61 FFVLSQDSRPSRWCNLPWFERISMLVLLNCVTLGMFRPCEDIAQDSQRCRILQAF 120

Db 61 FFVLSQDSRPSRWCNLPWFERISMLVLLNCVTLGMFRPCEDIAQDSQRCRILQAF 120

QY 121 DDFIFAFFAVEMVMVVALGIFGKCYLGTWNRDLDFIVIAAGMLEYSLDLQNVFSAVR 180

Db 121 DDFIFAFFAVEMVMVVALGIFGKCYLGTWNRDLDFIVIAAGMLEYSLDLQNVFSAVR 180

QY 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Db 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

QY 241 CFLPENFSLPSVDLERYVQTENEDESPFICSPRENGMRSCRSVPTLRDGGGGPPCGL 300

Db 241 CFLPENFSLPSVDLERYVQTENEDESPFICSPRENGMRSCRSVPTLRDGGGGPPCGL 300

QY 301 DYEAYNSSNTTCVNNQYVYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Db 301 DYEAYNSSNTTCVNNQYVYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360

QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLYLILKAAARLAQVSRAGVRVGLSSPAPLGGQETQPSS 480

Db 421 STLASFSEPGSCYEELLYLILKAAARLAQVSRAGVRVGLSSPAPLGGQETQPSS 480

QY 481 SCSRSRRLSVHLLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

Db 481 SCSRSRRLSVHLLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600

Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600

QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660

Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660

QY 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSIDLDPHSRRQRS LGPDA 720  
Db 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSIDLDPHSRRQRS LGPDA 720  
QY 721 EPSSVLAFWRLICDTFRKI VDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
Db 721 EPSSVLAFWRLICDTFRKI VDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIPDGVI VIVISVWEIVGQGGGLSVLRTFRLMR 840  
Db 781 VFTSLFALEMLLKLLVYGPFGYIKNPYNIPDGVI VIVISVWEIVGQGGGLSVLRTFRLMR 840  
QY 841 VLKLVRLPALQRLVVLMTMDNVATFCMLLM LFI FIFSI LGMHLFGCKFASERDGD TL 900  
Db 841 VLKLVRLPALQRLVVLMTMDNVATFCMLLM LFI FIFSI LGMHLFGCKFASERDGD TL 900  
QY 901 PDRKNFDSL LWAIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
Db 901 PDRKNFDSL LWAIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
QY 961 AILVEGFOAEISKREDASQ LSCIQLPVDSQGGDANKSESEPDFSPSLDGDGRKKCL 1020  
Db 961 AILVEGFOAE-----GDANKSESEPDFSPSLDGDGRKKCL 997  
QY 1021 ALVSLGEHPELRKSL LPLLIHTAATPM SLPKSTSTGLGEALGPASRR TSSSGSAEPGAA 1080  
Db 998 ALVSLGEHPELRKSL LPLLIHTAATPM SLPKSTSTGLGEALGPASRR TSSSGSAEPGAA 1057  
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140  
Db 1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117  
QY 1141 DEESSEEEERASPA GSDHRRGSLEREA KSSFDLPDTLQVPG LHRTASGRGSASEHQDCN 1200  
Db 1118 DEESSEEEERASPA GSDHRRGSLEREA KSSFDLPDTLQVPG LHRTASGRGSASEHQDCN 1177  
QY 1201 GKSASGRLARALRPDDPPLDGD DADDEGNLSKGERVRAWIRARLPACYL ERDSWSAYIFP 1260  
Db 1178 GKSASGRLARALRPDDPPLDGD DADDEGNLSKGERVRAWIRARLPACCL ERDSWSAYIFP 1237  
QY 1261 PQSRFRLLCHRIITHKMF DHHVVLVII FNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
Db 1238 PQSRFRLLCHRIITHKMF DHHVVLVII FNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297  
QY 1321 FLAEMTVKVVALGWC FGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1380  
Db 1298 FLAEMTVKVVALGWC FGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSGTKILGMLRVL 1357  
QY 1381 RLLRTLRLPLRVISRAOGLKLVVETLMSS LKPIGNIVVICAFFIIFGILGVQLFKGKFFV 1440  
Db 1358 RLLRTLRLPLRVISRAOGLKLVVETLMSS LKPIGNIVVICAFFIIFGILGVQLFKGKFFV 1417  
QY 1441 CQGEDTRNITNKS DCAEAS YRWRVHRKYNFNDNLGOALMSL FVLASKDGVWDIMYDGLDAVG 1500  
Db 1418 CQGEDTRNITNKS DCAEAS YRWRVHRKYNFNDNLGOALMSL FVLASKDGVWDIMYDGLDAVG 1477  
QY 1501 VDQQPI MNHPWMLLYFISFL LIVAFFVLNMFGVVVENFHKCRQHQBEEERREKRL 1560  
Db 1478 VDQQPI MNHPWMLLYFISFL LIVAFFVLNMFGVVVENFHKCRQHQBEEERREKRL 1537  
QY 1561 RRLEKRRKAOCKPYSDYSRFRLLVH LCTSHYLDLFI TGVIGLNVVTMAMEHYQQPQI 1620  
Db 1538 RRLEKRRKAOCKPYSDYSRFRLLVH LCTSHYLDLFI TGVIGLNVVTMAMEHYQQPQI 1597  
QY 1621 LDEALKICNYIFTVIFVLES VFKLVAFGFRFFQDRWNQOLDLAIVLLSIMGITLEEIVN 1680  
Db 1598 LDEALKICNYIFTVIFVLES VFKLVAFGFRFFQDRWNQOLDLAIVLLSIMGITLEEIVN 1657  
QY 1681 ASLPINPTIIRIMRVLR IARVLKLLKMAVGM RALLDVTVMQALPQVGNLGLLFFLFFIFA 1740  
Db 1658 ASLPINPTIIRIMRVLR IARVLKLLKMAVGM RALLDVTVMQALPQVGNLGLLFFLFFIFA 1717

QY 1741 ALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDCDQE 1800  
Db 1718 ALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDCDQE 1777  
QY 1801 STCYNTVISPIYFVS FVLTAQFVLNVVIAVLMKHLEESNKEAEAELEEMKTL 1860  
Db 1778 STCYNTVISPIYFVS FVLTAQFVLNVVIAVLMKHLEESNKEAEAELEEMKTL 1837  
QY 1861 SPQHPSP LGSFELWPGEVGPDS PKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP 1920  
Db 1838 SPQHPSP LGSFELWPGEVGPDS PKPGALHPAAHARSASHFSLEHPTMQPHPTELPGP 1897  
QY 1921 DLLTVRKSGVSRTHSLP NDSYMCRHGSTAEGPLCHRGWG LPKAQSGSVLSVHSQPADTSY 1980  
Db 1898 DLLTVRKSGVSRTHSLP NDSYMCRHGSTAEGPLCHRGWG LPKAQSGSVLSVHSQPADTSY 1957  
QY 1981 ILQLPKDAPHL LQPHSAPTWTGTIPKLPPPGRSPLAQ RPLRRQAAIRTDSDLVQGLGSRED 2040  
Db 1958 ILQLPKDAPHL LQPHSAPTWTGTIPKLPPPGRSPLAQ RPLRRQAAIRTDSDLVQGLGSRED 2017  
QY 2041 LLAEVSGSPPLARAYS FWGQSSTO AQOHSRSHSKI SKHMTPPAPCPGPEPNWGKPPET 2100  
Db 2018 LLAEVSGSPPLARAYS FWGQSSTO AQOHSRSHSKI SKHMTPPAPCPGPEPNWGKPPET 2077  
QY 2101 RSSLELDTLSWISG D LPPGGQEEPPSPRDLKCY SVEAQSCORRPTSWLDEQRRHSIA 2160  
Db 2078 RSSLELDTLSWISG D LPPGGQEEPPSPRDLKCY SVEAQSCORRPTSWLDEQRRHSIA 2137  
QY 2161 VSCLDSGSQPHLGTDP SNLGGQPLGGPSRPKKLSPP SITIDPPESQGPRTPPSPGICL 2220  
Db 2138 VSCLDSGSQPHLGTDP SNLGGQPLGGPSRPKKLSPP SITIDPPESQGPRTPPSPGICL 2197  
QY 2221 RRRAPSSDSKDPLAS GPPDSMAASPSPKKDVLSL SGLSSDPADLDP 2266  
Db 2198 RRRAPSSDSKDPLAS GPPDSMAASPSPKKDVLSL SGLSSDPADLDP 2243

RESULT 5  
AAAY14586

ID AAY14586 standard; protein; 2250 AA.  
XX  
AC AAY14586;  
XX  
DT 07-DEC-1999 (first entry)  
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a).  
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
KW Homo sapiens.  
XX WO9929847-A1.  
XX 17-JUN-1999.  
PF 30-OCT-1998; 98WO-US023161.  
XX 05-DEC-1997; 97US-00985809.  
PR (LOYO ) UNIV LOYOLA CHICAGO.  
XX Perez-Reyes E, Cribbs LL;  
PI WPI; 1999-394972/33.  
XX N-PSDB; AAX83481.  
PT New T-type voltage-gated calcium channels.  
XX  
PS Disclosure; Page 31-40; 138pp; English.  
XX  
CC This sequence represents a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane









QY 901 PDRKNFDSLLWAIIVTVFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLV 960  
Db 901 PDRKNFDSLLWAIIVTVFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLV 960  
QY 961 AILVEGFAEIEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFPSLSDGDGRKKCL 1020  
Db 961 AILVEGFAE-----GDANKSESEPDFFPSLSDGDGRKKCL 997  
QY 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080  
Db 998 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057  
QY 1081 HEMKSPPSARSPHSPWASAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1140  
Db 1058 HEMKSPPSARSPHSPWASAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1117  
QY 1141 DEESSEERASGASHRRHRSGLEREAKSSFOLDPTLQVPLHRTASGRSASEHODCN 1200  
Db 1118 DEESSEERASGASHRRHRSGLEREAKSSFOLDPTLQVPLHRTASGRSASEHODCN 1177  
QY 1201 GKSASGRALARALPDDPPLDGDADDDEGNLSKGERVRAWTRARLPACYLERDSWSAYIFP 1260  
Db 1178 GKSASGRALARALPDDPPLDGDADDDEGNLSKGERVRAWTRARLPACCLERDSWSAYIFP 1237  
QY 1261 PQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
Db 1238 PQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297  
QY 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLRVL 1380  
Db 1298 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLRVL 1357  
QY 1381 RLLRTRPLRVISRAQGLKVWETLMSLLKPIGNIVWICCAFFIIFGILGVQLFKGKFFV 1440  
Db 1358 RLLRTRPLRVISRAQGLKVWETLMSLLKPIGNIVWICCAFFIIFGILGVQLFKGKFFV 1417  
QY 1441 CQGEDTRNITKSDCAEASRVRWRHKYNFNDLQALMSLFLVLSKDGWVDIMYDGLDAVG 1500  
Db 1418 CQGEDTRNITKSDCAEASRVRWRHKYNFNDLQALMSLFLVLSKDGWVDIMYDGLDAVG 1477  
QY 1501 VDQQPMNHNPWMLLYFISFLIIVAFVFLNMFVGVVFNHFKCRQHOBEEEEARRREEKRL 1560  
Db 1478 VDQQPMNHNPWMLLYFISFLIIVAFVFLNMFVGVVFNHFKCRQHOBEEEEARRREEKRL 1537  
QY 1561 RRLEKKRR-----KAQCKPYSDYSRFRLLVHLCCTSHYLDLFTIGV 1602  
Db 1538 RRLEKKRRNMLDDVIASSGSASAASEAQCKPYSDYSRFRLLVHLCCTSHYLDLFTIGV 1597  
QY 1603 IGLNVVTWAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLDL 1662  
Db 1598 IGLNVVTWAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLDL 1657  
QY 1663 AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRAILLDTVMQAL 1722  
Db 1658 AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRAILLDTVMQAL 1717  
QY 1723 PQVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVST 1782  
Db 1718 PQVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVST 1777  
QY 1783 GDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKHEESNKE 1842  
Db 1778 GDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKHEESNKE 1837  
QY 1843 AKEEAELEAELEEMKTLSPQSPHPLGVPVGPVSDSPKPGALHPAAHARSASH 1902  
Db 1838 AKEEAELEAELEEMKTLSPQSPHPLGVPVGPVSDSPKPGALHPAAHARSASH 1897  
QY 1903 FSLHPTMQPHPTLPDGLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPK 1962  
Db 1898 FSLHPTMQPHPTLPDGLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPK 1957

QY 1963 AQSGSVLSVHSQPADTSYILQLPKDAPHLLOPHSAPTWTGTPKLPGRSPLAQRPLRRQ 2022  
Db 1958 AQSGSVLSVHSQPADTSYILQLPKDAPHLLOPHSAPTWTGTPKLPGRSPLAQRPLRRQ 2017  
QY 2023 AAIRTDSLDVQGLGSRREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHRSRSHSKISHMTP 2082  
Db 2018 AAIRTDSLDVQGLGSRREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHRSRSHSKISHMTP 2077  
QY 2083 PAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVEAQS 2142  
Db 2078 PAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVEAQS 2137  
QY 2143 CORRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDFSNLGGQPLGGGSRPKKLSPPSITI 2202  
Db 2138 CORRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDFSNLGGQPLGGGSRPKKLSPPSITI 2197  
QY 2203 DPPEOQPRTPPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPPKDVLSGLSSDPA 2262  
Db 2198 DPPEOQPRTPPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPPKDVLSGLSSDPA 2257  
QY 2263 DLDP 2266  
Db 2258 DLDP 2261  
RESULT 7  
AAAY14588  
ID AAAY14588 standard; protein; 2268 AA.  
XX  
AC AAAY14588;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1c).  
XX  
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
KW  
XX Homo sapiens.  
OS  
XX WO929847-A1.  
PN  
XX 17-JUN-1999.  
PD  
XX 30-OCT-1998; 98WO-US023161.  
PF  
XX 05-DEC-1997; 97US-00985809.  
PR  
XX (LOYO ) UNIV LOYOLA CHICAGO.  
PA  
XX Perez-Reyes E, Cribbs LL;  
PI  
XX WPI; 1999-394972/33.  
DR N-PSDB; AAX83483.  
DR  
XX New T-type voltage-gated calcium channels.  
PS Disclosure; Page 49-58; 138pp; English.  
XX  
CC This sequence represents a human T-type voltage-gated calcium (Ca)  
CC channel alpha-1-G designated hCavT1c. Voltage gated channels are membrane  
CC bound glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium

CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
XX acid, e.g. to treat cardiomyopathy, epilepsy, etc  
SQ Sequence 2268 AA;

QY	961	AILVEGFOAEIISKREDASQOLSCIQLPVD	SOQGDKANKSESEPDPFFSPSLDGDGRKKCL	1021
Db	961	AILVEGFOAE	-----GDANKSESEPDPFFSPSLDGDGRKKCL	997
QY	1021	ALVSLGEHPELRKSLPLPLI	IHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1080
Db	998	ALVSLGEHPELRKSLPLPLI	IHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1057
QY	1081	HEMKSPPSARSSPHSPWSAASSWT	SRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140
Db	1058	HEMKSPPSARSSPHSPWSAASSWT	SRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1117
QY	1141	DEESSEERASPGSDHRHGRGLEREA	KSFDLPDTLQVPLHRTASGRGSASEHQDCN	1200
Db	1118	DEESSEERASPGSDHRHGRGLEREA	KSFDLPDTLQVPLHRTASGRGSASEHQDCN	1177
QY	1201	GKSASGRLARALRPDDPPLDGD	DADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP	1260
Db	1178	GKSASGRLARALRPDDPPLDGD	DADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP	1237
QY	1261	QOSRFRLLCHRIITHKMF	DHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
Db	1238	QOSRFRLLCHRIITHKMF	DHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1297
QY	1321	FLAEMTVKVVALGWC	FGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSGTKILGMLRVL	1380
Db	1298	FLAEMTVKVVALGWC	FGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSGTKILGMLRVL	1357
QY	1381	RLLRTLRPLRVISRAQGLKLV	ETLMSLKPIGNIVWICCAFFIIFGILGVQLFKGKFFV	1440
Db	1358	RLLRTLRPLRVISRAQGLKLV	ETLMSLKPIGNIVWICCAFFIIFGILGVQLFKGKFFV	1417
QY	1441	CQGEDTRNITNKSDCAEAS	YRWRHKYNFNLGOALMSLVLASKDGVDMYDGLDAVG	1500
Db	1418	CQGEDTRNITNKSDCAEAS	YRWRHKYNFNLGOALMSLVLASKDGVDMYDGLDAVG	1477
QY	1501	VDQOPIMNHPWMLLYFIS	FLLLIVAFFVLNMFGVVVENFHKCRHQHEEAEARRREEKRL	1560
Db	1478	VDQOPIMNHPWMLLYFIS	FLLLIVAFFVLNMFGVVVENFHKCRHQHEEAEARRREEKRL	1537
QY	1561	RRLEKKRR	-----KAQCKPYSDYSRFRLLVHHLCTSHYL	1595
Db	1538	RRLEKKRRSKEKOMADLML	DDVIAAGSSASAASEAQCKPYSDYSRFRLLVHHLCTSHYL	1597
QY	1596	DLFITGVIGLVVVTWAMEHY	QQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQD	1655
Db	1598	DLFITGVIGLVVVTWAMEHY	QQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQD	1657
QY	1656	RWNQDLAI	VLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAL	1715
Db	1658	RWNQDLAI	VLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAL	1717
QY	1716	DTVMQALPQVGNLGLL	FMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFL	1775
Db	1718	DTVMQALPQVGNLGLL	FMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFL	1777
QY	1776	TLFRVSTGDNWNGIMKDTLR	DCDQESTCNTVISPIFYVSVFLTAQFVLVNVVIAVLMKH	1835
Db	1778	TLFRVSTGDNWNGIMKDTLR	DCDQESTCNTVISPIFYVSVFLTAQFVLVNVVIAVLMKH	1837
QY	1836	LEESNKEAKEAELEAELE	MEKTLSPQHSPLGSPFLWPVGEGDSDSPKPGALHPAA	1895
Db	1838	LEESNKEAKEAELEAELE	MEKTLSPQHSPLGSPFLWPVGEGDSDSPKPGALHPAA	1897
QY	1896	HARSASHFSLHPTMQPH	TELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGH	1955
Db	1898	HARSASHFSLHPTMQPH	TELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGH	1957
QY	1956	RGWGLPKAQSGSVLSVHSQ	PADTSYILQPKDAPHLLQPHSAPTWTGTPKLP	2015
Db	1958	RGWGLPKAQSGSVLSVHSQ	PADTSYILQPKDAPHLLQPHSAPTWTGTPKLP	2017

QY 2016 QRPLRQRAIRTDSDVQGLSREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSK 2075  
Db 2018 QRPLRQRAIRTDSDVQGLSREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSK 2077  
QY 2076 ISKHTPPAPCPGPEPNWGKGPETRRSSLELDTLSWISGDLPPGGQEEPPSPRDLKCC 2135  
Db 2078 ISKHTPPAPCPGPEPNWGKGPETRRSSLELDTLSWISGDLPPGGQEEPPSPRDLKCC 2137  
QY 2136 YSVEAQSCORRPTSWLDEQRRHSIAVCLDSGSPHLGTDPSNLGGQPLGPGSRPKKL 2195  
Db 2138 YSVEAQSCORRPTSWLDEQRRHSIAVCLDSGSPHLGTDPSNLGGQPLGPGSRPKKL 2197  
QY 2196 SPPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGPPDSMAASPSPKDVLSSL 2255  
Db 2198 SPPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGPPDSMAASPSPKDVLSSL 2257  
QY 2256 GLSSDPADLDP 2266  
Db 2258 GLSSDPADLDP 2268  
RESULT 8  
AAB66481  
ID AAB66481 standard; protein; 2266 AA.  
XX AAB66481;  
AC AAB66481;  
XX 09-APR-2001 (first entry)  
DT 09-APR-2001 (first entry)  
XX Human alpha-IG T-type calcium channel protein.  
DE Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;  
XX T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;  
KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.  
KW  
XX Homo sapiens.  
OS WO200102561-A2.  
XX PN 11-JAN-2001.  
XX PD 04-JUL-2000; 2000WO-CA000794.  
XX PF 02-JUL-1999; 99US-00346794.  
XX PR (NEUR-) NEUROMED TECHNOLOGIES INC.  
XX PA Snutch TP, Baillie DL;  
XX PI WPI; 2001-123111/13.  
XX DR N-PSDB; AAF31684.  
XX DR Novel T-type calcium channel alpha-1 subunit gene useful for treating  
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
PT epilepsy.  
XX  
PS Example 3; Fig 6; 103pp; English.  
XX  
CC The present sequence is given in a specification providing sequences and  
CC partial sequences for three types of mammalian (human and rat) T-type  
CC calcium channel subunits. An expression cassette has been generated which  
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha\_1  
CC subunit operably linked to control sequences to effect its expression.  
CC The novel calcium channel nucleic acids and proteins are useful for  
CC treating conditions characterised by undesirable levels of T-type calcium  
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
CC hypertension, sleep disorder and epilepsy  
XX  
SQ Sequence 2266 AA;  
Query Match 97.9%; Score 11653; DB 4; Length 2266;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 2239; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 MDEEDGAGAEESQPRSFMRNLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPVV 60  
Db 1 MDEEDGAGAEESQPRSFMRNLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPVV 60  
QY 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTGLMFRPCEDIAACDSQRCRILQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTGLMFRPCEDIAACDSQRCRILQAF 120  
QY 121 DDFFAFPAFVEMVVKVVALGIFGKKCYLGDWTNRLDFFIVIAAGMLEYSLDLQNVFSAVR 180  
Db 121 DDFFAFPAFVEMVVKVVALGIFGKKCYLGDWTNRLDFFIVIAAGMLEYSLDLQNVFSAVR 180  
QY 181 TVRVLRLRAINRVFSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
Db 181 TVRVLRLRAINRVFSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
QY 241 CFLPENFSLPLSVDLERYQTENEDESPFICSPRENGMRSCRVPTRLRGDGGGPPCGL 300  
Db 241 CFLPENFSLPLSVDLERYQTENEDESPFICSPRENGMRSCRVPTRLRGDGGGPPCGL 300  
QY 301 DYEAYNSSNTTCVNWNOYTYNCESAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEAYNSSNTTCVNWNOYTYNCESAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYEELLKYLVIYILRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSS 480  
Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSS 480  
QY 481 SCRSRHRRLSVHLLVHHHHHHHHYHLGNGILRAPRASPEIQDRDANGSRRLMLPPRSTP 540  
Db 481 SCRSRHRRLSVHLLVHHHHHHHHYHLGNGILRAPRASPEIQDRDANGSRRLMLPPRSTP 540  
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTSPPE 600  
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPPTLTSLNIPPGPYSSMHKLETOSTGACQSSCKISSPCLKADSG 660  
Db 601 TLKERALVEVAASSGPPPTLTSLNIPPGPYSSMHKLETOSTGACQSSCKISSPCLKADSG 660  
QY 661 ACGPDSQPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720  
Db 661 ACGPDSQPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720  
QY 721 EPSSVLAFWRLLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
Db 721 EPSSVLAFWRLLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLLKLIVYGPFGYIKNPYINFDGVIIVISVWEIVGQGGGLSVLRTFRLMR 840  
Db 781 VFTSLFALEMLLKLIVYGPFGYIKNPYINFDGVIIVISVWEIVGQGGGLSVLRTFRLMR 840  
QY 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMLEFIFISILGMHLFGCKFASERDGDTL 900  
Db 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMLEFIFISILGMHLFGCKFASERDGDTL 900  
QY 901 PDRKNFDSLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
Db 901 PDRKNFDSLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
QY 961 AILVEGFQAEIISKREDASQGLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020  
Db 961 AILVEGFQAEIISKREDASQGLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020  
QY 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSABPGAA 1080  
Db 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSABPGAA 1080



QY	1081	HEMKSPPSARSSPHSPWSAAASSWTSSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1141
Db			
Db	1081	HEMKSPPSARSSPHSPWSAAASSWTSSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140
QY			
Db	1141	DEESSEERASPAGSDHRHSGSLERAKSSFDLPDTLQVPLHRTASGRGSASEHQDCN	1200
QY			
Db	1141	DEESSEERASPAGSDHRHSGSLERAKSSFDLPDTLQVPLHRTASGRGSASEHQDCN	1200
QY			
Db	1201	GKSASGRLARALRPPDPLDGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP	1260
QY			
Db	1201	GKSASGRLARALRPPDPLDGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP	1260
QY			
Db	1261	PQSRFRLLCHRIITHKMFHDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
QY			
Db	1261	PQSRFRLLCHRIITHKMFHDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
QY			
Db	1321	FLAEMTVKVALGWCFGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380
QY			
Db	1321	FLAEMTVKVALGWCFGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380
QY			
Db	1381	RLRLTLRPLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV	1440
QY			
Db	1381	RLRLTLRPLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV	1440
QY			
Db	1441	CQGEDTRNITNKSDCAEASRVRWVKYFNFDNLGQALMSFLVLASKDQGWVIMYDGLDAVG	1500
QY			
Db	1441	CQGEDTRNITNKSDCAEASRVRWVKYFNFDNLGQALMSFLVLASKDQGWVIMYDGLDAVG	1500
QY			
Db	1501	VDQQPIMNHPNMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRL	1560
QY			
Db	1501	VDQQPIMNHPNMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRL	1560
QY			
Db	1561	RRLEKKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMAMEHYQQPOI	1620
QY			
Db	1561	RRLEKKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMAMEHYQQPOI	1620
QY			
Db	1621	LDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVN	1680
QY			
Db	1621	LDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVN	1680
QY			
Db	1681	ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTVMQALPOVGNLGLLFFMLFFIFA	1740
QY			
Db	1681	ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTVMQALPOVGNLGLLFFMLFFIFA	1740
QY			
Db	1741	ALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE	1800
QY			
Db	1741	ALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQE	1800
QY			
Db	1801	STCYNTVISPIYFVSFVLTAQFVLNVVIAVLKMHLEESNKEAKEEAELEAELEEMKTL	1860
QY			
Db	1801	STCYFTVISPIYFVSFVLTAQFVLVMVVIAVLKMHLEESNKEAKEEAELEAELEEMKTL	1860
QY			
Db	1861	SPQHSPLGSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQHPTELPGP	1920
QY			
Db	1861	SPQHSPLGSPFLWPGVEGPDSPDSPKPGALMPAAHARSASHFSLEHPTMQHPTELPGP	1920
QY			
Db	1921	DLLTVRKSGVSRTHSLPNDSSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY	1980
QY			
Db	1921	DLLTVRKSGVSRTHSLPNDSSYMCRRGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY	1980
QY			
Db	1981	ILQLPKDAPHLLOPHSAPTWTGTPKLPPLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED	2040
QY			
Db	1981	ILQLPKDAPHLLOPMSAPTWTGTPKLPPLPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRED	2040
QY			
Db	2041	LLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKISKHMTTPAPCPGPEPNWKGPPET	2100
QY			
Db	2041	LLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKISKHMTTPAPCAGPEPNWKGPPET	2100
QY			
Db	2101	RSSLELDTELSWISGDLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA	2160
QY			
Db	2101	RSSLELDTELSNISGDLPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIA	2160
QY			
Db	2161	VSCLDSGSQPHLGTDPNSNLGGQPLGGPGSRPKKLSPPSITIDPPESQGPRTPPSPGICL	2220

Db 2161 VSCLDSGSQPHLGTDPNSNLGGQPLGGPGSRPKKLSPPSITIDPPESQGRTTPSPGICL 2266  
 QY 2221 RRRAPSSDSKDFLASGPPDPSMAASPSPKDVLSSLGSLSSDPADLDP 2266  
 Db 2221 RRRAPSSDSKDFLASGPPDPSMAASPSPKDVLSSLGSLSSDPADLDP 2266

RESULT 9  
 AAY70720  
 ID AAY70720 standard; protein; 2428 AA.  
 XX  
 AC AAY70720;  
 XX  
 DT 18-JUL-2000 (first entry)  
 XX  
 DE Rat pancreatic T-type calcium channel.  
 XX  
 KW Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;  
 KW pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;  
 KW antidiabetic; calcium influx; L type calcium channel; NIDDM;  
 KW type II diabetes; non-insulin dependent diabetes mellitus.  
 OS Rattus sp.  
 XX

Key	Location/Qualifiers
Region	1. .52
	/note= "Region upstream to pancreatic T-type calcium channel protein"
Misc-difference 4	
	/note= "Encoded by in-frame stop codon TGA"
Protein	53. .2428
	/label= Pancreatic_T-type_calcium_channel_alpha1_subunit
	/note= "This region is claimed as SEQ ID NO: 2"
Region	53. .86
	/note= "Unique region that differs from amino acid sequence of neuronal T-type calcium channel alpha1 subunit (alpha1G)"
Region	1023. .1046
	/label= Intracellular_loop_I(II-III)
	/note= "Unique region that differs from amino acid sequence of neuronal T-type calcium channel alpha1 subunit (alpha1G)"
Region	1622. .1640
	/label= Intracellular_loop_L(III-IV)
	/note= "Unique region that differs from amino acid sequence of neuronal T-type calcium channel alpha1 subunit (alpha1G)"
Misc-difference 2341	
	/note= "Encoded by in-frame stop codon TGA"
Misc-difference 2371	
	/note= "Encoded by in-frame stop codon TAA"
XX	
PN	WO200015845-A1.
XX	
PD	23-MAR-2000.
XX	
PF	26-AUG-1999; 99WO-US019675.
XX	
PR	26-AUG-1998; 98US-0098004P.
PR	27-JAN-1999; 99US-0117399P.
XX	
PA	(SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.





Db 1853 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAFQVLVNVVIAVLMKHLESN 1912

Qy 1841 KEAKEAEAELEEMKTLSPQPHSPLGSPFLWPGVEGPDSPSPKPGALHPAAHARSA 1900

Db 1913 KEAKEAEAELEEMKTLSPQPHSPLGSPFLWPGVEGPNSPSPKPGAPHTTAHIGAA 1972

Qy 1901 SHFSLEHPTMQHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957

Db 1973 SGFSLEHPTMWPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHG 2032

Qy 1958 WGLPKAQSGSVLSVHSQPADTSYIILQPKDAPHLLOPHSAPTWTGIPKLPPLPPGRSPLAQR 2017

Db 2033 WGLPKAQSGSVLSVHSQPADTSCILQPKDVHYLLLOPHGAPTWGAIPKLPPLPPGRSPLAQR 2092

Qy 2018 PLRQAAIRTDSDVQGLGSRDGLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKIS 2077

Db 2093 PLRQAAIRTDSDVQGLGSRDGLLSEVSGPSPCLTRSSSFWGSSIQVQORSIGQSKVS 2152

Qy 2078 KHMTPPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCYS 2137

Db 2153 KHIRLPAPCPGLEPSPWAKDPPETRSSLELDTLSWISGDLPLSSQEEPLSPRDLKKCYS 2211

Qy 2138 VEAQSCORRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNSNLGQPLGGPSRPPKKLSP 2197

Db 2212 VETQSCRRRPPGSLDEQRRHSIAVSCLDGSGQPLCPSPSSLGQPLGGPSRPPKKLSP 2271

Qy 2198 PSITIDPPESQGRTPPSPGICLRRRAPSSDSKDPASGPPDSMAASPSPKDVLSLGL 2257

Db 2272 PSISIDPPESQSRPPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPSPKDVLSSGL 2331

Qy 2258 SSDPADLDP 2266

Db 2332 SSDPTDMDP 2340

RESULT 10

AA14593

ID AAY14593 standard; protein; 2247 AA.

XX

AC AAY14593;

XX 07-DEC-1999 (first entry)

DT

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavTid).

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO ) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR N-PSDB; AAX83488.

XX

PT New T-type voltage-gated calcium channels.

XX

PS Disclosure; Page 94-103; 138pp; English.

XX

CC This sequence represents a rat T-type voltage-gated calcium (Ca) channel

CC alpha-1-G designated rCavTid. Voltage gated channels are membrane bound

CC glycosylated proteins formed of several subunits. The large alpha

CC subunits form a pore in the membrane that is selective for a given ionic

CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and

CC each domain contains 6 putative transmembrane helical segments (S1-S6). T

CC -type Ca channels are activated at a lower voltage than L- or N-type

CC channels. Characteristics of T-type channels include short current time,

CC slow activation kinetics near threshold, fast inactivation kinetics and

CC slow tail current. The sequences AAX83481-X83492 represent novel T-type

CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca

CC -channels contains a putative IVS4 region comprising the amino acid.

CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium

CC channel proteins can be used to screen for drugs which affect calcium

CC channels. Methods are also disclosed for treating a disease or disorder

CC associated with a deficiency in a native T-type calcium channel nucleic

CC acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX

SQ Sequence 2247 AA;

Query Match 92.1%; Score 10962.5; DB 2; Length 2247;

Best Local Similarity 92.8%; Pred. No. 0;

Matches 2108; Conservative 33; Mismatches 101; Indels 29; Gaps 5;

Qy 1 MDEEEDGAGAEESGQPRSEMRNLDSGAGRPGGSAEKDPSADSEAEGLYPALAPVV 60

Db 1 MDEEEDGAGAEESGQPRSFQNLNDSGAGRQPGSTGTEKDPGSADSEAEGLYPALAPVV 60

Qy 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAF 120

Db 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAF 120

Qy 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSFSAVR 180

Db 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSFSAVR 180

Qy 181 TVRVLRLPLRAINRVPSMRILVTLTLLDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Db 181 TVRVLRLPLRAINRVPSMRILVTLTLLDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Qy 241 CFLPENFSLPLSVDLERYQOTENEDESPFCISQPRENGMRSCRSVPTLRGDDGGGPPCGL 300

Db 241 CFLPENFSLPLSVDLERYQOTENEDESPFCISQPRENGMRSCRSVPTLRGDDGGGPPCGL 300

Qy 301 DYEAYNSSNTTCVNNQYTYNCSAGEHNPFPKGAINFEDNIGYAWIAIFQVITLEGWVDIM 360

Db 301 DYEAYNSSNTTCVNNQYTYNCSAGEHNPFPKGAINFEDNIGYAWIAIFQVITLEGWVDIM 360

Qy 361 YFVMDAHSFYNFYIFILLIIVGSFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNFYIFILLIIVGSFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA 420

Qy 421 STLASFSEPGSCYEELLYLVRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480

Db 421 STLASFSEPGSCYEELLYLVRKAARRLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480

Qy 481 SCSRRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Db 481 SCSRRRLSVHHLVHHHHHHHHYHLNGTTLRVPRASPEIQDRDANGSRRLMLPPPSTP 540

Qy 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTSPPE 600

Db 541 TPSGGPPRGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTSPPE 600

Qy 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

Db 601 ILKDKALVEVAPSPGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

Qy 661 ACGPDCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSIGPD 719

Db 661 ACGPDCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRRRQRSIGPD 720

Qy 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHEQPEELTNALEISN 779

Db 721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYHEQPEELTNALEISN 780

Qy 780 IVFTSLFALEMLLKLIVYGPFGYIKPNYPNIFDGVIVVISVWEIVGQQGGGLSVLRTFLM 839

Db 781 IVFTSLFALEWLLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGSLVLRTRFLM 840  
QY 840 RVLKLVRELPALQRLVVLMTMDNVATFCMLLMLEFIFISILGMHLFGCKFASERDGD 899  
Db 841 RVLKLVRELPALQRLVVLMTMDNVATFCMLLMLEFIFISILGMHLFGCKFASERDGD 900  
QY 900 LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLE 959  
Db 901 LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLE 960  
QY 960 VAILVEGFOAEISKREDASGQLSCIQLPVDSSQCGDANKSESEPFFSPSLDGDGRK 1019  
Db 961 VAILVEGFOAE-----GDATAKSESEPFFSPSLDGDGRK 997  
QY 1020 LALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGEGALGPASRRTSSSGSAEP 1079  
Db 998 LALVALGEHAELRKSLPLPLIIHTAATPMHPKSSSTGVGEALGSGRRTSSSGSAEP 1057  
QY 1080 A-HEMKSPSPARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQ 1138  
Db 1058 AHHEMKCPSPARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEQ 1117  
QY 1139 SQDEEESSEERASPAAGSDHRRHRSLEAKSFDLPDLTQVPGHLRTASGRGSASEH 1198  
Db 1118 SQDEEESSEERASPAAGSDHRRHRSLEAKSFDLPDLTQVPGHLRTASGRGSASEH 1177  
QY 1199 CNGKSASGRALARALPDPPPLDGDADDGNLSKGERVRAWIRARLPACYLERDSWSAY 1258  
Db 1178 CNGKSASGRALARALTDDPQLDGDNDNDEGNLSKGERIQAWVRSRLPACCRERDSW 1237  
QY 1259 FPPQSRFRLCHRITHTKMFHDHVVLIIIFLNCITIAMERPKIDPHSAERIFLTLSNY 1318  
Db 1238 FPPQSRFRLCHRITHTKMFHDHVVLIIIFLNCITIAMERPKIDPHSAERIFLTLSNY 1297  
QY 1319 AVFLAEMTKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGML 1378  
Db 1298 AVFLAEMTKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILG 1357  
QY 1379 VLRLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVQLFKG 1438  
Db 1358 VLRLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVQLFK 1417  
QY 1439 FVCGEDTRNITNKSDCAEASRVRVRHKYNFEDNLGOALMSLFVLASKDGVWDIMYDGL 1498  
Db 1418 FVCGEDTRNITNKSDCAEASRVRVRHKYNFEDNLGOALMSLFVLASKDGVWDIMYDGL 1477  
QY 1499 VGVDOQPIMNHNPMMLLYFISFLLIIVAFVLMFVGVVVENFHKRQHOREEARRREK 1558  
Db 1478 VGVDOQPIMNHNPMMLLYFISFLLIIVAFVLMFVGVVVENFHKRQHOREEARRREK 1537  
QY 1559 RLRLLEKRRKAQCKPYYSYDSYRFRLLVHLCTSHYLDLFTITVGLNVVTMAMEHYQ 1618  
Db 1538 RLRLLEKRRKAQCKPYYSYDSYRFRLLVHLCTSHYLDLFTITVGLNVVTMAMEHYQ 1597  
QY 1619 QILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEE 1678  
Db 1598 QILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEE 1657  
QY 1679 VNASLPINPTIIRIMRVLRARVLRKLLKMAVGMRALLDVTMQALPQVGNLGLLFFL 1738  
Db 1658 VNLSLPINPTIIRIMRVLRARVLRKLLKMAVGMRALLDVTMQALPQVGNLGLLFFL 1717  
QY 1739 FAALGVLEFGDLECEDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDLR 1798  
Db 1718 FAALGVLEFGDLECEDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDLR 1777  
QY 1799 QESTCYNTVISPIYFVSFVLTQAQVFLVNVVIAVLMKHLSESNKEAKEAELEAELE 1858  
Db 1778 QESTCYNTVISPIYFVSFVLTQAQVFLVNVVIAVLMKHLSESNKEAKEAELEAELE 1837  
QY 1859 TSLSPQHPSPGLSPFLWPGVEGPDSPDPKPGALHPAAHARSASHFSLHPTWQPHPT 1918

Db 1838 TSLSPQHPSPGLSPFLWPGVEGVNSTDSPKPGAPHTTAHGAASGFSLEHPTWVHPPE 1897  
QY 1919 ---GPDLLITVRKSGVSRTHSLPNDSYMCRRHSGSTAEGPLGHRGWGLPKAQSGSVL 1975  
Db 1898 VPLGPDLLITVRKSGVSRTHSLPNDSYMCRRHSGSTAERSLGHGWGLPKAQSGSVL 1957  
QY 1976 ADTSYILQPKDAPHLLQPHSAPTGTIPKLPPLPPGRSPLAQRPLRRQAAIIRTDSDV 2035  
Db 1958 ADTSCILQPKDVHLLQPHGAPTGAIPKLPPLPPGRSPLAQRPLRRQAAIIRTDSDV 2017  
QY 2036 GSREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKISKHMTPPAPCPGPEPNW 2095  
Db 2018 GSREDLLSEVSGSPCLTRSSSFWSGSSIQVQORSIGIQSVKHIRLPAPCPGLEPS 2077  
QY 2096 GPPETRSSLLELDELTELWSIGDILLPPGQEEPPSPRDLKKCYSEVAQSCORRPT 2155  
Db 2078 DFPETRSSLLELDELTELWSIGDILL-PSQEEPLFPRDLKKCYSEVETQSCRRR 2136  
QY 2156 RHSIAVSCLDGSGQPHLGTDPNSNLGGQPLGGPSRPPKDLVLSGLSSDPADLDP 2215  
Db 2137 RHSIAVSCLDGSGQPHLGTDPNSNLGGQPLGGPSRPPKDLVLSGLSSDPADLDP 2196  
QY 2216 PGICLRRRAPSSDKDPLASGPPDPSMAASPPKDVLSGLSSDPADLDP 2266  
Db 2197 PGVCLRRRAPSSDKDPSVSSPLDSTAASPPKDTLSLSGLSSDPADLDP 2247

RESULT 11  
AAY14590  
ID AAY14590 standard; protein; 2254 AA.  
XX  
AC AAY14590;  
XX 07-DEC-1999 (first entry)  
XX  
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavTla).  
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX Rattus sp.  
OS  
PN WO9929847-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
XX N-PSDB; AAX83485.  
PT New T-type voltage-gated calcium channels.  
XX  
PS Disclosure; Page 67-76; 138pp; English.

This sequence represents a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCavTla. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca channels contains a putative IVS4 region comprising the amino acid

CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2254 AA;  
  
Query Match 91.9%; Score 10945; DB 2; Length 2254;  
Best Local Similarity 92.5%; Pred. No. 0;  
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;  
  
QY 1 MDEEDGAGAEESGQPRSMRLNDLSCAGGRPGGSAEKDPSADSEAEGLPYPALAPVV 60  
Db 1 MDEEDGAGAEESGQPRSFQNLNDLSCAGGRQGGSTEDKDPGADSEAEGLPYPALAPVV 60  
  
QY 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQDSQRCRIIQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQDSQRCRIIQAF 120  
  
QY 121 DDFFFAFAFVAVMVKQVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSAVR 180  
Db 121 DDFFFAFAFVAVMVKQVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSAVR 180  
  
QY 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLCCFFVFIFGIVGVQLWAGLLNR 240  
Db 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLCCFFVFIFGIVGVQLWAGLLNR 240  
  
QY 241 CFLPENFSLPSVDLERYQOTENEDSPFICSPRENGMRSCRSVPTLRGDDGGGPPCGL 300  
Db 241 CFLPENFSLPSVDLEPYQOTENEDSPFICSPRENGMRSCRSVPTLRGDDGGGPPCSL 300  
  
QY 301 DYEAYNSSNTTCVNWQYTYTNCASGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEYTNSSNTTCVNWQYTYTNCASGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
  
QY 361 YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
  
QY 421 STLASFSEPGCYEELLKYLVIILKKAARRLAQVSRAAGVVRVGLLSSPAPLGQETQPS 480  
Db 421 STLASFSEPGCYEELLKYLVIILKKAARRLAQVSRAIGVRAGLLSSPVARSQEPQPSG 480  
  
QY 481 SCSRSRRLSVVHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
Db 481 SCTRSHRRLSVHHLVHHHHHHHHYHLNGTTLRVPRASPEIQDRDANGSRRLMLPPSTP 540  
  
QY 541 ALSGAPPGGAEVSHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPE 600  
Db 541 TPGSGPPRGAEVSHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTSPPE 600  
  
QY 601 TLKEKALVEAASSGPPTLTSLNIPGPYSSMHKLLQTSQACQSSCKISSPCLKADSG 660  
Db 601 ILKDKALVEVAPSPGPPTLTSFNIPGPYSSMHKLLQTSQACQSSCKISSPCLKADSG 660  
  
QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQSLGPD 719  
Db 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQSLGPD 720  
  
QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALISN 779  
Db 721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALISN 780  
  
QY 780 IVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLM 839  
Db 781 IVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLM 840  
  
QY 840 RVLKLVRFPLALQRLVLMKTMNDNVATFCMLLMFIFISILGMHLFGCKFASERDGD 899  
Db 841 RVLKLVRFPLALQRLVLMKTMNDNVATFCMLLMFIFISILGMHLFGCKFASERDGD 900  
  
QY 900 LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 959

Db 901 LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 960  
  
QY 960 VAILVEGFQAEISKREDASGQLSCIQLPVDSSQGDANKSESEDPFFSPSLDGDGRKKC 1019  
Db 961 VAILVEGFQAE-----GDATESESEDPFFSPSVDDGDGRKKR 997  
  
QY 1020 LALVSLGEHPELRKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSSGAEPGA 1079  
Db 998 LALVALGEHAEHLRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSSGAEPGA 1057  
  
QY 1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRSLGRAPSLKRRSPSGERRSLLSGEQE 1138  
Db 1058 AHHEMKCPSARSSPHSPWSAASSWTSRRSSRSLGRAPSLKRRSPSGERRSLLSGEQE 1117  
  
QY 1139 SQDEEESSEERASPAAGSDHRRHRSLEAREAKSSFDLPDTLQVPLHRTASGRGSAEHQD 1198  
Db 1118 SQDEEESSEEDRASPAAGSDHRRHRSLEAREAKSSFDLPDTLQVPLHRTASGRGSAEHQD 1177  
  
QY 1199 CNGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWRARLPACYLERDSWSAYI 1258  
Db 1178 CNGKSASGRLARLTDDPQLDGDDEGNLSKGERIQAWRSRLPACRRERDSWSAYI 1237  
  
QY 1259 FPPQSRFRLLCHRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318  
Db 1238 FPPQSRFRLLCHRIITHKMFHVVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297  
  
QY 1319 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLDGLLVLSIVDILVSMVSDSGTKILGMLR 1378  
Db 1298 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLDGLLVLSIVDILVSMVSDSGTKILGMLR 1357  
  
QY 1379 VLRLRLTLRPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1438  
Db 1358 VLRLRLTLRPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1417  
  
QY 1439 FVCQGEDTRNITNKSDCAEASRYVRHKYNFDNLQALMSLFLVASKDGVWDIMYDGLDA 1498  
Db 1418 FVCQGEDTRNITNKSDCAEASRYVRHKYNFDNLQALMSLFLVASKDGVWDIMYDGLDA 1477  
  
QY 1499 VGVDQQPIMNHNPMWLLYFISFLLIIVAFVLMFVGVVVENPHKCRHQHEEEARRREK 1558  
Db 1478 VGVDQQPIMNHNPMWLLYFISFLLIIVAFVLMFVGVVVENPHKCRHQHEEEARRREK 1537  
  
QY 1559 RLRRLEKRR-----KAQCKPYSDYSRFRLLVHLCSTHYLDLFTITVIGLNVVTMA 1611  
Db 1538 RLRRLEKRRSKEQMAEAQCKPYSDYSRFRLLVHLCSTHYLDLFTITVIGLNVVTMA 1597  
  
QY 1612 MEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQDLAIIVLLSIMG 1671  
Db 1598 MEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQDLAIIVLLSIMG 1657  
  
QY 1672 ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDVTMOALPOVGNLGLL 1731  
Db 1658 ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDVTMOALPOVGNLGLL 1717  
  
QY 1732 FMLLFFIFAALGVLELFGDCEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791  
Db 1718 FMLLFFIFAALGVLELFGDCEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1777  
  
QY 1792 DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEESNKEAEAELEA 1851  
Db 1778 DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEESNKEAEAELEA 1837  
  
QY 1852 ELELEMKTLSPQPHSPGLSPFVPGVEGPDSPDPSKPGALHPAAHARSASHFSLEHPTMQ 1911  
Db 1838 ELELEMKTLSPQPHSPGLSPFVPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV 1897  
  
QY 1912 PHPTLEP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGKSTAEGLCHRGWGLPKAQSSV 1968  
Db 1898 PHPEEVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEBSLGRHWGLPKAQSGSI 1957  
  
QY 1969 LSVHSQPADTSYILQLPKDAPHLLQPHSAPTWTGTPKLPDPPGRSPLAQRLRRQAIIRD 2028



Db 1958 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPLPGRSPLAQRPLRRQAAIRTD 2017

QY 2029 SLDVQGLGSRREDLLAEVSGPPLARAYSFWGOSSTQAQHQHSRSHSKISKHMTTPPAPCPG 2088

Db 2018 SLDVQGLGSRREDLLSEVSGPPLTRSSSFWGSSIQVQORSIGQSVSKHIRLPAPCPG 2077

QY 2089 PEPNWGKPPETRSSLELDTLSWISGDLLPPGGQEEPPSPRDLKKCYSEVAQSCQRRPT 2148

Db 2078 LEPWAKDPETRSSLELDTLSWISGDLL-PSSQEEPLFPRDLKKCYSEVETQSCRRRPG 2136

QY 2149 SWLDEQRRHSIAVCLDSGSGQHLGTDPSNLGGQPLGGPSRPKKLSPPSITIDPPESQ 2208

Db 2137 FWLDEQRRHSIAVCLDSGSGQRLCPSPSSLGQPLGGPSRPKKLSPPSISIDPPESQ 2196

QY 2209 GPRTPPSGICLRRRAPSSDSKDPLASGPPDSMAASPKDVLSLSLSSDPADLDP 2266

Db 2197 GSRPPCSPGVCLRRRAPASDSKDPSSVSPLDSTAASPKKDTLSLSGLSSDPTDMDP 2254

RESULT 12

AAAY14591

ID AAY14591 standard; protein; 2265 AA.

XX AC AAY14591;

DT 07-DEC-1999 (first entry)

XX Rat T-type voltage-gated Ca channel alpha-1-G (rCav1b).

DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

OS Rattus sp.

XX WO9929847-A1.

XX 17-JUN-1999.

XX 30-OCT-1998; 98WO-US023161.

XX 05-DEC-1997; 97US-00985809.

XX (LOYO ) UNIV LOYOLA CHICAGO.

XX Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

DR N-PSDB; AAX83486.

XX New T-type voltage-gated calcium channels.

XX Disclosure; Page 76-85; 138pp; English.

XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel

CC alpha-1-G designated rCav1b. Voltage gated channels are membrane bound

CC glycosylated proteins formed of several subunits. The large alpha

CC subunits form a pore in the membrane that is selective for a given ionic

CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and

CC each domain contains 6 putative transmembrane helical segments (S1-S6). T

CC -type Ca channels are activated at a lower voltage than L- or N-type

CC channels. Characteristics of T-type channels include short current time,

CC slow activation kinetics near threshold, fast inactivation kinetics and

CC slow tail current. The sequences AAX83481-X83492 represent novel T-type

CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca

CC -channels contains a putative IVS4 region comprising the amino acid

CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium

CC channel proteins can be used to screen for drugs which affect calcium

CC channels. Methods are also disclosed for treating a disease or disorder

CC associated with a deficiency in a native T-type calcium channel nucleic

XX acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX Sequence 2265 AA;

1020 LALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA 1079

Query Match 91.9%; Score 10939.5; DB 2; Length 2265;

Best Local Similarity 92.0%; Pred. No. 0;

Matches 2107; Conservative 34; Mismatches 101; Indels 47; Gaps 6;

QY 1 MDEEDGAGAEESGQPRSFMRNLNDLSGAGRPGPGSAEKDPGSADEAGLPYPALAPVV 60

Db 1 MDEEDGAGAEESGQPRSFMRNLNDLSGAGRPGPGSAEKDPGSADEAGLPYPALAPVV 60

QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILNCVTLGMFPCEDIACDSQRCRILQAF 120

Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILNCVTLGMFPCEDIACDSQRCRILQAF 120

QY 121 DDFIFAFFAVEMVVMKVALGIFGKKCYLGDITWNRDLFFIVIAGMLEYSLDLQNVSFSAVR 180

Db 121 DDFIFAFFAVEMVVMKVALGIFGKKCYLGDITWNRDLFFIVIAGMLEYSLDLQNVSFSAVR 180

QY 181 TVRVLRLPRAINRVPSMRILVTLLDITLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Db 181 TVRVLRLPRAINRVPSMRILVTLLDITLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

QY 241 CFLPENFSLPSVDLERYQOTENEDESPFCISQPRENGMRSCRSVPTLRGGGGPPCGL 300

Db 241 CFLPENFSLPSVDLEPYQOTENEDESPFCISQPRENGMRSCRSVPTLRGGGGPPCGL 300

QY 301 DYEAYNSSNTTCVNNQYITNCAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Db 301 DYEAYNSSNTTCVNNQYITNCAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

QY 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

QY 421 STILASFSEPGSCYBEELLKYLVIILKKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPS 480

Db 421 STILASFSEPGSCYBEELLKYLVIILKKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPS 480

QY 481 SCSRRRLSVHLLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

Db 481 SCSRRRLSVHLLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRITVSGKVYPTVHTSPPE 600

Db 541 TPGGPPRGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRITVSGKVYPTVHTSPPE 600

QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSMHKLLETQSTGACQSSCKISSPCLKADSG 660

Db 601 ILKDKALVEVAPSPGPPTLTSLNIPPGPYSMHKLLETQSTGACQSSCKISSPCLKADSG 660

QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQSLGPD 719

Db 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720

QY 720 AEPSSVLAFWRLICDTFRKIIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISN 779

Db 721 AEPSSVLAFWRLICDTFRKIIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISN 780

QY 780 IVFTSLFALEMMLKLLVYGPFGYIKNPYNIFDGVIVVISWWEIVGQQGGLSVLRTFRML 839

Db 781 IVFTSLFALEMMLKLLVYGPFGYIKNPYNIFDGVIVVISWWEIVGQQGGLSVLRTFRML 840

QY 840 RVKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLIFIFLSILGMHLFGCKFASERDGD 899

Db 841 RVKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLIFIFLSILGMHLFGCKFASERDGD 900

QY 900 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 959

Db 901 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 960

QY 960 VAILVEGFQAEIEISKREDASQLSQIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKC 1019

Db 961 VAILVEGFQAEIEISKREDASQLSQIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKR 997



Db 998 LALVALGEAEELRKSLLPPLIIHTAATPMHPKSSSTGVGEALGSGSRRRTSSSGSAEPGA 1057  
QY 1080 A-HEMKSPPSARSPSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRSLLSGEQE 1138  
Db 1058 AHHEMKCPPSARSPSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRSLLSGEQE 1117  
QY 1139 SQDEEESSEERASDPAGSDHRRHGSLEREAKSSFDLPTDQLVPLHRTASGRSASEHQD 1198  
Db 1118 SQDEEESSEEDRASDPAGSDHRRHGSLEREAKSSFDLPTDQLVPLHRTASGRSASEHQD 1177  
QY 1199 CNGKSASGRALARPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYI 1258  
Db 1178 CNGKSASGRLARLTDDPQLDGDADDDEGNLSKGERIQAWVRSRLPACCRERDSWYI 1237  
QY 1259 FPPQSRFRLLCHRIITHKMFHVVLVIIPLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318  
Db 1238 FPPQSRFRLLCHRIITHKMFHVVLVIIPLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297  
QY 1319 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLGLLVLISVIDILVSMVSDSGTKILGMLR 1378  
Db 1298 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLGLLVLISVIDILVSMVSDSGTKILGMLR 1357  
QY 1379 VLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVQLFKGF 1438  
Db 1358 VLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICAPFIIFGILGVQLFKGF 1417  
QY 1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1498  
Db 1418 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDA 1477  
QY 1499 VGVDQOPIMHNPNWMLLYFISFLLIIVAFVLMFVGVVVENFHKRQHQQHEEERREEK 1558  
Db 1478 VGVDQOPIMHNPNWMLLYFISFLLIIVAFVLMFVGVVVENFHKRQHQQHEEERREEK 1537  
QY 1559 RLRLLEKKRR-----KAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 1600  
Db 1538 RLRLLEKKRRNMLDDVVIASGSSASAASEAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 1597  
QY 1601 GVIGLNVVTWAMEHYQQPQILDEALKICNIYIFTVIFVLESVKLVAFGRFRFFQDRWNQL 1660  
Db 1598 GVIGLNVVTWAMEHYQQPQILDEALKICNIYIFTVIFVESVKLVAFGRFRFFQDRWNQL 1657  
QY 1661 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDFTVMQ 1720  
Db 1658 DLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMRALDFTVMQ 1717  
QY 1721 ALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCEGLGRHATFRNFGMAFLTFRV 1780  
Db 1718 ALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCEGLGRHATFRNFGMAFLTFRV 1777  
QY 1781 STGDNWNGIMKDLTRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLKMLEESN 1840  
Db 1778 STGDNWNGIMKDLTRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLKMLEESN 1837  
QY 1841 KEAKEEALEAELEEMKTLSPQPHSPGLSPFLWPVGVEGPDSPDKPGALHPAAHARSA 1900  
Db 1838 KEAKEEALEAELEEMKTLSPQPHSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAA 1897  
QY 1901 SHFSLEHPTMQPHPTLTP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957  
Db 1898 SGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRG 1957  
QY 1958 WGLPKAQSGVLSVHSQPADTSYIQLPKDAPHLLQPHSAPTWGTIPKLPPLPPGRSPLAQR 2017  
Db 1958 WGLPKAQSGVLSVHSQPADTSYIQLPKDAPHLLQPHSAPTWGTIPKLPPLPPGRSPLAQR 2017  
QY 2018 PLRRQAARTDSDLVQGLSREDLLAEVSGSPPLARAYSFWGOSSTQAQOHSRSHSKIS 2077  
Db 2018 PLRRQAARTDSDLVQGLSREDLLSEVSGSPCLTRSSSFWGSSIQVQORSGIOQKVS 2077  
QY 2078 KHTMPPAPCPGPEPNWKGPPETRRSSLELDTELWSWISGDLPLPGQOEPPSPRDLKKCYS 2137

Db 2078 KHIRLPAPCGLEPSWAKOPPETRRSSLELDTELWSWISGDLPLPGQOEPPSPRDLKKCYS 2136  
QY 2138 VEAQSCORRPTSWLDQERRHSIAVSCLDGSGSQPHLGTDPNSLGGQPLGGPSRPPKKLSP 2197  
Db 2137 VETQSCRRRPGFWLDQERRHSIAVSCLDGSGSQPHLGTDPNSLGGQPLGGPSRPPKKLSP 2196  
QY 2198 PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPPKDVLSLSGL 2257  
Db 2197 PSISIDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPPKDVLSLSGL 2256  
QY 2258 SSDPADLDP 2266  
Db 2257 SSDPTDMDP 2265  
RESULT 13  
AAAY14592  
ID AAY14592 standard; protein; 2272 AA.  
XX  
AC AAY14592;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1.1c).  
XX  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.  
XX  
OS Rattus sp.  
XX  
PN WO9929847-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
DR N-PSDB; AAX83487.  
XX  
PT New T-type voltage-gated calcium channels.  
XX  
PS Disclosure; Page 85-94; 138pp; English..  
XX  
CC This sequence represents a rat T-type voltage-gated calcium (Ca) channel  
CC alpha-1-G designated rCav1.1c. Voltage gated channels are membrane bound  
CC glycosylated proteins formed of several subunits. The large alpha  
CC subunits form a pore in the membrane that is selective for a given ionic  
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and  
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T  
CC -type Ca channels are activated at a lower voltage than L- or N-type  
CC channels. Characteristics of T-type channels include short current time,  
CC slow activation kinetics near threshold, fast inactivation kinetics and  
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type  
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca  
CC -channels contains a putative IVS4 region comprising the amino acid  
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium  
CC channel proteins can be used to screen for drugs which affect calcium  
CC channels. Methods are also disclosed for treating a disease or disorder  
CC associated with a deficiency in a native T-type calcium channel nucleic  
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 2272 AA;

Query Match 91.8%; Score 10925; DB 2; Length 2272;  
Best Local Similarity 91.7%; Pred. No. 0;  
Matches 2106; Conservative 33; Mismatches 103; Indels 54; Gaps 6;

QY 1 MDEEDGAGAEESGQPRSFWRNLNDLSGAGRPGPGSAEKDPGSDADSEAEGLPYPALAPVV 60  
Db 1 MDEEDGAGAEESGQPRSFQNLNDLSGAGRPGPGSTKDPGSDADSEAEGLPYPALAPVV 60  
QY 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
QY 121 DDFIFAFFAVEMVVKWVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVFSAVR 180  
Db 121 DDFIFAFFAVEMVVKWVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVFSAVR 180  
QY 181 TVRVLRLPRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
Db 181 TVRVLRLPRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
QY 241 CFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGWRSCRSVPTLRDGGGGPPCGL 300  
Db 241 CFLPENFSLPLSVDLEPYQTENEDESPFICSQPRENGWRSCRSVPTLRDGGGGPPCGL 300  
QY 301 DYEAYNSSNTTCVNNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEAYNSSNTTCVNNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNFIFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNFIFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYEELLKYLVIYILRKAARLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480  
Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARLAQVSRAIGVRAGILLSSPVARSQEPQPSG 480  
QY 481 SCSRHRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
Db 481 SCSRHRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTP 540  
QY 541 ALSGAPPGAEVSHFYHADCHLEPVRQAPPPRSPSEASGRVTGSGKVYPTVHTSPPE 600  
Db 541 TPGGPPRGAESVSHFYHADCHLEPVRQAPPPRSPSEASGRVTGSGKVYPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660  
Db 601 ILKOKALVEVAPSGPPTLTSTFNIPPGPFSSMHKLLTQSTGACHSSCKISSPCKADSG 660  
QY 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS - RRQRSGLPD 719  
Db 661 ACPDSCPYCARTGAGEPESEDHVPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLPD 720  
QY 720 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779  
Db 721 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780  
QY 780 IVFTSLFALEMLLKLVLVYGPFGYIKNPYINFDGVIIVISWEIVGQGGGLSVLRTFRLM 839  
Db 781 IVFTSLFALEMLLKLVLVYGPFGYIKNPYINFDGVIIVISWEIVGQGGGLSVLRTFRLM 840  
QY 840 RVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGD 899  
Db 841 RVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGD 900  
QY 900 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959  
Db 901 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 960  
QY 960 VAILVEGFQAEIISKREDASGQLSCIQLPVDSSQGDANKSESEDPFSPSLDGDGDRKCC 1019  
Db 961 VAILVEGFQAE-----GDATKSESEDPFSPSLDGDGDRKCR 997  
QY 1020 LALVSLGHEPPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA 1079  
Db 998 LALVALGHEAELRKSLPLLIHTAATPMSHPKSSSTGVGEALGCSRRRTSSSGSAEPGA 1057  
QY 1080 A-HEMKSPPSARSPSPHSPWSAASWTSSRRSLGRAPSLKRRSPSGERRSLLSGEGOE 1138

Db 1058 AHHEMKCPPSARSPSPHSPWSAASWTSSRRSLGRAPSLKRRSPSGERRSLLSGEGOE 1117  
QY 1139 SODEEESSEERASGASDHRHRSGLEREAKSSFDPDLTQVPGHLRTASGRGSASEHQD 1198  
Db 1118 SODEEESSEEDRASGASDHRHRSGLEREAKSSFDPDLTQVPGHLRTASGRSSASEHQD 1177  
QY 1199 CNGKSASGRLARALRDPDPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYI 1258  
Db 1178 CNGKSASGRLARTLRTDDPQLDGDADDDEGNLSKGERROAWRSRLPACCRERDSWSAYI 1237  
QY 1259 FPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318  
Db 1238 FPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297  
QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGILLVLSVIDILVSMVSDSGTKILGMLR 1378  
Db 1298 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGILLVLSVIDILVSMVSDSGTKILGMLR 1357  
QY 1379 VLRLRLTLRLPLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438  
Db 1358 VLRLRLTLRLPLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417  
QY 1439 FVCOGEDTRNITNKSDCAEASRVRWRHKYNFNDLQALMSLFLVASKDGWVDIMYDGLDA 1498  
Db 1418 FVCOGEDTRNITNKSDCAEASRVRWRHKYNFNDLQALMSLFLVASKDGWVDIMYDGLDA 1477  
QY 1499 VGVDQOQIPMHNPMWMLLYFISFLIIVAFVFLNMFVGVVVENFHKCRHQHEEERREK 1558  
Db 1478 VGVDQOQIPMHNPMWMLLYFISFLIIVAFVFLNMFVGVVVENFHKCRHQHEEERREK 1537  
QY 1559 RLRRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSH 1593  
Db 1538 RLRRLEKKRRSKEQOMADMLDDVIASGSSASAAEQCKPYSDYSRFRLLVHHLCTSH 1597  
QY 1594 YLDLFTITGVIGLVNVTMAMEHYQQOQIILDEALKICNYIFTVIFVLESVFKLVAFGRFRFF 1653  
Db 1598 YLDLFTITGVIGLVNVTMAMEHYQQOQIILDEALKICNYIFTVIFVLESVFKLVAFGRFRFF 1657  
QY 1654 QDRWNQDLAIIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRA 1713  
Db 1658 QDRWNQDLAIIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRA 1717  
QY 1714 LLDTVMQALPOVGNLGLLFFIFAALGVLEFGDLECDETHCEGLGRHATFRNFGMA 1773  
Db 1718 LLHTVMQALPOVGNLGLLFFIFAALGVLEFGDLECDETHCEGLGRHATFRNFGMA 1777  
QY 1774 FLTLFRVSTGDNWNGIMKDTLRDCDOESTCVNTVISPIYFVSFVLTAQFVLNVVIAVLM 1833  
Db 1778 FLTLFRVSTGDNWNGIMKDTLRDCDOESTCVNTVISPIYFVSFVLTAQFVLNVVIAVLM 1837  
QY 1834 KHLEESNKEAKEAEAELEEMKTLSPQHPSPGSPFLWPVGVEGPDSPSPKPGALHP 1893  
Db 1838 KHLEESNKEAKEAEAELEEMKTLSPQHPSPGSPFLWPVGVEGPDSPSPKPGAPHT 1897  
QY 1894 AAHARSASHFSLEHPTMQPHTPLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAE 1950  
Db 1898 TAHIGAASGFSLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAE 1957  
QY 1951 GPLGHRGWGLPKAQSGSVLSVHSQPADTSYIOLPKDAPHLQLPHSAPTWTGTPKLPPLPG 2010  
Db 1958 RSLGHRGWGLPKAQSGSVLSVHSQPADTSYIOLPKDVHLLQPHGAPTWGAIPLKLPPLPG 2017  
QY 2011 RSPLAQRPLRQAAIRTDSDLDVQGLSREDLLAEVSGSPPLARAYSFWGQSSTQAQOHS 2070  
Db 2018 RSPLAQRPLRQAAIRTDSDLDVQGLSREDLLSEVSGSPCLTRSSSFVWGGSSIQVQORS 2077  
QY 2071 RSHKISKHMTPPAPCPGPEPNWKGPPETRSSLLELDTLSWISGDLPLPPGQEEPSPR 2130  
Db 2078 GIOSKVSXHIRLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLPSSQEEPSPR 2136  
QY 2131 DLKKCYSVAEQSCQRRTSWLDEQRHSTAVSCLDGSGQPHLGTDPNLSGQPLGGPSR 2190

Db 2137 DLKNCYSVETQSCRRRPFGLWDEQRRHSIAVSCLDGSGQPRLCPSRSSLGGQPLGGPSR 2196  
QY 2191 PKKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKD 2250  
Db 2197 PKKKLSPPSISIDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKD 2256  
QY 2251 VLSLSGLSSDPADLDP 2266  
Db 2257 TLSLSGLSSDPTDMDP 2272

RESULT 14  
AAB66475  
ID AAB66475 standard; protein; 2287 AA.  
XX  
AC AAB66475;  
XX  
DT 09-APR-2001 (first entry)  
XX  
DE Rat alpha-IG calcium channel protein.  
XX  
KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;  
KW hypotensive; cardiant; nootropic; T-type calcium channel subunit;  
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;  
KW epilepsy; alpha-IG calcium channel.  
XX  
OS Rattus sp.  
XX  
PN WO200102561-A2.  
XX  
PN 11-JAN-2001.  
PD  
XX  
PF 04-JUL-2000; 2000WO-CA000794.  
XX  
PR 02-JUL-1999; 99US-00346794.  
XX  
PA (NEUR-) NEUROMED TECHNOLOGIES INC.  
XX  
PI Snutch TP, Baillie DL;  
XX  
DR WPI; 2001-123111/13.  
DR N-PSDB; AAF31677.  
XX

PT Novel T-type calcium channel alpha-1 subunit gene useful for treating  
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
PT epilepsy.  
XX  
PS Disclosure; Page 63-72; 103pp; English.  
XX  
CC The present sequence is given in a specification providing sequences and  
CC partial sequences for three types of mammalian (human and rat) T-type  
CC calcium channel subunits. An expression cassette has been generated which  
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha\_1  
CC subunit operably linked to control sequences to effect its expression.  
CC The novel calcium channel nucleic acids and proteins are useful for  
CC treating conditions characterised by undesirable levels of T-type calcium  
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
CC hypertension, sleep disorder and epilepsy  
XX  
SQ Sequence 2287 AA;

Query Match 90.5%; Score 10774; DB 4; Length 2287;  
Best Local Similarity 92.3%; Pred. No. 0;  
Matches 2075; Conservative 33; Mismatches 105; Indels 36; Gaps 6;  
QY 30 GRPGPSAEKDPGSADSEAGLPYPALAPVFFYLSQDSRRPRSWCLRTVCNPFERISML 89  
Db 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVFFYLSQDSRRPRSWCLRTVCNPFERVSML 121  
QY 90 VILLNCVTGLMFRPCEDIAQDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149  
Db 122 VILLNCVTGLMFRPCEDIAQDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181

QY 150 DTWNRLDFFIVIAWMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 209  
Db 182 DTWNRLDFFIVIAWMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 241  
QY 210 MLGNVLLLCFFVFFIFIGIVGVQWAGLLRNRCFLPENFSLPLSDVLEYYQTENEDESPP 269  
Db 242 MLGNVLLLCFFVFFIFIGIVGVQWAGLLRNRCFLPENFSLPLSDVLEYYQTENEDESPP 301  
QY 270 ICSPRENGMRSCRSVPTLRGDDGGGPPCGLDYEAYNSSNTTCVNNQYTTNCSAGEHN 329  
Db 302 ICSPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNNQYTTNCSAGEHN 361  
QY 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389  
Db 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421  
QY 390 CLVVIATQFSETKQESQLMREQVRFLSNASTLASFSPGSCYEELLKYLVIILKKAAR 449  
Db 422 CLVVIATQFSETKQESQLMREQVRFLSNASTLASFSPGSCYEELLKYLVIILKKAAR 481  
QY 450 RLAQVSRAGVRVGLSSPAPLGQETQPSSSCSRSHRRRLSVHHLVHHHHHHHHYHLGN 509  
Db 482 RLAQVSRAGVRAGLLSSPVARSGQEPQPSGSCSTRSHRRRLSVHHLVHHHHHHHHYHLGN 541  
QY 510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRQ 569  
Db 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAEVHSFYHADCHLEPVRQ 601  
QY 570 APPPRSPSEASGRTVSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629  
Db 602 APPPRCPSEASGRTVSGKVYPTVHTSPPPEILKDKALVEVAPSGPPTLTSTFNIPPGPF 661  
QY 630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689  
Db 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721  
QY 690 SEAVYEFTQDAQHSDLRDPHS-RRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 748  
Db 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 781  
QY 749 IMIAILVNILSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 808  
Db 782 IMIAILVNILSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 841  
QY 809 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDVATF 868  
Db 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDVATF 901  
QY 869 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSILLWAIIVTFQILTQEDWNKV 928  
Db 902 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSILLWAIIVTFQILTQEDWNKV 961  
QY 929 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAEISKREDASGQLSCIQLP 988  
Db 962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFOAE----- 1003  
QY 989 VDSQGGDANKSESEPDFFPSLDGDRKKCLALVSLGHEPELRKSLPPLIIHTAATPM 1048  
Db 1004 -----GDATKSESEPDFFPSVDGDRKKRLALVALGEHAELRKSLPPLIIHTAATPM 1058  
QY 1049 SLPKSTSTGLGEALGPASRRRTSSGSAEPGAA-HEMKSPPSARSSPHSPWASAASWTSSR 1107  
Db 1059 SHPKSSSTGVGEALGSGRRRTSSGSAEPGAAHEMKPCPSARSSPHSPWASAASWTSSR 1118  
QY 1108 SSRNSLGRAPSLKRRSPSGERRSLISGEGQESQDEESESSEBERASAPAGSDHRHRSLERE 1167  
Db 1119 SSRNSLGRAPSLKRRSPSGERRSLISGEGQESQDEESESSEBERASAPAGSDHRHRSLERE 1178  
QY 1168 AKSSFDPDPTLQVPLHRTASGRGSASEHQDCNGKSGASGRLARALRPDDPPLDGDADD 1227  
Db 1179 AKSSFDPDPTLQVPLHRTASGRGSASEHQDCNGKSGASGRLARTLRDTPQLDGDND 1238  
QY 1228 GNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVILF 1287

Db 1239 GNLSKGERIQAWRSRLPACCRERDSWSAYIFFPQSRFRLLCHRIITHKMFHDVVLVIIF 1298  
Qy 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAGWCFGEQAYLRSSWN 1347  
Db 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAGWCFGEQAYLRSSWN 1358  
Qy 1348 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLTLRPLRVISRAOGLKLVVETLMS 1407  
Db 1359 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLTLRPLRVISRAOGLKLVVETLMS 1418  
Qy 1408 SLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITKNSDCAEASRWRHKY 1467  
Db 1419 SLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITKNSDCAEASRWRHKY 1478  
Qy 1468 NFDNLGQALMSLFVLASKDGWVDIMYDGLDVGVDQQPIMNHNPMWMLLYFISFLIVAFF 1527  
Db 1479 NFDNLGQALMSLFVLASKDGWVDIMYDGLDVGVDQQPIMNHNPMWMLLYFISFLIVAFF 1538  
Qy 1528 VLNMFVGVVVENFHKCRQHQQEERREERKRLRRLEKRR-----KAQCKPYYSYDYS 1580  
Db 1539 VLNMFVGVVVENFHKCRQHQQEERREERKRLRRLEKRRSKEKQMAEAQCKPYYSYDYS 1598  
Qy 1581 RFRLLVHLCTSHYLDLFTITGVIGLNVVTWAMEHYQQPQLDEALKICNYIFTVFVLES 1640  
Db 1599 RFRLLVHLCTSHYLDLFTITGVIGLNVVTWAMEHYQQPQLDEALKICNYIFTVFVES 1658  
Qy 1641 VFKLVAFGFRFFQDRWNQOLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIAR 1700  
Db 1659 VFKLVAFAFRFFQDRWNQOLDLAIVLLSIMGITLEEIEVNSLSPINPTIIRIMRVLIAR 1718  
Qy 1701 VLKLLKMAVGNRRALLDTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCEG 1760  
Db 1719 VLKLLKMAVGNRRALLHTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCEG 1778  
Qy 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCDQSTCYNTVISPIYFVSFVLTA 1820  
Db 1779 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPSPRDCDQSTCYNTVISPIYFVSFVLTA 1838  
Qy 1821 QFVLNVNVIIVLMKHLSEESNKEAEAELEAELELEMTLSPQPHSPGLSPFPLWPGVEGP 1880  
Db 1839 QFVLNVNVIIVLMKHLSEESNKEAEAELEAELELEMTLSPQPHSPGLSPFPLWPGVEGV 1898  
Qy 1881 DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLP 1937  
Db 1899 NSTDSPKPGAPHTTAHIGAAASGFSLEHPTWVPHEVPVPLGPDLLTVRKSGVSRTHSLP 1958  
Qy 1938 NDSYMCRHGSGTAEGPLHRCWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLOPHSA 1997  
Db 1959 NDSYMCRNSTAESRSLHRCWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGA 2018  
Qy 1998 PTWGTIPKLPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSRDLLAEVSGSPPLARAYS 2057  
Db 2019 PTWGAIPKLPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSRDLLSEVSGSPCLTRSSS 2078  
Qy 2058 FWGQSSTQAQHSRSHSKI SKHMTPPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDL 2117  
Db 2079 FWGSSIQVQORSQISQVSKHRLPAPCPGLEPSWAKPPETRRSSLELDTLSWISGDL 2138  
Qy 2118 LPPGGOEPPSPRDLKKCYVSAEQSCORRPTSWLDEQRHSTAVSCLDGSGQPHLGTDP 2177  
Db 2139 L-PSSQEEPLFRDLKKCYSVETQSCRRRPGFWLDEQRHSTAVSCLDGSGQPRLCPSPS 2197  
Qy 2178 NLGGQPLGGSPRPKKLSPPSITIDPPESQGRPTPPSPGICLRRRAPSSDSKDPLASGP 2237  
Db 2198 SLGGQPLGGSPRPKKLSPPSISIDPPESQGRPPCSPGVCCLRRRAPASDSKDPVS SSP 2257  
Qy 2238 PDSMAASPSPKDVLSSLSSDPAIDLDP 2266  
Db 2258 LDSTAASPSPKDVLSSLSSDPTDMDP 2286

AAU00474  
ID AAU00474 standard; protein; 1207 AA.  
XX  
AC AAU00474;  
XX  
DT 18-JUL-2001 (first entry)  
XX  
DE Human T-type calcium channel CACNA1G protein.  
XX  
KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B; APOB; caudal type homeobox transcription factor 2;  
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1; MINT31;  
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';  
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;  
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;  
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 17.  
XX  
OS Homo sapiens.  
XX  
PN WO200119845-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 14-SEP-2000; 2000WO-US025479.  
XX  
PR 15-SEP-1999; 99US-00398522.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Issa J;  
XX  
DR WPI; 2001-244777/25.  
DR N-PSDB; AAS01624.  
XX  
PT New nucleic acid molecule for use as a marker for screening cancer,  
PT comprises the coding region for a T-type calcium channel and regulatory  
PT sequences associated with the channel.  
XX  
PS Claim 9; Fig 3B; 125pp; English.  
XX  
CC The present sequence representing a novel human T-type calcium channel  
CC CACNA1G maps to chromosome 17. The methylation state of specific regions  
CC within CpG islands associated with the CACNA1G gene correlate with  
CC several cancerous phenotypes involving various tissue and cell types.  
CC Since aberrant methylation of normally unmethylated CpG islands is often  
CC observed in immortalised and transformed cells, CACNA1G is implicated in  
CC cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast  
CC and other cancers. The nucleic acid coding for CACNA1G is useful as a  
CC marker for screening cancer and age related diseases. A diagnostic kit  
CC containing primers (AAS01574-AAS01623) for amplification of a CpG-  
CC containing nucleic acid, where the primer hybridises with a target  
CC polynucleotide sequence (AAS01627-AAS01676), can be used for detecting  
CC aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are  
CC selected from genes encoding CACNA1G, apolipoprotein B (APOB), caudal  
CC type homeobox transcription factor 2 (CDX2), epidermal growth factor  
CC receptor (EGFR), fibrillin-1 (FBN1), G protein-coupled receptor 37  
CC (GPR37), heat shock 70kD protein 6 (HSP70B'; HSPA6), RasGAP-related  
CC protein (IQGAP2), klotho (KL), proteinase-activated receptor 2 (PAR2),  
CC paired-like homeodomain transcription factor 2 (PITX2), patched A and B  
CC (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT 31 sequence  
XX  
SQ Sequence 1207 AA;  
Query Match 53.1%; Score 6315.5; DB 4; Length 1207;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;  
Qy 1 MDEEDGAGAEESQPRSFMRNLDSGAGRPGSGAEKDPGSADSEAGLPYPALAPVV 60  
Db 1 MDEEDGAGAEESQPRSFMRNLDSGAGRPGSGAEKDPGSADSEAGLPYPALAPVV 60



QY 61 FFYLSQDSRPRSWCLRTVCNWPFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNWPFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180  
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180  
QY 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
Db 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
QY 241 CFLPENFSLPLSVDLERYYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300  
Db 241 CFLPENFSLPLSVDLERYYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300  
QY 301 DYEAYNSSNTTCVNNWNQYTYNCISAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEAYNSSNTTCVNNWNQYTYNCISAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINLCLVVIATQFSETKORESQLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINLCLVVIATQFSETKORESQLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYBELLYLVYILRKAARLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480  
Db 421 STLASFSEPGSCYBELLYLVYILRKAARLAQVSRAAGVRVGLLSSPAPLGGQETQPS 480  
QY 481 SCSRSRRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
Db 481 SCSRSRRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGSKVYPTVHTSPPE 600  
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGSKVYPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660  
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660  
QY 661 ACGPDCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPDA 720  
Db 661 ACGPDCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPDA 720  
QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
Db 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLLKLIVYGPFGYIKNPYNIQVGVIVISVWEIVGQGGGLSVLRTFRLMR 840  
Db 781 VFTSLFALEMLLKLIVYGPFGYIKNPYNIQVGVIVISVWEIVGQGGGLSVLRTFRLMR 840  
QY 841 VLKLVRLPALQRLVVLMTMDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGD TL 900  
Db 841 VLKLVRLPALQRLVVLMTMDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGD TL 900  
QY 901 PDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLV 960  
Db 901 PDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLV 960  
QY 961 AILVEGFQAEISKREDASQLSCIQLPVDSQGGDANKSESEDDFFPSLDGDGDRKKCL 1020  
Db 961 AILVEGFQAE-----GDANKSESEDDFFPSLDGDGDRKKCL 997  
QY 1021 ALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080  
Db 998 ALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1057  
QY 1081 HEMKSPPSARSSPHSPWSAASWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEQBSQ 1140  
Db 1058 HEMKSPPSARSSPHSPWSAASWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEQBSQ 1117  
QY 1141 DEESSEERASPAGSDHRRHGRSLEREAKSSFDPDLPTLQVPGHLHTASGRGSASEHQDCN 1200

Db 1118 DEESSEERASPAGSDHRRHGRSLEREAKSSFDPDLPTLQVPGHLHTASGRGSASEHQDCN 1177  
QY 1201 GKSASGRLARALRPDDPPPLDGGDDADDEGNL 1230  
Db 1178 GKSASGRLARALRPDDPPPLDGGDDADDEGNL 1207

Search completed: April 13, 2005, 16:34:38  
Job time : 256 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:30:32 ; Search time 57 Seconds  
(without alignments)  
2967.628 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKDVLSLGLSDPADLDP 2266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5
2	11241	94.4	2220	4	US-09-949-016-9730
3	6315.5	53.1	1207	4	US-09-398-522-52
4	6211	52.2	2353	3	US-08-984-709A-50
5	5492.5	46.1	2175	3	US-09-404-650-2
6	5492.5	46.1	2175	4	US-09-935-541-2
7	5484	46.1	2188	3	US-09-404-650-4
8	5484	46.1	2188	4	US-09-935-541-4
9	5366	45.1	1835	3	US-09-404-650-5
10	5366	45.1	1835	4	US-09-935-541-5
11	1750.5	14.7	2343	3	US-09-268-163-4
12	1749	14.7	2337	3	US-08-713-118-2
13	1749	14.7	2337	3	US-09-452-007-2
14	1748.5	14.7	2339	1	US-08-455-543A-47
15	1748.5	14.7	2339	2	US-08-223-305C-47
16	1746.5	14.7	2339	3	US-09-268-163-6
17	1743	14.6	2237	1	US-08-455-543A-48
18	1743	14.6	2237	2	US-08-223-305C-48
19	1741	14.6	2237	3	US-09-268-163-8
20	1722	14.5	2336	3	US-09-268-163-10
21	1632.5	13.7	1873	1	US-08-435-675B-4
22	1622.5	13.6	1873	1	US-08-336-257A-7
23	1619.5	13.6	1984	3	US-08-836-325-10
24	1619.5	13.6	1984	4	US-09-457-571-10
25	1619.5	13.6	1985	4	US-09-495-714C-6
26	1616	13.6	1872	6	5386025-6
27	1616	13.6	1872	6	5386025-6

28	1615.5	13.6	1989	3	US-08-836-325-12	Sequence 12, Appl
29	1615.5	13.6	1989	4	US-09-457-571-12	Sequence 12, Appl
30	1607.5	13.5	2516	3	US-08-374-077C-2	Sequence 2, Appli
31	1607.5	13.5	2516	3	US-08-895-590-2	Sequence 2, Appli
32	1607.5	13.5	2516	4	US-09-539-879A-2	Sequence 2, Appli
33	1601	13.4	1977	4	US-09-495-714C-4	Sequence 4, Appli
34	1601	13.4	2509	2	US-08-149-097D-35	Sequence 35, Appl
35	1596	13.4	1668	4	US-09-949-016-11611	Sequence 11611, A
36	1594.5	13.4	2546	4	US-09-949-016-9500	Sequence 9500, Ap
37	1594.5	13.4	2546	4	US-09-949-016-9501	Sequence 9501, Ap
38	1587	13.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
39	1587	13.3	2016	4	US-09-896-994-2	Sequence 2, Appli
40	1586	13.3	1969	3	US-08-836-325-16	Sequence 16, Appl
41	1586	13.3	1969	4	US-09-457-571-16	Sequence 16, Appl
42	1586	13.3	2016	3	US-09-634-920-4	Sequence 4, Appli
43	1586	13.3	2016	4	US-09-840-125-4	Sequence 4, Appli
44	1583	13.3	1977	4	US-09-976-594-757	Sequence 757, App
45	1583	13.3	1977	4	US-09-919-039-367	Sequence 367, App

ALIGNMENTS

RESULT 1  
US-09-426-998-5  
; Sequence 5, Application US/09426998  
; Patent No. 6358706  
; GENERAL INFORMATION:  
; APPLICANT: DUBIN, ADRIENNE E.  
; APPLICANT: PYATI, JAYASHREE  
; APPLICANT: ZHU, JESSICA Y  
; APPLICANT: ERLANDER, MARK G  
; APPLICANT: GALINDO, JOSE E  
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM  
; FILE REFERENCE: ORT-1057  
; CURRENT APPLICATION NUMBER: US/09/426.998  
; CURRENT FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PATENTIN VER. 2.0  
; SEQ ID NO 5  
; LENGTH: 2273  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-426-998-5

QY	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGGSAEKDPGSADSEAEGLYPALAPVV	60
Db	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGGSAEKDPGSADSEAEGLYPALAPVV	60
QY	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTGLMFRPCEDIACDSQRCRILQAF	120
Db	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTGLMFRPCEDIACDSQRCRILQAF	120
QY	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVTAGLMLEYSLDLQNVSPSAVR	180
Db	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVTAGLMLEYSLDLQNVSPSAVR	180
QY	181	TVRVLRLPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240
Db	181	TVRVLRLPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240
QY	241	CFLPENFSLPSVDLERYQYQTENEDESPFICSQPRENGMRSCRSVPTLRDGGGGPPCGL	300
Db	241	CFLPENFSLPSVDLERYQYQTENEDESPFICSQPRENGMRSCRSVPTLRDGGGGPPCGL	300
QY	301	DYEAYNSSNTTCVNNQYTYNCNCSAGEHNPFKGAINFNDIGNYAWIAIFQVITLEGWVDIM	360
Db	301	DYEAYNSSNTTCVNNQYTYNCNCSAGEHNPFKGAINFNDIGNYAWIAIFQVITLEGWVDIM	360

QY 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGETQPS 480  
Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGETQPS 480  
QY 481 SCSRRRLSVHHLVHHHHHHHHHVLGNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
Db 481 SCSRRRLSVHHLVHHHHHHHHHVLGNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540  
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600  
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660  
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660  
QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSDLRDPHSRRQRSLGPD 720  
Db 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQSDLRDPHSRRQRSLGPD 720  
QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGGIMIAILLVNTLSMGLYHEQPEELTNALEISNI 780  
Db 721 EPSSVLAFWRLICDTFRKIVDSKYFGGIMIAILLVNTLSMGLYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIIVISVWEIVGQGGGLSVLRTFLMR 840  
Db 781 VFTSLFALEMLKLLVYGPFGYIKNPYINFDGVIIVISVWEIVGQGGGLSVLRTFLMR 840  
QY 841 VLKLVFLPALQRLVLMKTMNDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGT 900  
Db 841 VLKLVFLPALQRLVLMKTMNDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGT 900  
QY 901 PDRKNFDSLLWAIIVTFQILTOEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLLV 960  
Db 901 PDRKNFDSLLWAIIVTFQILTOEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLLV 960  
QY 961 AILVEGFOAEISKREDASQOLSCIQLPVDOSQGDANKSESEDPFFSPSLDGDGRKKCL 1020  
Db 961 AILVEGFOAEISKREDASQOLSCIQLPVDOSQGDANKSESEDPFFSPSLDGDGRKKCL 1020  
QY 1021 ALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080  
Db 1021 ALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080  
QY 1081 HEMKSPPSARSPPHSPWASAASWTSSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140  
Db 1081 HEMKSPPSARSPPHSPWASAASWTSSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140  
QY 1141 DEEESSEERASPDGHRHRSGLEREAQSSFDLPDTLQVPLHRTASGRGSAEHQDCN 1200  
Db 1141 DEEESSEERASPDGHRHRSGLEREAQSSFDLPDTLQVPLHRTASGRGSAEHQDCN 1200  
QY 1201 GKSASGRALARALPDPPDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260  
Db 1201 GKSASGRALARALPDPPDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260  
QY 1261 PQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
Db 1261 PQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320  
QY 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVMSVSDSGTKILGMLRVL 1380  
Db 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVMSVSDSGTKILGMLRVL 1380  
QY 1381 RLRLTLRPLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440  
Db 1381 RLRLTLRPLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440

QY 1441 CQGEDTRNITNKSDCAEASRWRVRHKYNFDNLQALMSLFLVASKDQWVDIMYDGLDAVG 1500  
Db 1441 CQGEDTRNITNKSDCAEASRWRVRHKYNFDNLQALMSLFLVASKDQWVDIMYDGLDAVG 1500  
QY 1501 VDOQPMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVFNHFKCRQHQBEEAARRRREKRL 1560  
Db 1501 VDOQPMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVFNHFKCRQHQBEEAARRRREKRL 1560  
QY 1561 RRLEKKRR-----KQACKPYYSYDSYRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAME 1613  
Db 1561 RRLEKKRRSKEQMAEQACKPYYSYDSYRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAME 1620  
QY 1614 HYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLDLAIVLLSIMGIT 1673  
Db 1621 HYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLDLAIVLLSIMGIP 1680  
QY 1674 LEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRRALLDTVMQALPQVGNLGLLFM 1733  
Db 1681 LEQIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRRALLDTVMQALPQVGNLGLLFM 1740  
QY 1734 LLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDT 1793  
Db 1741 LLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDT 1800  
QY 1794 LRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEAKEAELEAEL 1853  
Db 1801 LRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEAKEAELEAEL 1860  
QY 1854 ELEMKTLSPOPHSPGLSPFLWPVEGDPSPSPKPGALHPAAHARSASHFSLEHPTMQPH 1913  
Db 1861 ELEMKTLSPOPHSPGLSPFLWPVEGDPSPSPKPGALHPAAHARSASHFSLEHPTMQPH 1920  
QY 1914 PTELPGDILLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1973  
Db 1921 PTELPGDILLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1980  
QY 1974 OPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQRPLRRAIRTDSDLVQ 2033  
Db 1981 OPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQRPLRRAIRTDSDLVQ 2040  
QY 2034 GLGSREDLLAEVSGSPPLARAYSFWGQSSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNW 2093  
Db 2041 GLGSREDLLAEVSGSPPLARAYSFWGQSSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNW 2100  
QY 2094 GKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPDLKCCYSVEAQSCORRPTSWLDE 2153  
Db 2101 GKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPDLKCCYSVEAQSCORRPTSWLDE 2160  
QY 2154 QRRHSIAVSCLDGSGQPHLGTDPNSNLGGQPLGGPGSRPKKLSPPSITIDPPESQGPRT 2213  
Db 2161 QRRHSIAVSCLDGSGQPHLGTDPNSNLGGQPLGGPGSRPKKLSPPSITIDPPESQGPRT 2220  
QY 2214 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSSLGLSSDPADLDP 2266  
Db 2221 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSSLGLSSDPADLDP 2273

RESULT 2

US-09-949-016-9730  
; Sequence 9730, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498



; PRIOR FILING DATE: 2000-09-08									
; NUMBER OF SEQ ID NOS: 207012									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 9730									
; LENGTH: 2220									
; TYPE: PR									
; ORGANISM: Human									
US-09-949-016-9730									
Query Match 94.4%; Score 11241; DB 4; Length 2220;									
Best Local Similarity 95.1%; Pred. No. 0;									
Matches 2162; Conservative 1; Mismatches 1; Indels 110; Gaps 4;									
QY	1	MDEEDGAGAESGQPRSFMRNDLSGAGRPGPSAEKDPGSADSEAEGLPYPALAPVV	60						
DB	49	MDEEDGAGAESGQPRSFMRNDLSGAGRPGPSAEKDPGSADSEAEGLPYPALAPVV	108						
QY	61	FFYLSQDSRPSWCLRTVCNP-WFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQA	119						
DB	109	FFYLSQDSRPSWCLRTVCNPTWFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQA	168						
QY	120	FDDFIFAFPAVEMVVMVALGIFGKKCYLGDWTNRLDFFIVTAGMLEYSLDLQNVSFSAV	179						
DB	169	FDDFIFAFPAVEMVVMVALGIFGKKCYLGDWTNRLDFFIVTAGMLEYSLDLQNVSFSAV	228						
QY	180	RTVRVLRPLRAINRVPSMRILVTLTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRN	239						
DB	229	RTVRVLRPLRAINRVPSMRILVTLTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRN	288						
QY	240	RCFLPENFSLPSVDLERYQOTENEDSPFICSQPRENGMRSCRSVPTLRGDGGGPPCG	299						
DB	289	RCFLPENFSLPSVDLERYQOTENEDSPFICSQPRENGMRSCRSVPTLRGDGGGPPCG	348						
QY	300	LDYEAYNSSNTTCVWNQYYTNCISAGEHNPFGKAINFDNIGYAWIAFQVITLEGWVDI	359						
DB	349	LDYEAYNSSNTTCVWNQYYTNCISAGEHNPFGKAINFDNIGYAWIAFQVITLEGWVDI	408						
QY	360	MYFVMDAHSFNFIYPILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSN	419						
DB	409	MYFVMDAHSFNFIYPILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSN	468						
QY	420	ASTLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAAGVVRVGLLSSPAPLGGQETQPS	479						
DB	469	ASTLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAAGVVRVGLLSSPAPLGGQETQPS	528						
QY	480	SSCSRSHRRLSVHHLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPST	539						
DB	529	SSCSRSHRRLSVHHLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPST	588						
QY	540	PALSGAPPGBAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPP	599						
DB	589	PALSGAPPGBAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPP	648						
QY	600	ETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADS	659						
DB	649	ETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADS	708						
QY	660	GACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPD	719						
DB	709	GACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPD	768						
QY	720	AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALBEISN	779						
DB	769	AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALBEISN	828						
QY	780	IVFTSLFALEMLLKLIVYGPFGYIKNPYNIIPDGVIIVISVWEIVGQGGGLSVLRTFRLM	839						
DB	829	IVFTSLFALEMLLKLIVYGPFGYIKNPYNIIPDGVIIVISVWEIVGQGGGLSVLRTFRLM	888						
QY	840	RVLKLVRFPLAQRLQVLVLMKTMNDNATFCMLLMLFIFIFSILGMHLFGCKFASERDGD	899						
DB	889	RVLKLVRFPLAQRLQVLVLMKTMNDNATFCMLLMLFIFIFSILGMHLFGCKFASERDGD	948						

QY	900	LPDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	959						
DB	949	LPDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	1008						
QY	960	VAILVEGFOAEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKC	1019						
DB	1009	VAILVEGFOAE-----GDANKSESEPDFFSPSLDGDGDRKKC	1045						
QY	1020	LALVSLGEHPBLRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA	1079						
DB	1046	LALVSLGEHPBLRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA	1105						
QY	1080	AHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQES	1139						
DB	1106	AHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQES	1165						
QY	1140	QDEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQDC	1199						
DB	1166	QDEEESSEERASPAGSDHRHRGSLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQDC	1225						
QY	1200	NGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIF	1259						
DB	1226	NGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIF	1285						
QY	1260	PPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA	1319						
DB	1286	PPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA	1345						
QY	1320	VFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLLVISVIDILVSMVSDSGTKILMLRV	1379						
DB	1346	VFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLLVISVIDILVSMVSDSGTKILMLRV	1405						
QY	1380	LRLRLTLRPLRVISRAOGLKLVETIMSSSLKPIGNIVVICAPFIIIFGILGVQLFKGKFF	1439						
DB	1406	LRLRLTLRPLRVISRAOGLKLVETIMSSSLKPIGNIVVICAPFIIIFGILGVQLFKGKFF	1465						
QY	1440	VCQGEDTRNITNKSDCAEASVWRVHKYNFDNLGQALMSLFLVASKDGVVDIMYDGLDAV	1499						
DB	1466	VCQGEDTRNITNKSDCAEASVWRVHKYNFDNLGQALMSLFLVASKDGVVDIMYDGLDAV	1525						
QY	1500	GVDQOPIMNHPMMLLYFISFLLIIVAFVFLNMFGVVVENFHKCRHQHEEEARRREEKR	1559						
DB	1526	GVDQOPIMNHPMMLLYFISFLLIIVAFVFLNMFGVVVENFHKCRHQHEEEARRREEKR	1585						
QY	1560	LRRLEKKR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLNVVTMAM	1612						
DB	1586	LRRLEKKRSEKQMAEAOCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLNVVTMAM	1645						
QY	1613	EHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIIVLLSIMGI	1672						
DB	1646	EHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIIVLLSIMGI	1705						
QY	1673	TLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLF	1732						
DB	1706	TLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLF	1765						
QY	1733	MLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD	1792						
DB	1766	MLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD	1825						
QY	1793	TLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVMLKHEESNKEAEAELEAE	1852						
DB	1826	TLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVMLKHEESNKEAEAELEAE	1885						
QY	1853	LELEMTLSQPSPHSPGLSPFLWPVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQP	1912						
DB	1886	LELEMTLSQPSPHSPGLSPFLWPVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQP	1945						
QY	1913	HPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVH	1972						
DB	1946	HPTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVH	2005						
QY	1973	SQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAIRTDSDLV	2032						

Db 2006 SQPADTSYILQLPKADAPHLLOPHSAPTWTGTPKLPPLPGRSPLAQRPLRRQAAIRTDSDLV 2065  
QY 2033 QGLGSREDLLAEVSGSPPLARAYFWGQSSTQAQQHSRSHSKISKHMTTPAPCPGPEPN 2092  
Db 2066 QGLGSREDLLAE----- 2077  
QY 2093 WKGPPETRSSLELDTLSWISGDLPLPPGGQEEPPSPRLDKKCYSAQAQSCRRPTSWLD 2152  
Db 2078 -----EPPSPRLDKKCYSAQAQSCRRPTSWLD 2106  
QY 2153 EORRHSAVSCLDGSGOPHLGTPNSILGGQPLGGPGSRPKKLSPPSITIDPPESQGPRT 2212  
Db 2107 EORRHSAVSCLDGSGOPHLGTPNSILGGQPLGGPGSRPKKLSPPSITIDPPESQGPRT 2166  
QY 2213 PPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2266  
Db 2167 PPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP 2220

RESULT 3  
US-09-398-522-52  
; Sequence 52, Application US/09398522  
; Patent No. 6783933  
; GENERAL INFORMATION:  
; APPLICANT: Issa, Jean-Pierre  
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: JHU1590  
; CURRENT APPLICATION NUMBER: US/09/398,522  
; CURRENT FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 1207  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel  
US-09-398-522-52

Query Match 53.1%; Score 6315.5; DB 4; Length 1207;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY 1 MDEEEDGAGAEESQPRSFMRNLNDSGACGRPGPSAEKDPGSADSEAEGLPYPALAPVV 60  
Db 1 MDEEEDGAGAEESQPRSFMRNLNDSGACGRPGPSAEKDPGSADSEAEGLPYPALAPVV 60  
QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSPSAVR 180  
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSPSAVR 180  
QY 181 TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240  
Db 181 TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240  
QY 241 CFLPENFSLPLSVDLERYQYQTENEDESPFICSQPRENMRSCRSVPTLRDGGGGPPCGL 300  
Db 241 CFLPENFSLPLSVDLERYQYQTENEDESPFICSQPRENMRSCRSVPTLRDGGGGPPCGL 300  
QY 301 DYEAYNSSNTTCVWNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEAYNSSNTTCVWNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQMLREQVRFLSNA 420  
Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQMLREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLYLVYILRKAARLAQVSRAGVRVGLSSPAPLGGQETQPSS 480  
Db 421 STLASFSEPGSCYEELLYLVYILRKAARLAQVSRAGVRVGLSSPAPLGGQETQPSS 480  
QY 481 SCSRSHRRLSVHHLVHHHHHHHHYHLNGTFLRAPRASPEIQDRDANGSRRLMLPPPSTP 540  
Db 481 SCSRSHRRLSVHHLVHHHHHHHHYHLNGTFLRAPRASPEIQDRDANGSRRLMLPPPSTP 540  
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVSGKYVPTVHTSPPE 600  
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVSGKYVPTVHTSPPE 600  
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660  
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660  
QY 661 ACGPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRRQRSGLGPA 720  
Db 661 ACGPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHSRRQRSGLGPA 720  
QY 721 EPSSVLAFWRLICDTFRKIIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
Db 721 EPSSVLAFWRLICDTFRKIIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780  
QY 781 VFTSLFALEMLLKLIVGPGFYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLMR 840  
Db 781 VFTSLFALEMLLKLIVGPGFYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLMR 840  
QY 841 VLKLVRFPLPALQRLVVLMTMDNVATFCMLMLFIFIFSILGMLHFGCKFASERDGTTL 900  
Db 841 VLKLVRFPLPALQRLVVLMTMDNVATFCMLMLFIFIFSILGMLHFGCKFASERDGTTL 900  
QY 901 PDRKNFDSLLWAIIVTFQIILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
Db 901 PDRKNFDSLLWAIIVTFQIILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV 960  
QY 961 AILVEGFQAEISKREDASQGLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020  
Db 961 AILVEGFQAE-----GDANKSESEPDFFSPSLDGDGDRKKCL 997  
QY 1021 ALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080  
Db 998 ALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1057  
QY 1081 HEMKSPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRRLLSGEGQESQ 1140  
Db 1058 HEMKSPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRRLLSGEGQESQ 1117  
QY 1141 DEEESSEERASPAGSDHHRHGRSLEREAKSSFDLPTLQVPLHRTASGRGSAEHQDCN 1200  
Db 1118 DEEESSEERASPAGSDHHRHGRSLEREAKSSFDLPTLQVPLHRTASGRGSAEHQDCN 1177  
QY 1201 GKSASGRLARALRPDDPPLDGDADDEGNL 1230  
Db 1178 GKSASGRLARALRPDDPPLDGDADDEGNL 1207

RESULT 4  
US-08-984-709A-50  
; Sequence 50, Application US/08984709A  
; Patent No. 6320032  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Stauderman, Kenneth A.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McAuliffe  
; STREET: 4250 Executive Square, Suite 700  
; CITY: La Jolla  
; STATE: California



1597 LFITGVIGLVNVTMAMEHYQQOILDEALKICNYITFTVIFVLESVEFKLVAFGFRFFQDR 1656  
1621 LFITFIICVNVITMSMEHYNQPSLDEALKYCNYVFTIVFVEAALKLVAFGFRFFKDR 1680  
1657 WNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRALLD 1716  
1681 WNQDLAIVLLSLMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRALLD 1740  
1717 TVMQALPQVGNLGLLMLFFIIPAAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLT 1776  
1741 TVQALPQVGNLGLLMLFFIIPAAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLT 1800  
1777 LFRVSTGDNWNGIMKDTLRDC---DQESTCYNTVISPFIYFVSFVLTAQFVLNVVAVLVM 1833  
1801 LFRVSTGDNWNGIMKDTLRDCSREDKHCLSYLPALSPYVFTFVLVAQFVLNVVAVLVM 1860  
1834 KHEESNKEAEAEAELEEMKTLSPQPHSPGLSPFLWPVGVEGPDSP---DSPKPGA 1890  
1861 KHEESNKEAREDAELDAEIELEM-----AQPGSARRVDADRP-- 1899  
1891 LHPAAHARSASHFSLEHPTMQPHPTLP---PDLLTVRKSGVSRTHSLPNDSYMCRHG 1946  
1900 -----PLQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV 1937  
1947 STAEGP-----LHGRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSA 1997  
1938 VPASAPHRPLQEVEMETYGATP---LGSVASVHSPPAESCASLQIP-----LAVSSPA 1989  
1998 PTWGTIPKLPPEG--RSPLAQRPLRQAAIRTDSDLDVQGLSREDLL--AEVSGPSP--P 2051  
1990 RSGEPLHALSPRGARSPSLRLLCRQEAHVHTDSLEGK-IDSPRDTLDPAPGEGEKTVPVRP 2048  
2052 LARAYSFWG--QSSTQAQQHSRSHKISKHMTTPAP-CPGPEPNWKGPPETRSLSLELD 2108  
2049 VTQGGSLQSPRSPRSPASVTRKHT-FGQHCVSRRPAAPGGE-----EAEADPADE 2099  
2109 ELSWISGDLLP-----PGQEEPP---SPRDLKKCYSVAEACQRRRPTSWLDEQRHSI 2159  
2100 EVSHITSSACPWQPTAEPHGPEASPVAGGERDLRLYSVDAQGLDKP-GRADQWRPSA 2158  
2160 AVSCLDSGSPHLGTDPSNLGGQPLGGPGRPKKLSPPSITDPP-ESQGPRTTSPSP-- 2216  
2159 ELGSGEPGEAKAWPE-----AEP--ALGARKKKWSPPCISVEPPAEDEGSARPSAEG 2211  
2217 -GICLRRRAPSSDSK-----DPLASGPPDSMAASPSPKDVLSSLGLSS 2259  
2212 GSTILRRRTPSCEATPHRESLEPTEGSGAGGDPAAKGERWGQA---SCRAEHLTVPSFAF 2268  
2260 DPADL-----DP 2266  
2269 EPLDLGVPSGDP 2280

RESULT 5  
US-09-404-650-2  
; Sequence 2, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-404-650-2

Query Match 46.1%; Score 5492.5; DB 3; Length 2175;  
Best Local Similarity 51.3%; Pred. No. 0;  
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;  
QY 31 RPPGSAEKDPSADSEAE-----LPYPALAPVVFYLLSQDSRPSRCLRTVTCNWPFERI 86  
Db 25 QPGPRSPSPSPGLEEPLDGADPHVPHDLAPIAFFCLRTTSPRNCIKMVCNWPFEVCV 84  
QY 87 SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVMVKMVALGIFGKKC 146  
Db 85 SMLVILLNCVTLGMYPQCDMDCLSDRCKILQVDDFIFFAMEMVLKMWALGIFGKKC 144  
QY 147 YLGDTWNLDFIIVAGMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVPSMRILVTLLED 206  
Db 145 YLGDTWNLDFIIVAGMVEYSLDLQNLINLSAIRTVRLRPLKAINRVPSMRILVNLLED 204  
QY 207 TLPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLNRNRCFLPENFSLPLSDVLERYQYOTENEDE 266  
Db 205 TLPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLNRNRCFLEENFTIQGDVALPPYQPEEDE 264  
QY 267 SPFICSQPRENGMRSRCSVPTLRGDGGGPPCGL-----DYAXNSSSNTT--CVNWNQ 318  
Db 265 MPFICSLSGDNGIMGCHIEPPLKEQ---GRECLSKDDVYDFGAGRQDLNAGLCVNWNR 321  
QY 319 YVTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGVDMYFVMDAHSFYNYFIYFILL 378  
Db 322 YVNCRTGSANPHKGAINDNIGYAWIVIFQVITLEGVWEIMYVMDAHSFYNYFIYFILL 381  
QY 379 IIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELK 438  
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS--SSTVASAEPGDCYEEIFQ 440  
QY 439 YLVYILRKAARRLAQVSRAGVRVGLLSPPAPLGGQETQPSSSCSRRRLSVHHLVHH 498  
Db 441 YVCHILRKAKR-----RALGLYQALQSRRLQALG----- 468  
QY 499 HHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYH 558  
Db 469 -----PEAPA--PAKPGP-----H 480  
QY 559 ADCHLEPVRCAQAPPSPSPSASGRVTGSKVYPTVHTSPPPETLKEKALVEVAASSGPPT 618  
Db 481 AK---EPRHYQLCPQHSPLDPTL-----VQPIPATL----- 511  
QY 619 LTSNLTPPGPYSSMHKLELTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672  
Db 512 -----ASDPASCPCQCHEDGRRP 529  
QY 673 AGAGEVELADREMPDSDSEAVVEFTQDAHQHSDLRDPHSRRQRSLGPDAPSSVL----- 726  
Db 530 SGLGSTD--SQEGSGSGSSAGGE--DEADGDGARSSDGDGASSELGKEEEEEQADGAVWL 586  
QY 727 --AFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGLEYHEQPEELTNALISNIVFTS 784  
Db 587 CGDVWRETRAKLRGIVDSKYFNFRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS 646  
QY 785 LFALEMLKLLVYGPFGYIKNPYNIQFDGVIIVISVWEIVGQGGGLSVLRTFRLMRVLKL 844  
Db 647 MFALEMLKLAAGLFDYLRNPYNIFDSIIIVISIWEIVGQADGGLSVLRTFRLMRVLKL 706  
QY 845 VRFLPALQRLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKFASERD-GDTLPDR 903  
Db 707 VRFPALRRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKFSLRTDGTGTVPDR 766  
QY 904 KNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALFYALMTFGNYVLFNLVAIL 963  
Db 767 KNFDSLLWAIIVTFQILTQEDWNVVLNGMASTSPWASLYFVALMTFGNYVLFNLVAIL 826  
QY 964 VEGFOAEIISKREDASGQLSCIQLPVDGQGDANKSESEPDFSPS-----LDGD 1013  
Db 827 VEGFOAE-----GDANRSYDEQSSSNIIEFDKLEGLDSS 863



QY 1014 GDRKKCLALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRT----- 1069  
Db 864 GDPKLCPIWTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRLSLQPD 906  
QY 1070 -----SSSGAEPGAHEMKSPPSARSSPHSPWSAASSWTSSRNSRLGRAPSLK 1120  
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYYGPWGRSAAWASRRSSWN-----SLK 960  
QY 1121 RRSPSGERRSLSGE-QGESQDEEESSEE--ERASPAAGSDH-----RHRG 1162  
Db 961 HKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHITHHGPLAHRRHRR 1020  
QY 1163 SLEREAKSSFDPDLTQVPLHRTASGR--GSASEHQDCNGKSASGRALARALRPDDPDL 1220  
Db 1021 TLSLDNRDSVDLAEVLPAVGAHPRAAWRAAGAPAGHEDCNGRMPSIAKDVFTKMGDRGR 1080  
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSPRLLCHRIITHKMF 1280  
Db 1081 GED-ESEIDYTLCPVRKMDIVYKPDWCVEVEDWSVYLFSPENRFRVLCQTIIAHKLF 1139  
QY 1281 VVLVIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFGEOA 1340  
Db 1140 VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTKVWSLGLYFGEQA 1199  
QY 1341 YLRSSWNVLDGLLVLISVIDILVSMVSDSTKILGMLRVLRLRLRLPLRVISRAOGLKL 1400  
Db 1200 YLRSSWNVLDGLFVFSIIDIVVSLASAGAKILGVLRLRLRLPLRVISRAPGLKL 1259  
QY 1401 VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNITNKSDCAEASY 1460  
Db 1260 VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGFYHCLGVDTRNITNRSDCMAAY 1319  
QY 1461 RWVRHKYNFNLGQALMSLFVLASKDGVVDIMYDGLDAVGVDQOPIMNHNPMMLLYFISF 1520  
Db 1320 RWVHKYNFNLGQALMSLFVLASKDGVWVIMYNGLDVAVDQPVTNHNPMMLLYFISF 1379  
QY 1521 LLIVAFFVLNMFVGVVVENFHKRQHOBEEARRREEKRLRLLEKRRKAQCKPYVSDYS 1580  
Db 1380 LLIVSFFVLNMFVGVVVENFHKRQHOBEEARRREEKRLRLLEKRRKAQRLPYVATYC 1439  
QY 1581 RFRLLVHLCTSHYLDLFTIGVLNVVTWAMEHYQQOILDEALKICNYIFTVIFVLES 1640  
Db 1440 HTRLLIHSMTCTSHYLDIFITFIICLVNVVWMSLEHYNQPTSLTALKYCNMFTTVFVLEA 1499  
QY 1641 VFKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLIEEIEVNASLIPNPTIIRIMRVLRIAR 1700  
Db 1500 VLKLVAFGLRRFFKDRWNQDLAIIVLLSVNGITLIEEIEINAAIPNPTIIRIMRVLRIAR 1559  
QY 1701 VLKLLKMAVGMRALLDVTVMQALPOVGNLGLLFLMLFFIFFAALGVELFGDLECEHPCEG 1760  
Db 1560 VLKLLKMATGMRALLDVTVMQALPOVGNLGLLFLMLFFIYAALGVELFGKLVNDENPCEG 1619  
QY 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1817  
Db 1620 MSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDCTHDSRCLSSLQFVSPLYFVSFV 1679  
QY 1818 LTAQFVLNVVAVLVMKHLLEESNKEAKEBAELEAELELEM-KTISPPQSPHSPGLSPFLWPG 1876  
Db 1680 LTAQFVLINVVAVLVMKHLDDSNKEAQEAEMDAELEMAHGLGPGPRLPTGSPGA-PG 1738  
QY 1877 VEGPDSPD-----SPKPGAL-----HPAAHA----- 1897  
Db 1739 -RPGGAGGGGTEGGLCRRCYSPAQDSLEGELTIIDNLSGSIFHHYSSPAGCKKCHHDK 1797  
QY 1898 -----RSAS-----HFSLEHPTMQP-----HTELPGPDLLTVRKSG-- 1929  
Db 1798 QEVQLAETEAFSLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPPEPMRVGDLGEC 1857  
QY 1930 ---VSRTHSLPN-DSYMCRRHGSTAEGPLGHRGWLPLKAQSGSVLSVHSPADTSYILQLP 1985  
Db 1858 FFLPLSSTAVSPDPENFLCEMEEIIPFNPV--RSW--LKHDSQAQPPSPFSPDASSPLLPMP 1913  
QY 1986 KDAPH-----LLQPHSAPTWTGTIPKLPPPG-----RSPLAQRLRRQAAIIRTDSDLVQG 2034

Db 1914 AEFHHPAVSASQKPEKGTGTGLPKJALQGSWASLRSPRVNCTLLRQATGSDTSLD--- 1970  
QY 2035 LGSREDLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTTPAPCPGPEPNWG 2094  
Db 1971 -----ASPSSAGSLQTTLEDLSLSDSPRA-----LGPPAPAPGPRAGLS 2012  
QY 2095 KGPPETRSSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCYSEVAQSCQRRRTSWLDEQ 2154  
Db 2013 ---PAARRRLSL-----RGRGLFSLRGLRA-----HQ 2036  
QY 2155 RRHSIAVCLDSGSPHLGTDPN---LGGQPLGGGSRPKKLSPPSIT---IDPPESQ 2208  
Db 2037 RSHSSGGS-TSPGCTHDSMDPSDEEGRGAGGAGSEHSETLSLSLTSLFCPPP--- 2092  
QY 2209 GPRTPPSPGICLRRRAPSSDS---KDPASGPPDSMAASPSPKDVLSSLGLSSDPADL 2264  
Db 2093 ---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-----RSKDPGPR 2143  
QY 2265 DP 2266  
Db 2144 AP 2145  
  
RESULT 6  
US-09-935-541-2  
; Sequence 2, Application US/09935541  
; Patent No. 6589787  
; GENERAL INFORMATION:  
; APPLICANT: McGivern, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/935,541  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2175  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-541-2  
  
Query Match 46.1%; Score 5492.5; DB 4; Length 2175;  
Best Local Similarity 51.3%; Pred. No. 0;  
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;  
  
QY 31 RPPGSAEKDPGSADSEAG---LPYPALAPVFFYLSQDSRPRSWCLRTVCNPFERI 86  
Db 25 QGPRSPSPSPGLEEPLDGADPHVPHDLAPIAFFCLRTTSPRNWCIKWCNPFECV 84  
QY 87 SMLVILLNCVTILGMFRPCEDIACDSORCIRILOAFDDFIFAFFAVEMVVMVALGIFGKKC 146  
Db 85 SMLVILLNCVTILGMVQPCDDMDCLSDCKILQVFDFFIFIFFAMVLMKVALGIFGKKC 144  
QY 147 YLGDTWNRDLFFIAGLMLEYSLDLQNVSPSAVRTVRLRPLRAINRVPSMRILVTLILD 206  
Db 145 YLGDTWNRDLFFIVMAGMVEYSLDLQINLSAIRTVRLRPLKAINRVPSMRILVNLILD 204  
QY 207 TLPMLGNVLLLCFFVFFIFIGVGVQLWAGLLNRCLPENSPLSVDLERYYQTENEDE 266  
Db 205 TLPMLGNVLLLCFFVFFIFIGIIGVQLWAGLLNRCLFLENFTIQGDVALPPYQPEEDE 264  
QY 267 SPFICSQPRENGMRSCRSVPTLRGDCGGGPPCCGL-----DYEAYNSSSNTT--CVNNWQ 318  
Db 265 MPFICSLSGDNGIMGCHEIPLPLEQ---GRECCLSKODVYDFGAGRQDLNASGLCVNNWR 321  
QY 319 YYTNCESAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILL 378  
Db 322 YYNVCRGTSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFYIFILL 381



QY 379 IIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELK 438  
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASAEPGDCYEEIFQ 440  
QY 439 YLVYILRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH 498  
Db 441 YVCHILRKAH-----RALGLYQALQSRRALG----- 468  
QY 499 HHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYH 558  
Db 469 -----PEAPA--PAKPGP-----H 480  
QY 559 ADCHLEPVRQCAPPSPSEASGRIVGSKVYPTVHTSPPETLKEKALVEVAASSGPPT 618  
Db 481 AK---EPRHYQLCPQHSPLDATPHL-----VQIPATL----- 511  
QY 619 LTSLNIPPGPYSSMHKLLLETOSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672  
Db 512 -----ASDPASCPCQCHEDGRRP 529  
QY 673 AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRSGLGPDAAEPSVL----- 726  
Db 530 SGLGST-D-SQEGSCSGSSAGGE--DEADGDGARSSDGGASSELGKEEEEEQADGAOWL 586  
QY 727 --AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALAEISNIVFTS 784  
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHQPEELTNILEICNVVFTS 646  
QY 785 LFALEMLLKLAVYGPFGYIKNPYNIFDGVIVVISWEIVGQCGGLSVLRTFRMLRVLKL 844  
Db 647 MFALEMILKLAAGLFDYLRNPYNIFDSIIVISWEIVGQADGGLSVLRTFRLLRVLKL 706  
QY 845 VRFLPALQRLVLMKTMNDNVATFCMLMLFIFISILGMHLFGCKFASERD-GDTLPDR 903  
Db 707 VRFPALRRQLVLMKTMNDNVATFCMLMLFIFISILGMHIFGCKFSRLTDTGDTVDR 766  
QY 904 KNFDSLLWAIIVTFOILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFLNLVAIL 963  
Db 767 KNFDSLLWAIIVTFOILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYVLFLNLVAIL 826  
QY 964 VEGFOAEISKREDASQQLSCIQLPVDSSQGDANKSESEPDFFSPS-----LDGD 1013  
Db 827 VEGFOAE-----GDANRSYDEDDQSSNIEEFDKLEGLDSS 863  
QY 1014 GDRKKCLALVSLGEHPELRKSLPLPPLIHTAATPMSLPKSTSTGLGEALGPASRRT---- 1069  
Db 864 GDFKCLPIPMTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRLSLQPD 906  
QY 1070 -----SSSGSAEPGAAHEMKSPPSARSPSPWASAASSWTSSRRSSRNSLGRAPSLK 1120  
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYGPWGRSAAWASRRSSWN-----SLK 960  
QY 1121 RRSFSGERRSLLSGE-GOESQDEEESSE--ERASPAAGSDH-----RHRG 1162  
Db 961 HKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHHIHGPHLAHRHRHRR 1020  
QY 1163 SLREBAKSSFDLPDTLQVPLHRTASGR--GSASEHQDCNGKSASGRLARALRPDDPPLD 1220  
Db 1021 TSLDNRDSVDLAELVPVAGAHPRAAWRAAGPAPGHEDCNGRMPSTAKDVFTKMGDRGDR 1080  
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERSWSAYIFPPQSRFRLLCHRIITHKMFH 1280  
Db 1081 GED-BEEDYTLCFVRVKMIDVYKPDWCEVRDWSVYLFSPENRFRVLCQTIIAHLKFDY 1139  
QY 1281 VVLVIIFLNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVVALGWCFGEOA 1340  
Db 1140 VVLAFLIFLNCITIALERPQIFAGSTERIFLTVSNYIFTAIFVGEMTLKVVSGLYFGEQA 1199  
QY 1341 YLRSSWNVLGGLVLISVIDILVSMVSDSGTKILGMLRVLRLLRTRPLRVRISRAQGLKL 1400  
Db 1200 YLRSSWNVLGGLVFLVFSIIDIIVVSLASAGGAKILGVLRVLRLLRTRPLRVRISRAPGLKL 1259

QY 1401 VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASY 1460  
Db 1260 VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFFYHCLGVDTNRITNRSDCMAANY 1319  
QY 1461 RWVRHKYNFDNLGQALMSFLVASKDGVWVIMYDGLDAVGVDQOQIMNHNPMWMLLYFISF 1520  
Db 1320 RWVHKYNFDNLGQALMSFLVASKDGVWVIMYNGLDADAVDQOQVNTNHNPMWMLLYFISF 1379  
QY 1521 LLIVAFFVLNMFVVVENFHKRQHQBEEARRRERKRLRLEKKRRKAQCKPYYSYDYS 1580  
Db 1380 LLIVSFFVLNMFVVVENFHKRQHQBEEARRRERKRLRLEKKRRKAQRLPYATYC 1439  
QY 1581 RPELLVHLCCTSHYLDLFIITGVIGLVNVTWAMEHYQOQIILDEALKICNYIFTVIFVLES 1640  
Db 1440 HTRLLIHSMTCTSHYLDLFIITICLVNVTWMSLEHYNQPTSLETALKYCNMYFTTVFVLEA 1499  
QY 1641 VFKLVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIAR 1700  
Db 1500 VLKLVAFGLRRFFKDRWNQDLAIIVLLSVMGITLEEIEINAALPINPTIIRIMRVLIAR 1559  
QY 1701 VLKLLKMAVGMRALDVTMQALPOVGNLGLLFFMLFFIFAALGVLEFGDLECDETHPCGE 1760  
Db 1560 VLKLLKMATGMRALDVTVQALPOVGNLGLLFFMLFFIYAALGVLEFGKLVNDENPCGE 1619  
QY 1761 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCVNTV--ISPIYFVSFV 1817  
Db 1620 MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCSLQFVSPLYFVSFV 1679  
QY 1818 LTAQFVLNVVIAVLMKHLEESNKEAKEAELEAELELEM-KTLPSPHSPGLSGPFLWPG 1876  
Db 1680 LTAQFVLNVVAVLMKHLDSDNKEAQEDAENDAELEMAHGLGPGRLPTGSPGA-PG 1738  
QY 1877 VEGDPSD-----SPKPGAL-----HPAABA----- 1897  
Db 1739 -RPGGAGGGDTEGGLCRRCYSPAQDSLEGELTIIDNLGSIFFHYSSPAGCKKCHHDK 1797  
QY 1898 -----RSAS-----HFSLEHPTMQP-----HPTELPGDILLTVRKSG-- 1929  
Db 1798 QEVQLAETEAFLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGEC 1857  
QY 1930 ---VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSQADTSYIQLP 1985  
Db 1858 FFPLSSTAIVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSFSPDASSPLLPMP 1913  
QY 1986 KDAPH-----LLQPHSAPTWGTIPKLPPPG-----RSPLAQRLRQAAIRTDSDVQG 2034  
Db 1914 AEFHHPAVSASOKGPEKGTGTLPKIALQGSWASILRSPRVNCTLLRQATGSDTSLD--- 1970  
QY 2035 LGSREDLLAEVSGSPPLARAYSFVGQSSSTQAOQHSHSRSHSKISKHMTTPPAPCPGPEPNWG 2094  
Db 1971 -----ASPSASSAGSLQTTLEDSTLSDSPRA-----LGPPAPAPGPRAGLS 2012  
QY 2095 KGPPETRSSLDELDTLSWISGDLPPGGQEEPPSPRDLKKCYVEAQSCQRRPTSWLDEQ 2154  
Db 2013 ---PAARRRLSL-----RGRGLFSLRLRA-----HQ 2036  
QY 2155 RRHSIAVSCLDSDGSOPLGTDPN---LGGQPLGGPGSRPKKLSPPSIT---IDPPESQ 2208  
Db 2037 RSHSSGGS-TSPGCTHDSMDPSDEGRGGAGGGAGGAGSEHSETLSSLSLTSFCEPPP--- 2092  
QY 2209 GPRTPPSPGICLRRRAPSSDS----KDPLASGPPDMSMAASPSPKDVLSSLGSSDDPADL 2264  
Db 2093 ---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-----RSKDPFGR 2143  
QY 2265 DP 2266  
Db 2144 AP 2145

GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2188  
; TYPE: prt  
; ORGANISM: Homo sapiens  
US-09-404-650-4

Query Match 46.1%; Score 5484; DB 3; Length 2188;  
Best Local Similarity 51.1%; Pred. No. 0;  
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

QY 31 RPPGSAEKDPSADSEAE-----LPYPALAPVWFFYLSQDSRPSRWCLRTVCNPFERI 86  
Db 25 QGPRSPSPSGLEELDGDADPHVPHDLAPIAFFCLRTQTSRPNWCIKWVCPNPFECV 84

QY 87 SMLVILLNCVTLCGMFRPCEDIACDSQRCILQAFDDFIFAFVAVEMVVKVALGIFGKCC 146  
Db 85 SMLVILLNCVTLCGMYPQCDMDCLSDRCKILQVDFDFIFIFAMEMVVKVALGIFGKCC 144

QY 147 YLGDWTNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLD 206  
Db 145 YLGDWTNRLDFFIVMAGMVEYSLDLQNLNSAIRTVRVLRLKAINRVPSMRILVNLLD 204

QY 207 TPLMLGNVLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPLSVDLERYYQTEDE 266  
Db 205 TPLMLGNVLLCFFVFFIFGIIQVQLWAGLLNRNRCFLEENFTIQGDVALPPYYQPEEDDE 264

QY 267 SPFICSQPRENGWRSRCSVPTRLRGDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318  
Db 265 MPFICSLSGDNGIMGCHEIPLKEQ---GRECCLSKDDVDFGAGRQDLNASGLCVNWNR 321

QY 319 YITNCSAGEHNPFGAINFDNIGYAMIAIFQVITLEGWDMYFVMDAHSFYNFIFILL 378  
Db 322 YINVCRGTSANPHKGAINFDNIGYAMIVIFQVITLEGWVEIMYVMDAHSFYNFIFILL 381

QY 379 IIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNASTLASFSEPGSCYEELLK 438  
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS--SSTVASYAEPGDCYEEIFQ 440

QY 439 YLVYILRKAAARLAQVSRAGVRVGLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH 498  
Db 441 YVCHILRKAKR-----RALGLYQALQSRRQALG----- 468

QY 499 HHHHHYHLGNTLRAPRASPEIQDRDANGSRRLMLPPSPALSGAPPGAESVHSFYH 558  
Db 469 -----PEAPA--PAKPGP-----H 480

QY 559 ADCHLEPVRCAQPPRSPSEASGRITVSGKVYPTVHTSPPPETLKEKALVEVAASSGPPT 618  
Db 481 AK---EPRHYQLCPQHSPLDTPHTL-----VQIPATL----- 511

QY 619 LTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYPAR----- 672  
Db 512 -----ASDPASCPCQCHEDGRRP 529

QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLGPAEPSSVL----- 726  
Db 530 SGLGSTD--SGQEGSGSGSSAGGE--DEADGDGARSSSEDGASSELGKEEEEEQADGAVWL 586

QY 727 --AFWRLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVETS 784  
Db 587 CGDVWRETRAKLRGIVDSKYFNRGINMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS 646

QY 785 LFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKL 844

Db 647 MFALEMILKLAAGFLDYLRNPYNIFDSIIIVISIWEIVGQADGGLSVLRTFRLLRVLKL 706

QY 845 VRFLPALQRLVVLMTMDNVATFCMLLMFLFIFISILGMHLFGCKFASERD-GDTLPDR 903  
Db 707 VRFPALRRQLVVLMTMDNVATFCMLLMFLFIFISILGMHLFGCKFSLRTDGTVPDR 766

QY 904 KNFDSLLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL 963  
Db 767 KNFDSLLWAIWTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL 826

QY 964 VEGFQAEIEISKREDASGQLSCIQLPVDQGGDANKSESEPDFFSPS-----LDGD 1013  
Db 827 VEGFQAE-----GDANRSYDEDDQSSSNIIEEFDKQEGLDSS 863

QY 1014 GDRKKCLALVSLGEHPELRKSLPPLIHTAATPMSLPKSTSTGLGEALGPASRRT---- 1069  
Db 864 GDPKLCPIPMTPNGH-----LDP-----SLPLGGHLGPAGAAGPAPRLSLQPD 906

QY 1070 -----SSSGSAEPGAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLK 1120  
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSSYGPGWGRSAWASRRSSWN-----SLK 960

QY 1121 RRSPPGERRSLLSGE--GOESQDEEESSEE--ERASPAAGSDH-----RHRG 1162  
Db 961 HKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHIIHGHPLAHRHRHRR 1020

QY 1163 SLEREAKSSFDLPDTLQVPLGHLRTASGR--GSASEHQDCNGKSASGLARALRPDDPPLD 1220  
Db 1021 TSLDNRDSDVLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGR 1080

QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFEDH 1280  
Db 1081 GED-EEEDYTLCFRVRKMDIVYKPDWCEVREDWSVYLFSEPNRFRVLCQTIIAHKLFDY 1139

QY 1281 VVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFFEQA 1340  
Db 1140 VVLAFLFLNCITIALERPOIEAGSTERIFLTVSNYIFTAVFVGMTLKVSVSLGLYFGEQA 1199

QY 1341 YLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRPLRVIISRAQGLKL 1400  
Db 1200 YLRSSWNVLDGFLVFSIIDIVVSLASAGGAKILGVLRLRLRPLRPLRVIISRAPGLKL 1259

QY 1401 VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCGQEDTRNITNKSDCAEASY 1460  
Db 1260 VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGFHCLGVDTNRNITNRSDCMAANY 1319

QY 1461 RWVRHKYNFDNLGQALMSLFLVASKDQGWVDIMYDGLDAVGVDQQPIMNHNPMMLLYFISF 1520  
Db 1320 RWVHKYNFDNLGQALMSLFLVASKDQGWVIMYNGLDVAVDQQPVTNHNPMMLLYFISF 1379

QY 1521 LLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRRREEKRLRLEKKRKAQCKPYYSYS 1580  
Db 1380 LLIVSFFVLNMFVGVVVENFHKCRQHQEAEEARRRREEKRLRLEKKRKAQRLPYVATYC 1439

QY 1581 RFRLVHHLCTSHYLDLFTIGVLNVVTMAMEHYQQQIILDEALKICNYIFTVIFVLES 1640  
Db 1440 HTRLIHSMTCTSHYLDIFITFIICLVNVVTMSLEHYNQTSLETALKYCNMFTTFFVLEA 1499

QY 1641 VFKLVAFGFRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIAR 1700  
Db 1500 VLKLVAFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIAR 1559

QY 1701 VLKLLKMAVGMRRALLDTVMQALPQVGNLGLLFFMLFFIFAALGVELFGDLECEDETHPCEG 1760  
Db 1560 VLKLLKMATGMRRALLDTVVQALPQVGNLGLLFFMLFFIYAALGVELFGKLVNDENPCEG 1619

QY 1761 LGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1817  
Db 1620 MSRHATFRNFGMAFLTILFQVSTGDNWNGIMKDTLRDCTHDSRCLSSQLQFVSPLFVSFV 1679

QY 1818 LTAQFVLVNVVIAVLMKHLEESNKEAEAELEAELEEM-KTSLSPQPHSPLGSPFLMPG 1876

Db 1680 LTAQFVLINVVAVLKMHLDDSNKEAQAEDAEMLMAHGLGPGPRPTGSPGA-PG 1738

Qy 1877 VEGPD-----SP-----DSPKPGALH-- 1892

Db 1739 -RPGGAGGGGDETEGGLRRCYSPAENLWLDVSLIIKDSLEGELTIIDNLGSGIFHHY 1797

Qy 1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTPLP 1918

Db 1798 SSPAGCKKHDKQEVQLAETEAFSLNSDRSSILLGGDLSLEDTACPPGRKDSKGELD 1857

Qy 1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMRHGSTABEGLGHRGWGLPKAQSGSVLSVH 1972

Db 1858 PPEPMRVGDLGECFFPLSSSTAVSPDENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSP 1913

Qy 1973 SQPADTSYIILQPKDAPH-----LLQPHSAPTGTIPKLPPLPG-----RSLAQRLRR 2021

Db 1914 FSPDASSPLPMPAEFFHPAVSASQKPEKGTGTGLPKIALQGSWASLRSRPNCTLLR 1973

Qy 2022 QAAIRTDSDVQGLGSRDRELLAEVSGSPPLARAYFWGQSSSTQAQHSRSHSKSKHMT 2081

Db 1974 QATGSDTSLD-----ASPSSAGSLQTTLEDSTLSDSPRA-----LG 2012

Qy 2082 PPAPCPGPEPNWCKGPPETRSSLELDTLSWISGDLPLPGQGEPPSPRDLKKCYVSAEQ 2141

Db 2013 PPAPAGPRAGLS---PAARRLSL-----RGRGLFSLRGLRA- 2047

Qy 2142 SCQRRPTSWLDERRHSIAVCLDSGQPHLGTDPN---LGGQPLGGPGSRPKKLSP 2198

Db 2048 -----HQRSHSSGGS-TSPGCTHDSMDPSDEGRGAGGAGGSEHSETLSSL 2095

Qy 2199 SIT---IDPPESQGPRTPPSPGICLRRRAPSSDS---KDPPLASGPPDMSAASPSKKDV 2251

Db 2096 SLTSLFCPPP-----PPAPGLTPARKFSTSSLAAPGRPHAAALAHGLARSPSWAAD- 2148

Qy 2252 LSLSGLSDDPADLDP 2266

Db 2149 -----RSKDPGGRAP 2158

RESULT 8

US-09-935-541-4

; Sequence 4, Application US/09935541

; Patent No. 6589787

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 2188

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-935-541-4

Query Match 46.1%; Score 5484; DB 4; Length 2188;

Best Local Similarity 51.1%; Pred. No. 0;

Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

Qy 31 .RPGGSAEKDPSADSEAG-----LPYPALAPVVFYFLSQDSRPRSWCLRTVCNPFERI 86

Db 25 QGPRSPSPSPGLEEPLDGADPHVPHPDLPAPFCLRTQTTSPRNWCIMVNCNPFECV 84

Qy 87 SMLVILLNCVTLMGFRPCEDACDSQRCRILQAFDDIPAFPAFVEMVVMVALGIFGKKC 146

Db 85 SMLVILLNCVTLMGYQPCDDMDCLSDRCKILQVDFDIFIFFAMEMVLKMVALGIFGKKC 144

Qy 147 YLGDTWNRLDFFIAGMLEYSLDLQNVFSFAVRTVRVLRPLRAINRVPSMRILVTLLED 206

Db 145 YLGDTWNRLDFFIWMAGMVEYSLDLQINILSAIRTVRVLRLKAINRVPSMRILVNLLED 204

Qy 207 TLPMLGNVLLCCFFVFFIFIGIVGVQLWAGLLRNCFLPENFSLPLSVDLERYQYQTEDE 266

Db 205 TLPMLGNVLLCCFFVFFIFIGIVGVQLWAGLLRNCFLPENFTIQGDVALPPYQPEEDE 264

Qy 267 SPFICSQPRENGMRSCRSVPTLRGDDGGGPPCCGL-----DYAYNSSNTT--CVNNNQ 318

Db 265 MPFICSLSGDNGMGCHIEIPPLKEQ---GRECLSKDDVDYDFGAGRQDLNASGLCVNNNR 321

Qy 319 YYTNCAGEHNPFKAINFDNIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYFIYFILL 378

Db 322 YYNVCRGTGSANPHKGAINFDNIGYAWIVIFQVITLEGVWEIMYVMDAHSFYFIYFILL 381

Qy 379 IIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELK 438

Db 382 IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQYLS-SSTVASYAEPGDCYEEIFQ 440

Qy 439 YLVYILRKAARLQVSRRAAGVRVGLLSPAPLGGQETQPSSSCSRSHRRLSVHHLVHH 498

Db 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468

Qy 499 HHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH 558

Db 469 -----PEAPA--PAKPGP-----H 480

Qy 559 ADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTSPPTLKEKALVEVAASSGPPT 618

Db 481 AK---EPRHYQLCPQHSPLDAPHTL-----VQPIPATL----- 511

Qy 619 LTSLNIPPGPYSSMHKLELTQSTGACQSSCKIISPCLKADSGACGPDSCPYCAR----- 672

Db 512 -----ASDPASCPCCQHEDGRRP 529

Qy 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVL----- 726

Db 530 SGLGSTD-SGQEGSGSGSAGGE--DEADGDGARSEDGASSELGKEEEEEQADGAVWL 586

Qy 727 --AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 784

Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPEELTNIILEICNVFTS 646

Qy 785 LFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKL 844

Db 647 MFALEMLLKLAAFGFLDYLRPNYIFDSIIIVISWEIVGQADGGLSVLRTFRLLRVLKL 706

Qy 845 VRFLPALQRLVVLMTKMDNVATFCMLLMFLFIFISILGMHLFGCKFASERD-GDTLPDR 903

Db 707 VRFPALRRQLVVLMTKMDNVATFCMLLMFLFIFISILGMHIFGCKFSLRTDGTVPDR 766

Qy 904 KNFDSLILWAIVTVFQILTQEDWNKVLYNGMASTSSWAALFYALMTFGNYVLENLLVAIL 963

Db 767 KNFDSLILWAIVTVFQILTQEDWNKVLYNGMASTSPWASLYFVALMTFGNYVLENLLVAIL 826

Qy 964 VEGFQAEIISKREDASGQLSCIQLPVDQSQGDANKSESEPDPFFSPS-----LDGD 1013

Db 827 VEGFQAE-----GDANRSYDDEDQSSNIEEFDKLEGLDSS 863

Qy 1014 GDRKKCLALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGEALGPASRRT---- 1069

Db 864 GDPKLCPIPMTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRLSLQPD 906

Qy 1070 -----SSSGSAEPGAHEMKSPPSARSSPHSPWSAASSWTSSRRSSRNSLGRAPSLK 1120

Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYYGPGWGRSAAWASRRSSWN-----SLK 960

Qy 1121 RRSPPSGERRSLSGE-GQESQDEEESSEE--ERASPAQSDH-----RHRG 1162

Db 961 HKPPSAEHESLLSAERGGGARVCEVADEGPPRAAPLHTTHAHHHGPHLAHRHRHRR 1020

Qy 1163 SLEREAKSSFDLPDTLQVPLGHLRTASGR--GSASEHQDCNGKSASRLARALRPDDPPLD 1220





Db 478 ---HAK---EPHCKLCPRHSPLD-----PTPHTLVQP----- 504

QY 615 GPPTLTSLNIPPGPYSSMHKLETTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-- 672

Db 505 -----ISAILASD-----PSSCPHCHEA 523

QY 673 ----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGDAEPSSVLA- 727

Db 524 GRRPSGLGSTD-SGOEGSGGGSABAEANGDG---LQSSDGVSSDLGKEEEOEDGAAR 578

QY 728 ----FWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALISNIVFT 783

Db 579 LCGDVWRETRKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFT 638

QY 784 SLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIIVISVWEIVGQGGGLSVLRTFRLMRVLK 843

Db 639 SMFALEMILKLAAGFLDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLMRVLK 698

QY 844 LVRELPALQRLVVLVMTMDNVATFCMLLMFIFIFISILGMHLFGCKFASERD-GDTLPD 902

Db 699 LVREMPALRRQLVVLVMTMDNVATFCMLLMFIFIFISILGMHIFGCKFSLRTDGTVPD 758

QY 903 RKNFDSLLWAIIVTFQILTQEDWNKVLNMGMASTSSWAALYFIALMTFGNVYVFLNLLVAI 962

Db 759 RKNFDSLLWAIIVTFQILTQEDWNVVLNMGMASTTPWASLYFVALMTFGNVYVFLNLLVAI 818

QY 963 LVEGFOAEIISKREDASQLSCIQLPVDSQGDANKSESEDPFFSPS-----LDG 1012

Db 819 LVEGFOAE-----GDANRSCSDEDDQSSNLEEFKLPGLDN 855

QY 1013 DGDRKKCLALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071

Db 856 SRDLKLCPIPMTPNGH-----LDP-----SLP-----LGAHLGPAGTMGTAP 892

QY 1072 SGSAEPG-----AAHEMKSPPSARSSPHSPWSAASSWTSRRSRNSL 1113

Db 893 RLSLQPDVPLVALDSRKSSVMSLGRMSYDQRLSSSRSSYYGPWGRSGTWASRRSSWN-- 950

QY 1114 GRAPSLKRRSPSGERRSLLSGEGQESQDEE-ESSEEE---RASPAQSDH----- 1158

Db 951 ----SLKHKPPSAEHESLLSGEGGSCVRACEGAREEAPTRAPLHAPHAHHAHPHLA 1006

QY 1159 ----RHGSLEREAKSFDLPDTLQVPGHLRTAS--GRGSASEHQDCNGKSASGLARAL 1212

Db 1007 HRHRHRRRTLSLDRDSVDLDELVPVVGASRAAWRGAGQAPGHEDCNGRMPNIAKVFT 1066

QY 1213 RPDDPPLDGDDADDEGNLSKGERVAVIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI 1272

Db 1067 KMDRRDRGED-EEEDYTLCFVRKMDIVYKPDWCEVREDWSVYLFSPENKFRILCQTI 1125

QY 1273 ITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1332

Db 1126 IAHKLFYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVS 1185

QY 1333 GWCFFEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGLMLRVLRLRLTLRLRVI 1392

Db 1186 GLYFGEQAYLRSSWNVDGLFVFSIIDIVSVASAGGAKILGLVLRVLRLLTLRLRVI 1245

QY 1393 SRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK 1452

Db 1246 SRAPGLKLVVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGKFFHCLGVDTNRITNR 1305

QY 1453 SDCAEASRWRVHKYNFNLQALMSLFLVASKDGVVDIMYDGLDAVGDQOQPMHNHPW 1512

Db 1306 SDCVAANYRWVHKYNFNLQALMSLFLVASKDGVWNIMYNGLDVAVDQOQPVTHNHPW 1365

QY 1513 MLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHQEAEARRRREKRLRRLEKRRKAQC 1572

Db 1366 MLLYFISFLLIIVSFFVLNMFVGVVVENFHKCRQHQEAEARRRREKRLRRLEKRRKAQR 1425

QY 1573 KPYVSDYSRFRLLVHLCCTSHYDLFITIGVGLNVVTMAMEHYQQQILDEALKICNYIF 1632

Db 1426 LPYVATYCPTRLIIHSMCTSHYDLFITFIICLNVVTMSLEHYNQPTSETALKYCNYMF 1485

QY 1633 TVIFVLESVFKLVAFGRFFQDRWNQDLAIVLLSIMGITLEIEVNASLPINPTIIRI 1692

Db 1486 TTTFVLEAVLKLAFGLRRFFKDRWNQDLAIVLLSVMGITLEIEINAALPINPTIIRI 1545

QY 1693 MRVLRIRAVLKLKMAVGMRALLDVTVMQALPOVGNLGLLMLFFIFAALGVELFGDLEC 1752

Db 1546 MRVLRIRAVLKLKMAVGMRALLDVTVMQALPOVGNLGLLMLFFIFAALGVELFGKLV 1605

QY 1753 DETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS 1809

Db 1606 NDENPCEGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCLSSQLQFVS 1665

QY 1810 PIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAEAELEAELEEM-KTILSPQPHSPL 1868

Db 1666 PIYFVSFVLTAQFVLNVVIAVLMKHLDSDNKEAQAEDAEMDAEIELEMAHGLGPCP--- 1721

QY 1869 GSPFLWPVGEGPDSPPKPGALHPAAHARSASHFSLEHPTMQPHTELPGPDLLTV--- 1925

Db 1722 -----GPCPG-----PCPCPCPCPCAGPRLPTSSPG 1747

QY 1926 ---RKSQSVRTHSLPNDSYMCRH 1945

Db 1748 APGRSGGAGAGG-DTESHLCRH 1769

RESULT 10

US-09-935-541-5

; Sequence 5, Application US/09935541

; Patent No. 6589787

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-935-541-5

Query Match 45.1%; Score 5366; DB 4; Length 1835;

Best Local Similarity 56.8%; Pred. No. 0;

Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;

QY 27 GAGGRPGSGSAEKDPGSADSEAG---LPYPALAPVVFYLSQDSRPSRWCURTVCPNW 82

Db 19 GITEQGPGRSPSPPPGLEEPLGEGTNPDPVHPDLAPVAFCLRQTTSPRNWCIKMWCPNW 78

QY 83 FERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIAPFAVEMVVMVALGIF 142

Db 79 FECVSMVLILLNCVTLMGYQPCDDMECLSDRCKILQVDFDIFIFFAMEMVLKMWALGIF 138

QY 143 GKCYLGDWTNRLDFFIVIAAGMLEYSLDLQNVFSAVTRVRLPLRPLRINRVPSMRILVT 202

Db 139 GKCYLGDWTNRLDFFIVMAGMVEYSLDLQNLNLSAIRTVRLPLKAINRVPSMRILVN 198

QY 203 LLLDTLPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVLERYQTE 262

Db 199 LLLDTLPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFTIQGDVALPPYQPE 258

QY 263 NEDESPFICSPRENGMRSRCSVPTRLRGDGGGPPCGL-----DYEAYNSSNTT--CV 314

Db 259 EDEMPFICSLTGDNGIMGCHIEIPLKEQ---GRECCLSKDDVYDFGAGRQDLNASGLCV 315

QY 315 NWNQYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNYFI 374





Db 85 KYAKRITWPPFEYMLATILIANCIVLAL-----EQLPDGDKTPMSERLDDTEPYFIGI 140  
QY 128 FAVEMVVMVALG-IFGKKCYLGDWNRLLDFFIVIAWLEYS--LDLQNVSFSAVRTVR 183  
Db 141 FCFEAGIKIALGFVFKGSLRNGWNVDMFVVVLGTILATAGTDFDLR-----TLRAVR 195  
QY 184 VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNCFL 243  
Db 196 VLRPLKLVSGIPSLQVLKSIKAMVPLLIQIGLLFFAILMFAIIGLEFYMGKFHKA CF- 254  
QY 244 PENFSLPLSVDLERYYYQ TENEDESPFCISQPRENGMRSRVSPTLRGDCGGGPPCGLDYE 303  
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273  
QY 304 AYNSSNTTCVNMNQYNTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363  
Db 274 ARLCEDTEC-----REYWP-----GPNFGITNFDNILFAILTVFQCITMEGWDILYNT 323  
QY 364 MD-AHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKORES-----QLMREQRVRF 416  
Db 324 NDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLSEFAKERERVENRRAFLKLRQQOIE- 382  
QY 417 LSNASTLASFSEPGSCYEELLYLVLIRKAARRLAQVSRAGVRVGLLSSPAPLGGQET 476  
Db 383 -----RELNGYLEWIFPKAEVMLAEEDRNA-----EEK 410  
QY 477 QPSSSCSRSHRRLSVHHLVHHHHHHHHLNGTLRAPRASPEIQDRDANGSRRLMLPP 536  
Db 411 SPLDVLKRAATKKSRLDLI-----ABEGEDRFAD-----440  
QY 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSKVYPTVHTS 596  
Db 441 -----440  
QY 597 PPPETLKEKALVEVAASSGPPTLTSLNIPGPYSSMHKLETOSTGACQSSCKISSPCLK 656  
Db 441 -----LCAVGSPEAR 450  
QY 657 ADGACGPDPCPYCARACAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS 716  
Db 451 ASLKGKTESSESYFR-----KEKMR-----473  
QY 717 GPDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMIALVNTLSMGLEYHEQPEELTNALE 776  
Db 474 -----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTY 515  
QY 777 ISNIVFTSLFALEMLKLVGPPFYIKNPNYIFDGVIVIVISWEIVGQ-----QGGGLS 831  
Db 516 FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFCDFGVIVGSVFVWAAIKPGSSFGIS 575  
QY 832 VLRTFRIMRVLKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLIFISILGMHLFGCKF 891  
Db 576 VLRALRLRIFKVTKYWSSLRNLVWSLLNSMKSISLLFLFLFVIVV FALLGMQLFGGQF 635  
QY 892 ASERDGDTLPRKNFDSLWAIWTVVFOILTQEDWNKVLYNGM-----ASTSSWAALYFIA 946  
Db 636 NFQDETPT-----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGVSKGMFSSFYFIV 691  
QY 947 LMTFGNYVFLNLLVAILVEGF-QAEEISK-----REDASGQ-----LSCIQ 986  
Db 692 LTLFGNYTLNVFLAIAVDNLANAQELTKDEEEMEEAANQKALQAKEVAEVSMPMAAN 751  
QY 987 LPVDSQGGDANKSESEPDFFSILDGDGDRKKCLALVSLGE-----HPELRK 1033  
Db 752 ISIAARQONSAKARSVWEQASQLRQLNLRASCEALYSEMDPEERLRFATRHRLRPDMKT 811  
QY 1034 SLLPPLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSSG-----1073  
Db 812 HLDRLVLVLRDGDGARGPVGGKARPEAAEAPGVDPPRRHHRDKDKTPAAGDQDRAEA 871  
QY 1074 -----SAEPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW 1103

Db 872 PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGEGRRHRRGSPPEAAERE 931  
QY 1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLS GEGQESQDEHEESSEE-----ERASP- 1153  
Db 932 PRRHRAHRH---QDPSKECAGAKGERRARHRRGGPRAGPREAESGEEPARRHRAHKAQPA 988  
QY 1154 -----AGSDHRRHRSGLEREAKSSFDLPD TLQVPLGHLRTASGRG 1191  
Db 989 HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGT VTPGPMHTLPSTCL 1048  
QY 1192 SASEHQDCNGKSASRLARALRPDDP-----PLDGDADDEGNL-----SKGE 1234  
Db 1049 QKVEEQPEDADNQNRNVTMGSPQPPDNTIVHIPVMLTGPLGEATVVP SGNVLDLESQAEGK 1108  
QY 1235 R-----VRAMIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHVVLVIF 1287  
Db 1109 KEVEADDVMRSRGPPIVPYS-----SMFCLSPTNLLRRFCHYIVTMYFEVVILVIA 1161  
QY 1288 LNCITIAMERPKIDPHSAERIFLTLNYYITAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347  
Db 1162 LSSIALAAEDP-VRTDSPRNALKYLDYFTGVFTFEMVIKIMIDGLLLHPGAYFRDLWN 1220  
QY 1348 VLDGLLVLSVIDI-LVSMVSDSGTKILGLMLRVLRLLRPLRVISRAQGLKLVVETLM 1406  
Db 1221 ILDFIVVSGALVAFAPSSVFGSGKGDINTIKSLRVLRLPLKTLKRLPKLKAVFDCVV 1280  
QY 1407 SSKKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQE-----DTRN--ITNKSDCAEA 1458  
Db 1281 NSLKNVLNLIIVYMLFIFAVIAVQLFKGKFFCYCTDESKELERDCRGQYLDYEKEEVEA 1340  
QY 1459 SYR-WVRHKYNFDNLGOALMSLFLVASKDGVVDIMYDGLDVGVDQQPI MNHNPMWLLYF 1517  
Db 1341 QPRQWKYDFHYDNVLWALLTLFTVSTGEGVMVLKHSVDATYEEQGPSGPMELSI FY 1400  
QY 1518 ISFLLI VAFVFLNMFVGVVVENFHKCRHQHEEEARRRREKRLRLEKKRKA-----QC 1572  
Db 1401 VVYFVFPFFFFVNFVALIITF-----QEQGDKVMSE---CSLEKNERACIDFAISA 1450  
QY 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKIC 1628  
Db 1451 KPLTRYMPQNRQSFQYKWTWVVSPPFEYFIMAMIALNTVLMKFDAPY EYELMLKCL 1510  
QY 1629 NYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAI VLLSIMGITLEEI-EVNASLPINP 1687  
Db 1511 NIVFTSMFSMECVLKI AFGVLNVFRDANWVDFVTVLG SITDILVTEIAETN-----NF 1565  
QY 1688 TIIRIMRVLRIARVLKLLKMAVGMRALLDVTVMQALPQVGNLGLL FMLFFIFAALGVLEF 1747  
Db 1566 INLSFLRLFRAARLIKLLRQGYTIRILLTWTVQSFALPYVCLLIAMLFFIYAI GMQVF 1625  
QY 1748 GDLECDETHPCGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRD--CDQE--STC 1803  
Db 1626 GNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1682  
QY 1804 YNTVISPIYFVSFVLTAQFVLNVVIAVLM-----KHLEE-----1838  
Db 1683 CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1742  
QY 1839 -----1838  
Db 1743 AACGRISYNDMFEMLKHMSPPPLGLKKCPARVAYKRLVRNMNPI SNEDMTVHFTSTLMAJ 1802  
QY 1839 -----SNKEAKEAEAELEEMKTLSPQHSPLGSPFLWPVGEGDSDSP 1886  
Db 1803 IRTALEIKLAPAGTKHQHCDALRKEISVVWANL-PQKTLDLLVP-----PHKPEM 1853  
QY 1887 KPGALHPA-----AHARSASHFSLEHPTM---QPHPTLPGLPD 1921  
Db 1854 TVGKVAALMIFDYKQNKTRDQMOQAPGLSQMGVSLFPHLPKATLEQTQPAVLRGAR 1913  
QY 1922 LLTVRKSGVSRTHSLPNDSYMCRCRHSFAGPLGHRGWGLPKAQSGSVLSVHSQPADTSYI 1981  
Db 1914 VFLRQKSSSTSLN-----GGAIQNESGIKESV-----SWG 1944

QY 1982 LQLPKDAPHLLQP-----HSAPTWTGTPKLPPLPPGRSPLAQRLRRQAAIR-----TDS 2029  
Db 1945 TQRTQDAPHEARPPLERGHSTEI-----PVGRSGALAVDVQMOSITRRGPDGEQPG 1996  
QY 2030 LDVQGLSREDLLAEVSGP---SPPLARAYFWGQSSTQAQOHSRSHSKISKHMTTPAPC 2086  
Db 1997 LESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPRGTHLCST---TPDRPP 2047  
QY 2087 PG-----PEPNWGKPPETRRSSLELDTLSWISGDLPLPPGGQEEPPSP 2129  
Db 2048 PSQASSHHHRRCHRRDRKQSRLEKGP---SLSADMDGAPSSAVGGLPPG---EGPTGC 2102  
QY 2130 RDLKCYSEVAQSCQRR-PTSWLDEQRRHSIAVSCLDG-----SQPHLG 2173  
Db 2103 RRERRRQERGRSQRRQPSSSSSEKQRF---YSCDRFGGREPPKPKPSLSHPTSPTAG 2159  
QY 2174 TDP-----SNLGGQPL-----GGGSRPKKKLSP-PSITI-----DPESQG 2209  
Db 2160 QEPGPHQSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITYKTANSSPIHFAG 2219  
QY 2210 PRT--PP-SPG-----ICLRRRAPSSDSKDPLASGPPDSMAASPPKDVLSLGL 2257  
Db 2220 AQTSLPAFSPGRLSRGLSEHNALLQRDPLS---QPLAPG-----SRI 2258  
QY 2258 SSDP 2261  
Db 2259 GSDP 2262

RESULT 12

US-08-713-118-2  
; Sequence 2, Application US/08713118  
; Patent No. 6040436  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2337 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-713-118-2

Query Match 14.7%; Score 1749; DB 3; Length 2337;

Best Local Similarity 24.3%; Pred. No. 3.5e-133;  
Matches 645; Conservative 359; Mismatches 832; Indels 820; Gaps 86;  
QY 14 GQPRSFMRNLDSGAGRPGPGSAEKDPGSDADSEAEGLYPALAPVVF----- 61  
Db 13 GPGGGERARG-GGAGGAGGPGGLQPGQRLVKQSIQARTMALYNPIPVKQNCFTV 71  
QY 62 ----FYLSDSRPRRWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIACDSQRCRIL 117  
Db 72 NRSLFVSEDNVVRKYAKRITWPPPEYMLATIANCIVLAL-----EQHLPDGDKTPMS 127  
QY 118 QAFDD---PIFAFFAVEMVMVMVALG-IFGKKCYLGDWNRDLDFVIVAGMLEYS---LD 170  
Db 128 ERLDDTEPYFIGFCFEAGIKIIALGFVFKGSLRNGWNWMDFVVVLTGILATAGTDFD 187  
QY 171 LQNVFSAVRTVRLPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGV 230  
Db 188 LR-----TIRAVRVLRLKLVSGIPSLQVVLKIMKAMVPLLIQIGLLFFAILMFAIGL 242  
QY 231 QLWAGLLNRNRCFLPENFSLPLSDLERYYYQTENEDESPFICSPRENGMRSCRSVPTLRG 290  
Db 243 EFYMGKFHKACF-----PNSTDAE-----PV--- 263  
QY 291 DGGGPPCGLDYEAYNSSNTTCVNMNQYTNCSAGEHNPKGAINFDNIGYAWIAIFQV 350  
Db 264 ---GDFPCGKEAPARLCEGTEC---REYWP-----GNPFGITNFDNIFALTVPQC 310  
QY 351 ITLEGWVDIMYFVMD-AHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRES--- 406  
Db 311 ITMEGTDILYNTNDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENRR 370  
QY 407 ---QLMREQVRFLSNASTLASFSEPGSCYEELLYVILRKAARRLAQVSRAAGVRVG 463  
Db 371 AFLKLRQQQIE-----RELNGYLEWIFKAEVMLAEEDRNA----- 407  
QY 464 LLSSPAPLGGQETQPSSSCSRSHRRLSVHLLVHHHHHHHHHGLNGTLRAPRASPEIQD 523  
Db 408 -----EEKSPLDVLKRAATKKSRNDLIH-----AEEGED 436  
QY 524 RDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVRVCQAPPPRSPSEASGRT 583  
Db 437 READ----- 440  
QY 584 VSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTQSTGA 643  
Db 441 ----- 440  
QY 644 QSSCKISSPCLKADSGACPDSPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHS 703  
Db 441 ---LCAVSPFARASLKSGETESSYFRR-----KEKMFRE----- 473  
QY 704 DLDRPHRRQRSGLPDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIE 763  
Db 474 -----FIRRMVKAQSFYVWVLCVVALNTLCVAMV 502  
QY 764 YHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIV 823  
Db 503 HYNQPRRLTTLTYFAEFVFLGLFTEMSLKMYGLPSPRSYFRSSFCDFGVIVGSVFEVV 562  
QY 824 GQ-----QGGGLSVLRTFRLMRVLKLVRLPALQRLVVLMTMDNVATFCMLMLFIFI 878  
Db 563 WAAIKPGSSFGISVLRALRLRLRIFKVTKYWSSLRLNLVSLNSMKSIISLLFLFLFIVV 622  
QY 879 FSILGMHLFGCKFASERDGTDLDRKNFDSLWAIIVTVFOILTQEDWNKVLNYGM----- 933  
Db 623 FALLGMQLFGGQFNQDETPT-----TNFDTPAAILTVEQILTGEDWNAVMYHIESQGG 678  
QY 934 ASTSSWAALYFIALMTFGNVLENLLVAILVEGF-QAEIESK-----REDASGQ----- 981  
Db 679 VSKGMFSSFYFIVLTLFGNTLLNVFLAIVDNLANAQELTKDEEEMEEAANQKALQKA 738  
QY 982 -----LSCIQLPVDSDQGGDANKSESEPDFFPSPLDGDGDRKKCLALVS----- 1024

Db 739 KEVAEVSMSAANISIAARQNSAKARSVWEQASQLRLQNLRASCEALYSEMDPEERLR 798  
QY 1025 -----LGEHDELKSLPLIHTAATPMSLP-----KSTSTGLGEALGPASR----- 1067  
Db 799 FATTHRRPDMKTHLDRPLVVELGRDARGPVGGKARPEAAEAPEGVDPPRRHHRDKD 858  
QY 1068 RTSSSG-----SAEPGA-----AHMKSPPSARS-----SPH----- 1094  
Db 859 KTPAAGDQDRAEAPKAESGEPGAREERPRPHRSHSKAAGPPEARSERGRGPGEGGRRH 918  
QY 1095 -----SPWSAASWTSR-RSSRNLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEE- 1148  
Db 919 HRRGSPEEAEREPRRHRHRH-----QDPSKECAGAKGERRARHRRGGPRAGPRAESGEEP 975  
QY 1149 -----ERASP-----AGSDHHRGSLEREAKSFDLPDTL 1178  
Db 976 ARHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTV 1035  
QY 1179 QVPLHRTASGRGSASEHQDCNGKSASGLARALRPDDP-----PLDGDADD 1226  
Db 1036 TVGPMHTLPSTCLQKVEEQPEDADNQRNVRMGSPQDPDNTIVHIPVMLTGPLGEATVVP 1095  
QY 1227 EGNL-----SKGER-----VRAMIRARLPACYLERDSWASAYIFPPQSRFRLLCHRIIT 1274  
Db 1096 SGNVDLESQAEGKKEVEADVMRSGRPPIVPS-----SMFCLSPTNLLRRFCHYIVT 1148  
QY 1275 HKMFDHVVLVILFNCITIAMERPKIDPHSAERIFLTLSNVIPTAVFLAEMTKVVALGW 1334  
Db 1149 MRYFEVILVIALSSIALAAEDP-VRTDSPRNALKYLDYFTGVFTFEMVIKIDLGL 1207  
QY 1335 CFGEQAYLRSSWNVDGLLVLSVIDILVMV-SDSGTKILGMLRVLRLRLTLRLRVLIS 1393  
Db 1208 LLHPGAYFRDLWNILD-----FIVVSGALVAFAPSGSGKGDINTIKSLRVLRLPLKTIK 1263  
QY 1394 RAQGLKLVETLMSSLKPIGNIVVICCAFFIIFGILGVOLFKEFFVCOGE-----DTR 1447  
Db 1264 RLPKLVAVFDCVNSLKNVLNIIIVYMLFEMFIFAVIAVOLFKEFFYCTDESKELERDCR 1323  
QY 1448 N--ITNKSDCAEASR-WVRHKYNFNLGOALMSLFLVASKDQWVDIMYDGLDAVGVDQO 1504  
Db 1324 QOYLDYEKEEVEAQPRQWKKYDFHYDNVLMALLTLFTVSTGEGPMVLKHSVDATYEEQG 1383  
QY 1505 PIMNHNPMWLLYFISFLIVAFVFLNMFGVVVENFHKCRHQHEEEAARRREKRLRLE 1564  
Db 1384 PSPGYRMELSIYVYVVFVVFVFFVFNIFVLIITF-----QEQDKVMSE-----CSLE 1433  
QY 1565 KKRKA-----QCKPY--YSDYSR--FRLVHHLCTSHYLDLFTGVIGLVNVTWAMEHY 1615  
Db 1434 KNERACIDFAISAKPLTRYMPQNRQSFQYKWTWVFWSPPEYFIFAMIALNTVLMKPY 1493  
QY 1616 QOQOILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQLDLAIVLLSIMGITLE 1675  
Db 1494 DAPYEYELMKCLNIVFTSMFSMECVLKIIFAGVNLVFRDAMNVDFVTVLGSITDILVT 1553  
QY 1676 EIEVNASLPINPTIIRIMRVLRIARVLKLMKMAVGMRALLDVTVMQALPQVGNLGLLMLL 1735  
Db 1554 EIANNF---IN---LSFLRLFRAARLIKLRQGYTIRILLTTFVQSFKALPYVCLLIAML 1607  
QY 1736 FFIFAALGVLEFGDLECDETHPCGLGRHATERNFGMAFLTFLRVSTGDNWNGIMKDTLR 1795  
Db 1608 FFIYAIIGMQVFGNIALDDD---TSINRHNFRFTLOALMLLFRSATGEAWHEIMLSCLS 1664  
QY 1796 D--CDQE--STCYNTVISPIYFVSFVLTAQFVLNVVIAVLM-----KHL 1836  
Db 1665 NQACDEQANATECGDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEXLTRDSSILGPHHL 1724  
QY 1837 EE----- 1838  
Db 1725 DEFIRVWAEYDPAACGRISYNDMFEMLKHMSPLGLGKKCPARVAYKRLVRMNPISNED 1784  
QY 1839 -----SNKEAKEAELEAELEMLEMKTLSQPSPHSPGLSPFLW 1874  
Db 1785 MTVHFTSTLMALIRTALEIKLAPAGTKHQHQCDAELRKEISVVWANL-PQKTLDLLVP--- 1840

QY 1875 PGVEGPDSPDSPKPGALHPA-----AHARSASHFSLEHPTM--- 1910  
Db 1841 -----PHKPDGMTVGVYAAALMIFDFYKQNKTTTRDQMQAQPGGLSQMGVPVSLFHLKATL 1895  
QY 1911 -QPHPTLPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLHGRWGLPKAQSGSVL 1969  
Db 1896 EQTPAVLRGARVFLRQKSSLSLN-----GGAIONQESGIKE 1933  
QY 1970 SVHSQPADTSYILQPKDAPHLLQP-----HSAPTWTGTIPKLPSPGRSPLAQRPLRQAA 2024  
Db 1934 SV-----SWGTQRTQDAPHEARPPLERGHSTEI-----FVGRSGALAVDVQMOSI 1978  
QY 2025 IR-----TDSLVOGLGSRREDLLAEVSGP---SPPLARAYSFWQSSTQAQOHSRSHS 2074  
Db 1979 TRRGPDGEPQGLSQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPGRGTHL 2032  
QY 2075 KISKHMTPPAPCPG-----PEPNWGKPPPETRSSLELDTLSWISGDL 2117  
Db 2033 CST---TPDRPPPSQASSHHHHRCHRRDRKQRSLEKGP---SLSADMDCAPSSAVGPG 2086  
QY 2118 LPPGQEEPPSPRDLKKCYSVEAQSCORR-PTSWLDEQRRHSIAVSCLDG----- 2167  
Db 2087 LPPG-EGPTGCRERRERQERSRSQERRQPSSESSEKQRF---YSCDRFGGREPPKPKP 2141  
QY 2168 -----SQPHLGTD-----SNLGGQPL-----GGPGSRPKKLSLSP-PSITI 2202  
Db 2142 SLSSHTSPTAGQEPGPHQSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITY 2201  
QY 2203 -----DPPEOQPRTP-PP-SPG-----ICLRRRAPSSDSKDPLASGPPDSMAASP 2245  
Db 2202 KTANSSPIHFAGAQTSLPFSPGRLSRGLSEHNALLQDPLS---QPLAPG----- 2249  
QY 2246 SPKDVLSLGLSSDP 2261  
Db 2250 -----SRIGSDP 2256

RESULT 13

US-09-452-007-2  
; Sequence 2, Application US/09452007  
; Patent No. 6140485  
; GENERAL INFORMATION:  
; APPLICANT: Franco, Rodrigo  
; APPLICANT: Sun Chen, Ai Ru  
; APPLICANT: Suey, David J.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/452,007  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,118  
; FILING DATE: 16-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mata, Elizabeth W.  
; REGISTRATION NUMBER: 38,236  
; REFERENCE/DOCKET NUMBER: ACC96-01  
; TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 617-861-6240  
/ TELEFAX: 617-861-9540  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 2337 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-09-452-007-2

Query Match 14.7%; Score 1749; DB 3; Length 2337;  
Best Local Similarity 24.3%; Pred. No. 3.5e-133;  
Matches 645; Conservative 359; Mismatches 832; Indels 820; Gaps 86;

QY 14 QPGRSFMRNLDSGAGRPGPGSAEKDPGSADEGLPYPALAPVVF----- 61  
Db 13 GPGGGERARG-GGAGGAGGPGGGLQPGQVRVLYKQSIARARTMALYNPIPVKQNCFTV 71

QY 62 ----FYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMFRPCEDIACDSQRIL 117  
Db 72 NRSLFVSEDNVVRKYAKRITETWPPPEYMILATIANCIVLAL----EQHLPDGDKTPMS 127

QY 118 QAFDD---FIFAFVAVEMVVKMALG-IFGKCYLGDVTNRLDFFIVIAGMLEYS---LD 170  
Db 128 ERLDDTEPYFIGFCEAGIKIIIALGFVPHKGYLRNGWNVMDFVVVLTGILATAGTDFD 187

QY 171 LQNVFSAVRTVRVLRPLRAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGV 230  
Db 188 LR-----TLRAVRVLRPLKLVSGIPSLQVVLKSIKAMVPLLIQIGLLFFAILMFAIGL 242

QY 231 QLWAGLLRNRCFLPENFSLPSVLDLERYYYQTENEDESPFICQPRENGMRSCRSVPTLRG 290  
Db 243 ERYMGKFHKACF-----PNSTDAE-----PV--- 263

QY 291 DGGGPPCGLDYAYNSSNTTCVNNWQYNTCSAGEHNPFGAINFDNIGYAWIAIFQV 350  
Db 264 ---GDFPCGKEAPARLCEGDTEC---REYWP-----GPNFGITNFDNIFAILTVFQC 310

QY 351 ITLEGWVDIMYFMD-AHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRES--- 406  
Db 311 ITMEGWTDLIYNDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENRR 370

QY 407 ---QLMREQRVFLSNASTLASFSEPGSCYEELLYVILRKAARRLAQVSRAAGVRVG 463  
Db 371 AFLKLRQQOIE-----RELNGYLEWIFKAEVVMLEEDRNA----- 407

QY 464 LLSSPAPLGGQETQPSSSCSRSHRRLSVHVLVHHHHHHHHYHLNGTGLRAPRASPEIQD 523  
Db 408 -----EEKSPDLVLKRAATKKSNDLIH-----AEEGED 436

QY 524 RDANGSRRLMLPPPSTPALSGAPPGGABSVHSFYHADCHLEPVRCQAPPPRSPSEASGRT 583  
Db 437 RFAD----- 440

QY 584 VSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPGPYSSMHKLLETQSTGA 643  
Db 441 ----- 440

QY 644 QSSCKISSPCLKADSGACGPDSCPYCAPAGAGEVELADREMPDSDSEAVYEFTQDAQHS 703  
Db 441 ---LCAVGSPPFARASLKSCKTESSESYFR-----KEKMFRE----- 473

QY 704 DLRDPHSRRQRSGLGDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIE 763  
Db 474 -----FIRRMVKAQSFYVWVLCVVALNTLCVAMV 502

QY 764 YHEQPEELTNALETGNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIV 823  
Db 503 HYNQPRRLTTTLYPAEFVFLGLFTLEMSLQWYGLGPRSYFRSSPNCDFGVIGSVFEV 562

QY 824 GQ-----QGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMLEIFI 878  
Db 563 WAAIKPGSSFGISVLRALRLRLRIFKVTKYWSSLRNLVSVLLNSMKSIIISLLFLFLFIVV 622

QY 879 FSILGMHLFGCKPASERDGTLPDRKNFDSLLWAIYTVFQILTQEDWNKVLYNGM----- 933  
Db 623 FALLGMQLFGGQNFQDETPT-----TNEDTFPAAILTVFQILTGEDWNVAMVHGIESQGG 678

QY 934 ASTSSWAALYFIALMTFGNYVLFNLLVAILVEGF-QAEEISK-----REDASGQ----- 981  
Db 679 VSKGMFSSFYFIVTLTFLGNYTLLNVLFLAIVADNLANAQELTKDEEEMEAAQNKLALQKA 738

QY 982 -----LSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCLALVS----- 1024  
Db 739 KEVAEVSPTSAAANISIAARQQNSAKARSWEQASQLRLQNLRASCEALYSEMDPEERLR 798

QY 1025 ----LGEHPELRKSLPLPLIIHTAATPMSLP-----KSTSTGLGEALGPASR----- 1067  
Db 799 FATTRHRRRPMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHRHRDKD 858

QY 1068 RTSSSG-----SAEPGA-----AHMKSPSPARS-----SPH----- 1094  
Db 859 KTPAAGDQDRAEAPKAESGEPGAREERPRPHRSHSKEAAGPEARSEGRGPGPEGGRRH 918

QY 1095 ----SPWSAASSWTSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEEESSEE- 1148  
Db 919 HRRGSPEEAAREPRRHRHRH---QDPSKECAGAKGERRARHRRGGPRAGPREAESGEEP 975

QY 1149 -----ERASP-----AGSDHRHRCGLEREAKSSFDPDLPTL 1178  
Db 976 ARHRARHKAQPAHEAVEKETTEKEATEKEAEIIVEADKEKELRNHQPREPHCDLETSGTV 1035

QY 1179 QVPLHRTASGRGSASEHQDCNGKSASGRALARALRPDDP-----PLDGDADD 1226  
Db 1036 TVGPMHTLPSTCLQKVEEQPEDADNQNRNVRMGSPQPPDNTIVHIPVMLTGPLGEATVVP 1095

QY 1227 EGNL-----SKGER-----VRWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIIT 1274  
Db 1096 SGNVDLESQAEGKKEVEADDVMRSGRPPIVPS-----SMFCLSPTNLLRRFCHYIVT 1148

QY 1275 HKMFDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIPTAVFLAEMTVKVVALGW 1334  
Db 1149 MRYFEVVILVVLSSIALAAEDP-VRTDSPRNALKYLDIYFTGVFTFEMVIKMDLGL 1207

QY 1335 CFGEQAYLRSSWNVDGLLVLSIVDILVSMV-SDSGTKILGMLRVLRLTLRPLRVIS 1393  
Db 1208 LLHPGAYFRDLWNILD---FIVVSGALVAFAFSGSKGDKDINTIKSLRVLRLPLKTIK 1263

QY 1394 RAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGE-----DTR 1447  
Db 1264 RLPKLKAVFDCVNSLKNVLNIVMLFMFIFAVIAVQLFKGFFYCTDESKELERDCR 1323

QY 1448 N--ITNKSDEAEASYR-WVRHKYNFDNLQALMSLFLVASKDGVVDIMYDGLDAVGVDQQ 1504  
Db 1324 GOYLDYEKEEVEAQPQWKYDFHYDNVWALLTLFTVSTGEGWPMVLKHSVDATYEEQG 1383

QY 1505 PIMNHNPMWLLYFISFLLLIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRLRLE 1564  
Db 1384 PSPGYRMELSIFVYVVFVFPFFVFVNIIFVALIITF-----QEQQDKVMSE-----CSLE 1433

QY 1565 KRRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLEITGVIGLNVVTMAMEHY 1615  
Db 1434 KNERACIDFAISAKPLTRYMPQNRQSFQYKTWTTFVSPFPFEYFIMAMIALNTVVLMMKFY 1493

QY 1616 QPQILDEALKICNYIFTVIFVLESVPKLVAFGRFRFFQDRWNQDLAIVLLSIMGITLE 1675  
Db 1494 DAPYEYELMKCLNIVFTSMFMECVLKIIAFGLVNLFRDAMNVDFVTVLGSITDILVT 1553

QY 1676 EIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLML 1735  
Db 1554 EIANNF---IN---LSFLRLFRAARLKLRLQGYTIRILLTWTTFQSFKALPYVCLLIAML 1607

QY 1736 FFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLR 1795  
Db 1608 FFIIYIIGMQVFGNIALDDDD---TSINRHNFRFTLOALMLLFRSATGEAWHEIMLSCLS 1664



Qy	1796	D	--CDQE--	--STCVNTVISPIYFVSVLTAQFVLNVNVI	AVLM-----KHL	1836
Db	1665	NQACDEQANATECGSD	FAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHL	1724		
Qy	1837	EE	-----	-----	-----	1838
Db	1725	DEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPGLGKKCPARVAYKRLVRMNPISNED	1784			
Qy	1839	-----	-----SNKEAKEEALEAELEEMKTLSPQPHSPGLGSPFLW	1874		
Db	1785	MTVHFTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANL-PQKTLDLLVP	-----	1840		
Qy	1875	PGVEGPDSPDPKPGALHPA	-----AHARSASHFLEHPTM	-----	1910	
Db	1841	-----PHKPDENTGVKYAALMIFDYKONKTTTRDQMQAPGGLSQMGFVSLFHLKATL	1895			
Qy	1911	-QPHPTELPGDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVL	1969			
Db	1896	EQTQPAVLRGARVFLRQKSTSLN	-----GGAIQNESGIKE	1933		
Qy	1970	SVHSQPADTSYIQLPKDAPHLLOP	-----HSAPTWTGTIPKLPPPGRSPLAQRPLRRQAA	2024		
Db	1934	SV	-----SWGTQRTQDAPHEARPPLERGHSTEI	-----PVGRSGALAVDVQMOSI	1978	
Qy	2025	IR	-----TDSLVDQGLGSRREDLLAEVSGP	-----SPPLARAYSFWQSQSSTQAQOHSRSHS	2074	
Db	1979	TRRGPDGEPQGLSQGRAASMPRLAAETQPVTDASPMKRSI	-----STLAQRPGRGTHL	2032		
Qy	2075	KISKHMTTPAPCPG	-----PEPNWKGPPETRRSSLELDTELSWISGDL	2117		
Db	2033	CST	-----TPDRPPPSQASSHHHHHRRRRDRKQRSLEKGP	-----SLSADMGAPSSAVGPG	2086	
Qy	2118	LPPGGQEEPPSPDLKKCYSV	EAQSCQRR-PTSWLDEORRHSAVSCLD	SG-----	2167	
Db	2087	LPPG	-----EGPTGCRRRERQRQSRSQERRQPSSSSSKQRF	-----YSCDRFGGREPPKPKP	2141	
Qy	2168	-----SQPHLGTDP	-----SNLGGQPL	-----GGPGSRPKKKLSP-PSITI	2202	
Db	2142	SLSSHPTSPTAGQEPGPHQSGSVNGSP	LLSTSGASTPGRGRRQLPOTPLTPRPSITY	2201		
Qy	2203	-----DPPE SQPRT	-----PP-SPG	-----ICLRRRAPSSDSKDPLASGPPDSMAASP	2245	
Db	2202	KTANSSPIHFAGAQTSLEAFSPGRLSRGLSEHNALLORDPLS	-----QPLAPG	-----	2249	
Qy	2246	SPKKDVL	SLSGLSSDP	2261		
Db	2250	-----SRIGSDP	2256			

RESULT 14  
US-08-455-543A-47  
; Sequence 47, Application US/08455543A  
; Patent No. 5792846

GENERAL INFORMATION:  
APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
APPLICANT: Brenner, Robert  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
; US-08-455-543A-47

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Query Match	14.7%;	Score 1748.5;	DB 1;	Length 2339;
Best Local Similarity	24.2%;	Pred. No. 3.8e-133;		
Matches 641;	Conservative 359;	Mismatches 825;	Indels 819;	Gaps 85;

QY	27	GAGGRPGGSAEKDPG	SADSEAEGLPY	PALAPVVF	----	FYLSQDSRP	70
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QY	71	RSWCLRTVCNPWF	ERISMLVILLNC	VTGLMFRPCED	IACDSORCILQ	AFDD---	127
		:	:	:	:	:	
Db	85	RKYAKRITETWPP	FENMILATI	IANCIVLAL---	EQHLPDGDKTP	MSERLDDTE	140
QY	128	FAVEMVVKMVALG	-IFGKKCYLGDT	WNRLDFFIVIA	GMLEYS---	LDLQNVSFSA	183
		:	:	:	:	:	
Db	141	FCFEAGIKIIALG	FVHKGSYLRNG	WNVMDFVVULT	GILATAGTDF	DLR----	195
QY	184	VLRLPRAINRVPS	MRILVTLLDLT	PLMIGNVLLLC	FFVFIFGIVG	VQLWAGLLNR	243
			: : : : :	: :		: : : :	
Db	196	VLRLPLVSGIPSL	QVVLKSIKAM	VPLLOIGLLLF	AILMFAIIGL	EYFMGKFHKA	254
QY	244	PENFSLPLSVDL	ERYQTENEDES	PFICSQPRENG	MRSRCSVPTLR	GDGGGGPPCG	303
Db	255	-----PNSTDAE	-----	-----PV	-----	GDFFPCGKEAP	273
QY	304	AYNSSNTTTCVN	WNQYNTNCSA	GEHNPFKGAIN	FDNIGYAWIA	IPQVITLEGW	363
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Db	274	ARLCEGDTEC---	REYWP-----	GPNFGITNFD	NILFAILTV	QCITMEGWTD	323



Db 2156 QEPGHPQSGSVNGSPLSTSGASTPGRGRRQLPQTPLTPRPSITYKTKTANSSPIHFAG 2215  
QY 2210 PRT--PP-SPG-----ICLRRAPSSDSKDXPLASGPPDMSMAASPSPKKDVLISLGL 2257  
Db 2216 AQTSLPAFSPGLSRGLSEHNALLQDPLS---QPLAPG-----SRI 2254  
QY 2258 SSDP 2261  
Db 2255 GSDP 2258

RESULT 15  
US-08-223-305C-47  
; Sequence 47, Application US/08223305C  
; Patent No. 5851824  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/223,305C  
; FILING DATE: April 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/868,354  
; FILING DATE: April 10, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/745,206  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/620,250  
; FILING DATE: 30-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/482,384  
; FILING DATE: 20-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/603,751  
; FILING DATE: 04-APR-1989  
; APPLICATION NUMBER: WO PCT/US89/01408  
; FILING DATE: 04-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/176,899  
; FILING DATE: 04-APR-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 52516 (P519739)  
; TELEPHONE: (619)238-0999  
; TELEFAX: (619)238-0062  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2339 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-223-305C-47  
Query Match 14.7%; Score 1748.5; DB 2; Length 2339;  
Best Local Similarity 24.2%; Pred. No. 3.8e-133;  
Matches 641; Conservative 359; Mismatches 825; Indels 819; Gaps 85;  
QY 27 GAGGRPGSAEKDPGSADEAGLPYPALAPVVF-----FYLSDQSRP 70  
Db 25 GAGGAGGPGGLQPGQVLYKQSIARARTMALYNPIPVKQNCFTVNRSLFVSEDNVV 84  
QY 71 RSWCLRTVCNPWFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAFDD---FIFAF 127  
Db 85 RKYAKRITWPPFENMILATIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI 140  
QY 128 FAVEMVVMVALG-IFGKKCVLGDWTNRLDFFIVIAAGMLEYS---LDLQNVSPSAVRTVR 183  
Db 141 FCFEAGIKIIALGFVHKGSYLNRGNVMDVTVVLTGILATAGTDFDLR-----TLRAVR 195  
QY 184 VLRPLRAINRVPSMRILVTLDDTLPLMLGNVLLCFVFFIFIGIVGVQLWAGLLNRNCF 243  
Db 196 VLRPLKLVSGIPSLQVVLKSIKAMVPLLIQIGLLLPAILMFAIIGLEFYMGKFKACF- 254  
QY 244 PENFSLPLSVDLERYQYOTENEDESPFICSPRENGMRSCRVPVTLRGDGGGPGCGLDYE 303  
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273  
QY 304 AYNSSNTTCVNMNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363  
Db 274 ARLCEGTEC---REYWP-----GPNFGITNFDNIFAILTVFQCITMEGWTDILYNT 323  
QY 364 MD-AHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQRES-----QLMREQRVRF 416  
Db 324 NDAAGTNWNLWYFIPLIIIGSFMLNLVLGVLSGEFAKERVENRRRAFLKLRQQQIE- 382  
QY 417 LSNASTLASFPSEPGSCYEELKLVYILRKAARRLAQVRAAGVRVGLLSPPAPLGGQET 476  
Db 383 -----RELNGYLEWIFKAEVVMLEEDRNA-----EKK 410  
QY 477 QPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPP 536  
Db 411 SPLDVLKRAATKKSNDLIH-----AEEGEDRFAD----- 440  
QY 537 PSTPALSAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTS 596  
Db 441 ----- 440  
QY 597 PPTETLKEKALVEVAASSGPPITLSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLK 656  
Db 441 -----LCAVGSPPAR 450  
QY 657 ADGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRRQRS 716  
Db 451 ASLKSCKTESSESYFRR-----KEKMRP----- 473  
QY 717 GPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALE 776  
Db 474 -----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTY 515  
QY 777 ISNIVFTSLFALEMLLKLVLVYGPFGYIKPNYNIFDGVIVVISWEIVGQ-----QGGGLS 831  
Db 516 FAEFVFLGLFLEMSLKMVGLGPRSYFRSSFCDFGIVGVSFVFEVVAWAAIKPGSSFGIS 575  
QY 832 VLRTRFLMRVLKVRFLPALORQLVVLMTKMDNVATFCMLLMFLFIFISILGMHLFGCKF 891  
Db 576 VLRALRLRIFKVTKYWSSLRNVLVSLNSMKSIIISLLFLFLFVIFVALLGMQLFGGQF 635  
QY 892 ASERDGDTLPDCKNFDLSLLWAVTVFQILTQEDWNKVLNMG-----ASTSSWAALYFIA 946  
Db 636 NFQDETPT-----TNFDTFPAILTVFQILTGEDWNAVWYHGIESQGGVSKGMFSSFYFIV 691

[illegible]

Search completed: April 13, 2005, 16:50:54  
Job time : 91 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: April 13, 2005, 16:39:37 ; Search time 213 Seconds  
(without alignments)  
3535.925 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAEESGQPRFSM.....PKDVLSLSSDPADLDP 2266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues  
Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	11815.5	99.3	2377	16	US-10-757-262-16
2	11758.5	98.8	2243	16	US-10-408-765A-625
3	11111	93.3	2374	10	US-09-383-894-2
4	11111	93.3	2425	10	US-09-383-894-4
5	6315.5	53.1	1207	17	US-10-930-301-52
6	6212	52.2	2353	16	US-10-408-765A-1128
7	5492.5	46.1	2175	9	US-09-935-541-2
8	5492.5	46.1	2175	14	US-10-425-800-2
9	5484	46.1	2188	9	US-09-935-541-4
10	5484	46.1	2188	14	US-10-425-800-4
11	5366	45.1	1835	9	US-09-935-541-5
12	5366	45.1	1835	14	US-10-425-800-5
13	3959.5	33.3	1853	9	US-09-030-482B-19

14	3564.5	29.9	1657	15	US-10-369-493-6836	Sequence 6836, Ap
15	1753	14.7	2264	15	US-10-627-370-2	Sequence 2, Appli
16	1750.5	14.7	2343	13	US-10-033-026-4	Sequence 4, Appli
17	1748.5	14.7	2339	15	US-10-375-253-12	Sequence 12, Appl
18	1746.5	14.7	2339	13	US-10-033-026-6	Sequence 6, Appli
19	1743	14.6	2237	15	US-10-375-253-14	Sequence 14, Appl
20	1741	14.6	2237	13	US-10-033-026-8	Sequence 8, Appli
21	1722	14.5	2336	13	US-10-033-026-10	Sequence 10, Appl
22	1673.5	14.1	1745	15	US-10-627-370-4	Sequence 4, Appli
23	1667	14.0	2313	16	US-10-322-696-178	Sequence 178, App
24	1665	14.0	2270	15	US-10-375-253-40	Sequence 40, Appl
25	1663.5	14.0	2251	15	US-10-375-253-38	Sequence 38, Appl
26	1659	13.9	2270	16	US-10-322-696-176	Sequence 176, App
27	1657.5	13.9	2251	16	US-10-322-696-84	Sequence 84, Appl
28	1632	13.7	1873	13	US-10-029-413A-22	Sequence 22, Appl
29	1625.5	13.7	1748	16	US-10-408-765A-1968	Sequence 1968, Ap
30	1619.5	13.6	1984	10	US-09-457-571-10	Sequence 10, Appl
31	1615.5	13.6	1989	10	US-09-457-571-12	Sequence 12, Appl
32	1602	13.5	2016	16	US-10-632-342-2	Sequence 2, Appli
33	1602	13.5	2510	15	US-10-375-253-34	Sequence 34, Appl
34	1598.5	13.4	2015	16	US-10-632-342-6	Sequence 6, Appli
35	1597.5	13.4	2157	16	US-10-467-491-2	Sequence 2, Appli
36	1596.5	13.4	2151	16	US-10-467-491-4	Sequence 4, Appli
37	1594	13.4	2016	16	US-10-632-342-4	Sequence 4, Appli
38	1591	13.4	1854	13	US-10-029-413A-2	Sequence 2, Appli
39	1590.5	13.4	2015	14	US-10-077-054-2	Sequence 2, Appli
40	1590.5	13.4	2015	16	US-10-632-342-8	Sequence 8, Appli
41	1587	13.3	2016	10	US-09-896-994-2	Sequence 2, Appli
42	1586	13.3	1969	10	US-09-457-571-16	Sequence 16, Appl
43	1586	13.3	2016	9	US-09-840-125-4	Sequence 4, Appli
44	1586	13.3	2016	15	US-10-333-191-2	Sequence 2, Appli
45	1586	13.3	2016	16	US-10-914-133-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-10-757-262-16  
; Sequence 16, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; TITLE OF INVENTION: 55053  
; FILE REFERENCE: MPI03-007P1RNMNIM  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156

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; PRIOR APPLICATION NUMBER: US 60/499,594									
; PRIOR FILING DATE: 2003-09-02									
; PRIOR APPLICATION NUMBER: US 60/506,332									
; PRIOR FILING DATE: 2003-09-26									
; NUMBER OF SEQ ID NOS: 136									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 16									
; LENGTH: 2377									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
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QY	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMPRPCEDIACDSQRILQAF	120						
Db	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMPRPCEDIACDSQRILQAF	120						
QY	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRLDFFIVIAGMLEYSLDLQNVFSAVR	180						
Db	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRLDFFIVIAGMLEYSLDLQNVFSAVR	180						
QY	181	TVRVLRPLRAINRVPSMRILVTLTLLDTLPMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240						
Db	181	TVRVLRPLRAINRVPSMRILVTLTLLDTLPMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240						
QY	241	CFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL	300						
Db	241	CFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL	300						
QY	301	DYEAVNSSNTTCVWNQYVYTCNSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360						
Db	301	DYEAVNSSNTTCVWNQYVYTCNSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360						
QY	361	YFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420						
Db	361	YFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420						
QY	421	STLASFEPGSCYEELKLVILRKAARRLAQVSRAAGVRVGLLSAPLGGQETQPS	480						
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QY	481	SCSRSHRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540						
Db	481	SCSRSHRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540						
QY	541	ALSGAPPGGAESVHSFYHADCHLEPVRCPQAPPSPSEASGRTVSGKVYPTVHTSPPE	600						
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QY	601	TLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLFTQSTGACQSSCKISSPCLKADSG	660						
Db	601	TLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLFTQSTGACQSSCKISSPCLKADSG	660						
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRSLGPD	720						
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRSLGPD	720						
QY	721	EPSSVLAFWRLTCDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780						
Db	721	EPSSVLAFWRLTCDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780						
QY	781	VFTSLFALEMLKLVYGPFGYIKNPYNIQVIVVIVSVWEIVGQGGGLSVLRTFRLMR	840						
Db	781	VFTSLFALEMLKLVYGPFGYIKNPYNIQVIVVIVSVWEIVGQGGGLSVLRTFRLMR	840						

QY	841	VLKVRFLPALQRLVVLMTKMDNVATFCMLLMFIPIFISILGMHLFGCKFASERDGTLL	900						
Db	841	VLKVRFLPALQRLVVLMTKMDNVATFCMLLMFIPIFISILGMHLFGCKFASERDGTLL	900						
QY	901	PDRKNFDSLWLAIWTVFQILTOBDWNKVLNGMASTSSWAALYFIALMTFNGVLFNLLV	960						
Db	901	PDRKNFDSLWLAIWTVFQILTOBDWNKVLNGMASTSSWAALYFIALMTFNGVLFNLLV	960						
QY	961	AILVEGFQAEISKREDASGQSCIQLPVDSQGGDANKSESEPFFSPSLDGDGRKKCL	1020						
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QY	1021	ALVSLGEHPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080						
Db	1021	ALVSLGEHPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080						
QY	1081	HEMKSPPSARSPHSPWSAASSWTSRRSSRSLGRAPSLKRRSPSGERRSLLSGEGESQ	1140						
Db	1081	HEMKSPPSARSPHSPWSAASSWTSRRSSRSLGRAPSLKRRSPSGERRSLLSGEGESQ	1140						
QY	1141	DEESSEERASPADSDHRRHGRSLEREAKSSFDLPDTLQVGLHRTASGRGSASEHQDCN	1200						
Db	1141	DEESSEERASPADSDHRRHGRSLEREAKSSFDLPDTLQVGLHRTASGRGSASEHQDCN	1200						
QY	1201	GKSASGRLARALRPPDPPDLGDDADDEGNLSKGERVRAWRIRARLPACYLERSWSAYIFP	1260						
Db	1201	GKSASGRLARALRPPDPPDLGDDADDEGNLSKGERVRAWRIRARLPACYLERSWSAYIFP	1260						
QY	1261	POSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDHSAERIFLTLSNYIFTAV	1320						
Db	1261	POSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDHSAERIFLTLSNYIFTAV	1320						
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Db	1321	FLAEMTVKVVALGWCFCQAYLRSSWNVDGLLVLISVIDILYSMVSDSGTKILGMLRVL	1380						
QY	1381	RLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIIVICCAFFIIFGILGVQLFKGKFFV	1440						
Db	1381	RLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIIVICCAFFIIFGILGVQLFKGKFFV	1440						
QY	1441	COGEDTRNITNKSDCAEASRVRWKYFNDFNLGQALMSLFLVASKDGWVDIMYDGLDVG	1500						
Db	1441	COGEDTRNITNKSDCAEASRVRWKYFNDFNLGQALMSLFLVASKDGWVDIMYDGLDVG	1500						
QY	1501	VDQQPIMNHNPMWLLYFISFLLIVAFVFLNMFGVVVENFHKCRHQHEEEAARRREKRL	1560						
Db	1501	VDQQPIMNHNPMWLLYFISFLLIVAFVFLNMFGVVVENFHKCRHQHEEEAARRREKRL	1560						
QY	1561	RRLEKKRR-----KAQCKPYSDYSRFRLLVHLCCTSHYLDLFTGV	1602						
Db	1561	RRLEKKRRMLDDVIASSGSASAASEAQCKPYSDYSRFRLLVHLCCTSHYLDLFTGV	1620						
QY	1603	IGLNVVTWAMEHYQQOILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQLDL	1662						
Db	1621	IGLNVVTWAMEHYQQOILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQLDL	1680						
QY	1663	AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLDVTMQAL	1722						
Db	1681	AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLDVTMQAL	1740						
QY	1723	POVGNLGLLFMLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTFRVST	1782						
Db	1741	POVGNLGLLFMLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNFGMAFLTFRVST	1800						
QY	1783	GDWNWNGIMKDLTRDCDQESTCYNTVISPIYFVSFVLTQAQFVLVNVVIAVLMKHLEESNKE	1842						
Db	1801	GDWNWNGIMKDLTRDCDQESTCYNTVISPIYFVSFVLTQAQFVLVNVVIAVLMKHLEESNKE	1860						
QY	1843	AKBEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGPDSPSPKPGALHPAAHARSASH	1902						
Db	1861	AKBEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGPDSPSPKPGALHPAAHARSASH	1920						
QY	1903	PSLEHPT-----	1909						

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Db 1921 FSLEHPTDRQLFDTISLLIQGSLEWELKMDLAGPGGQPSAPPSAPSLGGSDPQIPLAE 1980
Qy 1910 -----MQPHPTELPGPDLLTVRKSG 1929
Db 1981 MEALSLTSEIVSEPSCSLALTDDSLDPDMHTLLLSALESNMQPHPTELPGPDLLTVRKSG 2040
Qy 1930 VSRTHSLPNDSYMCRHGSTAEGPLGHRGWLPKAQSGSVLSVHSPADTSYIILQPKDAP 1989
Db 2041 VSRTHSLPNDSYMCRHGSTAEGPLGHRGWLPKAQSGSVLSVHSPADTSYIILQPKDAP 2100
Qy 1990 HLLQPHSAPTGTIPKLPPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSREDLLAEVSGPS 2049
Db 2101 HLLQPHSAPTGTIPKLPPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSREDLLAEVSGPS 2160
Qy 2050 PPLARAYFWGQSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNWGKGGPPETRSSLELDT 2109
Db 2161 PPLARAYFWGQSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNWGKGGPPETRSSLELDT 2220
Qy 2110 LSWISGDLPPGGQEEPPSPRDLKKCYVSAQSCORRPTSWLDEQRRHSIAVSCLDGSGSQ 2169
Db 2221 LSWISGDLPPGGQEEPPSPRDLKKCYVSAQSCORRPTSWLDEQRRHSIAVSCLDGSGSQ 2280
Qy 2170 PHLGTDPSNLGQPLGGPSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDS 2229
Db 2281 PHLGTDPSNLGQPLGGPSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDS 2340
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Db 2341 KDPLASGPPDSMAASPSPKDVLSSLGSSDPADLDP 2377
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RESULT 2

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; Sequence 625, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 2243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-625
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Best Local Similarity 98.9%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

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Db 1 MDEEEDGAGAEESGQPRSFMRNLDSLGAAGRRPGGSAEKDPGSADSEAEGLPYPALAPVV 60

Qy 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFPCEDIACDSQRCRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFPCEDIACDSQRCRILQAF 120

Qy 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSAVR 180
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVTAGMLEYSLDLQNVFSAVR 180
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Qy 181 TVRVLRPLRAINRVPSMRILVTLTLLDTLPM LGNVLLLCFFVFFIFIGIVGVQLWAGLLRNR 240
Db 181 TVRVLRPLRAINRVPSMRILVTLTLLDTLPM LGNVLLLCFFVFFIFIGIVGVQLWAGLLRNR 240

Qy 241 CFLPENFSLPSVDLERYYYQTENEDESPFICSQPRENGMRSRCSVPPTLRGDGGGPPCGL 300
Db 241 CFLPENFSLPSVDLERYYYQTENEDESPFICSQPRENGMRSRCSVPPTLRGDGGGPPCGL 300

Qy 301 DYEAYNSSNTTTCVWNQYYTNC SAGEHNPFKGAINFNDIGNYAWIAIFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTTCVWNQYYTNC SAGEHNPFKGAINFNDIGNYAWIAIFQVITLEGWVDIM 360

Qy 361 YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Qy 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETOPSS 480
Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETOPSS 480

Qy 481 SCSRSRRRLSVHHLVHHHHHHHHYHLNGT LRAPRASPEIQDRDANGSRRLMLPPRSTP 540
Db 481 SCSRSRRRLSVHHLVHHHHHHHHYHLNGT LRAPRASPEIQDRDANGSRRLMLPPRSTP 540

Qy 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSKVYPTVHTSPPE 600
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSKVYPTVHTSPPE 600

Qy 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHK LLETOSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHK LLETOSTGACQSSCKISSPCLKADSG 660

Qy 661 ACGPDCPYCARAGAGEVELADREMPDS DSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 720
Db 661 ACGPDCPYCARAGAGEVELADREMPDS DSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 720

Qy 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMIA ILVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMIA ILVNTLSMGIEYHEQPEELTNALEISNI 780

Qy 781 VFTSLFALEMLJLKVYGPFGYIKNPYNI F DGVIVVISVWEIVGQGGGLSVLRTFLMR 840
Db 781 VFTSLFALEMLJLKVYGPFGYIKNPYNI F DGVIVVISVWEIVGQGGGLSVLRTFLMR 840

Qy 841 VLKLVRFALQRLVLMKTMNDNVATFCMLLM LFI FIFISILGMHLFGCKFASERDGT 900
Db 841 VLKLVRFALQRLVLMKTMNDNVATFCMLLM LFI FIFISILGMHLFGCKFASERDGT 900

Qy 901 PDRKNFDSLLWAI VTFQILTQEDWNKVLYNGMA STSSWAALYFIALMTFGNYVLFNLLV 960
Db 901 PDRKNFDSLLWAI VTFQILTQEDWNKVLYNGMA STSSWAALYFIALMTFGNYVLFNLLV 960

Qy 961 AILVEGFOAEISKREDASGQLSCIQLPVD SQGDANKSESEPDFFSPSLDGDGDRKKCL 1020
Db 961 AILVEGFOAE-----GDANKSESEPDFFSPSLDGDGDRKKCL 997

Qy 1021 ALVSLGEHPRLKSLLPPLIIHTAATPMSL PKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db 998 ALVSLGEHPRLKSLLPPLIIHTAATPMSL PKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057

Qy 1081 HEMKSPPSARSSPHSPWSAASWTSRRSR SRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
Db 1058 HEMKSPPSARSSPHSPWSAASWTSRRSR SRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117

Qy 1141 DEEESSEERASPA GSDHRRHRSGLEREAKSSF DLPTLQVPGLHRTASGRGSASEHODCN 1200
Db 1118 DEEESSEERASPA GSDHRRHRSGLEREAKSSF DLPTLQVPGLHRTASGRGSASEHODCN 1177

Qy 1201 GKSASGRLARALRPDDPPLDGDADDDEGNLS KGERVRAWIRARLPACYLERSDSWSAYIFP 1260
Db 1178 GKSASGRLARALRPDDPPLDGDADDDEGNLS KGERVRAWIRARLPACYLERSDSWSAYIFP 1237

Qy 1261 PQSRFRLLCHRIITHKMFHDHVVLVIIFLNCIT IAMERPKIDPHSAERIFLTLSNYIFTAV 1320
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1238 PQSRFLLCHRIITHKMFHDVJVLIFLNCITIANERP KIDPHSAERFLTLSNYIFTAV 1297  
1321 FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL 1380  
1298 FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL 1357  
1381 RLLRTLRLPLRVISRAOGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1440  
1358 RLLRTLRLPLRVISRAOGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV 1417  
1441 CQGEDTRNITNKSDCAEASRYWRHKYNFNDLGOALMSLFLVLASKDGWVDIMYDGLDAVG 1500  
1418 CQGEDTRNITNKSDCAEASRYWRHKYNFNDLGOALMSLFLVLASKDGWVDIMYDGLDAVG 1477  
1501 VDOQPIMNHPNMLLYFISFLLIIVAFFVLNMFVGVVVNFHKKRQHQQEERARRRREKRL 1560  
1478 VDOQPIMNHPNMLLYFISFLLIIVAFFVLNMFVGVVVNFHKKRQHQQEERARRRREKRL 1537  
1561 RRLEKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQPQI 1620  
1538 RRLEKRRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQPQI 1597  
1621 LDEALKICNYIFTVIFVLESVEFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVN 1680  
1598 LDEALKICNYIFTVIFVLESVEFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVN 1657  
1681 ASLPINPTIIRIMRVLIARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLFFLFFIFA 1740  
1658 ASLPINPTIIRIMRVLIARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLFFLFFIFA 1717  
1741 ALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDTLRDCDQE 1800  
1718 ALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDTLRDCDQE 1777  
1801 STCVNTVISPIYFVSFVLTAQFVLNVVIVIAVMKHLEESNKEAKEEAELELEMKTL 1860  
1778 STCVNTVISPIYFVSFVLTAQFVLNVVIVIAVMKHLEESNKEAKEEAELELEMKTL 1837  
1861 SPQHPSPGSPFLWPVGEGDSDSPKPGALHPAAHARSASHFSLSEHPTMQPHPTLPGP 1920  
1838 SPQHPSPGSPFLWPVGEGDSDSPKPGALHPAAHARSASHFSLSEHPTMQPHPTLPGP 1897  
1921 DLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY 1980  
1898 DLLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY 1957  
1981 ILQLPKDAPHLLOPHSAPTWTGTPKLPPLPPGRSPLAQRPLRQAAIRTDSDLVQGLGSRED 2040  
1958 ILQLPKDAPHLLOPHSAPTWTGTPKLPPLPPGRSPLAQRPLRQAAIRTDSDLVQGLGSRED 2017  
2041 LLAEVSGSPPLARAYSFWGQSTQAQHSRSHSKISKHMTTPAPCPGPEPNWGKGPPE 2100  
2018 LLAEVSGSPPLARAYSFWGQSTQAQHSRSHSKISKHMTTPAPCPGPEPNWGKGPPE 2077  
2101 RSSLELDTLSWISGDLPLPGQGEPPSPRDLKKCYSVQAEQSCQRRPTSWLDEQRRHSIA 2160  
2078 RSSLELDTLSWISGDLPLPGQGEPPSPRDLKKCYSVQAEQSCQRRPTSWLDEQRRHSIA 2137  
2161 VSCLDGSGQHLGTDPSNLGGQPLGGPSRPPKLSPPSITIDPPESQGPRTPPSPGICL 2220  
2138 VSCLDGSGQHLGTDPSNLGGQPLGGPSRPPKLSPPSITIDPPESQGPRTPPSPGICL 2197  
2221 RRRAPSSDSKDLASGPPDMSMAASPPKDVLSLSGLSSDPADLDP 2266  
2198 RRRAPSSDSKDLASGPPDMSMAASPPKDVLSLSGLSSDPADLDP 2243

RESULT 3  
US-09-383-894-2  
; Sequence 2, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:

APPLICANT: Li, Ming  
TITLE OF INVENTION: T-Type Calcium Channel  
FILE REFERENCE: 004.00191  
CURRENT APPLICATION NUMBER: US/09/383,894  
CURRENT FILING DATE: 1999-08-26  
EARLIER APPLICATION NUMBER: US 60/098,004  
EARLIER FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: US 60/117,399  
EARLIER FILING DATE: 1999-01-27  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 2374  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-09-383-894-2

Query Match 93.3%; Score 11111; DB 10; Length 2374;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEDGAGAEESQPRSFMRNLNLSGAGRRPGSGAEKDPGSDADSEAEGLPYPALAPVV 60  
Db 1 MDEEDGAGAEESQPRSFMRNLNLSGAGRRPGSGAEKDPGSDADSEAEGLPYPALAPVV 60  
QY 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
Db 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120  
QY 121 DDPIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVFSAVR 180  
Db 121 DDPIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVFSAVR 180  
QY 181 TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240  
Db 181 TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240  
QY 241 CFLPENFSLPLSVDLERYQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL 300  
Db 241 CFLPENFSLPLSVDLERYQTENEDESPFICSPRENGMRSCRSVPTLRGEAGGGPPCGL 300  
QY 301 DYEAYNSSNTTTCVNNQYTNCSAGEHNPFKAGNFDNIGYAWIAIFQVITLEGWVDIM 360  
Db 301 DYEAYNSSNTTTCVNNQYTNCSAGEHNPFKAGNFDNIGYAWIAIFQVITLEGWVDIM 360  
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420  
QY 421 STLASFSEPGSCYEELLYLIRKAARRLAQVSRAGVRLSSPAPLGGQETQPS 480  
Db 421 STLASFSEPGSCYEELLYLIRKAARRLAQVSRAGVRLSSPAPLGGQETQPS 480  
QY 481 SCSRSRRLSVHHLVHHHHHHHHYHLNGTTLRAPASPEIQDRDANGSRRLMLPPSTP 540  
Db 481 SCSRSRRLSVHHLVHHHHHHHHYHLNGTTLRAPASPEIQDRDANGSRRLMLPPSTP 540  
QY 541 ALSGAPPGCAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPPE 600  
Db 541 ALSGAPPGCAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPPE 600  
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660  
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660  
QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS -RRQSLGPD 719  
Db 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS -RRQSLGPD 720  
QY 720 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILLVNTLSMGIYHEQPEELTNALEISN 779  
Db 721 AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILLVNTLSMGIYHEQPEELTNALEISN 780



QY 780 IVFTSLFALEMLLKLVLVYGPFGYIKNPYNIPDGVIVVISVWEIVGQGGGLSVLRTFRLM 839  
Db 781 IVFTSLFALEMLLKLVLVYGPFGYIKNPYNIPDGVIVVISVWEIVGQGGGLSVLRTFRLM 840  
QY 840 RVLKLVRFPLALQRLVVLKMTMDNVATFCMLLMFLFIFISILGMHLFGCKFASERDGT 899  
Db 841 RVLKLVRFPLALQRLVVLKMTMDNVATFCMLLMFLFIFISILGMHLFGCKFASERDGT 900  
QY 900 LPDRKNFDSLWLAIWTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLL 959  
Db 901 LPDRKNFDSLWLAIWTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLL 960  
QY 960 VAILVEGFQAEESKREDASQOLSCIQLPVDSSQGGDANKSESEDFPSPSLDGDGRKKC 1019  
Db 961 VAILVEGFQAEESKREDASQOLSCIQLPVNSQGGDATKSESEDFPSPSVDGDRKKR 1020  
QY 1020 LALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079  
Db 1021 LALVALGEHAELRKSLPLPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSGSAEPGA 1080  
QY 1080 A-HEMKSPPSARSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPSGERRSLLSGEQE 1138  
Db 1081 AHHEMKSPPSARSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPSGERRSLLSGEQE 1140  
QY 1139 SQDEEESSEERASPAGSDHRRGSLEREAASSFDLPDTLQVPLGHLRTASGRGSASEHQD 1198  
Db 1141 SQDEEESSEEDRASPDHRRGSLEREAASSFDLPDTLQVPLGHLRTASGRSSASEHQD 1200  
QY 1199 CNGKSASGRLARALRPDDPPLDGDADDENGLSKGERVRAWTRARLPACYLERSWSAYI 1258  
Db 1201 CNGKSASGRLARLTDDPQLDGDADDENGLSKGERIQAWVRSLPACCRERDSWYI 1260  
QY 1259 FPPQSRFRLLCHRIITHKMFHDHVLVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318  
Db 1261 FPPQSRFRLLCHRIITHKMFHDHVLVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1320  
QY 1319 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1378  
Db 1321 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1380  
QY 1379 VLRLRLTLRPLRVISRAOGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1438  
Db 1381 VLRLRLTLRPLRVISRAOGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1440  
QY 1439 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSFLVASKDGVWDIMYDGLDA 1498  
Db 1441 FVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSFLVASKDGVWDIMYDGLDA 1500  
QY 1499 VGVDQQPIMNHNPMWMLLYFISFLLIVAFVLMFVGVVVENFHKRQHQEEEEARRREEK 1558  
Db 1501 VGVDQQPIMNHNPMWMLLYFISFLLIVAFVLMFVGVVVENFHKRQHQEEEEARRREEK 1560  
QY 1559 RLRRLEKKRR-----KAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 1600  
Db 1561 RLRRLEKKRRNMLDDVIAAGSSASAASEAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 1620  
QY 1601 GVIGLNVVTWAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGRFRFFQDRWNQL 1660  
Db 1621 GVIGLNVVTWAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGRFRFFQDRWNQL 1680  
QY 1661 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDFTVMQ 1720  
Db 1681 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDFTVMQ 1740  
QY 1721 ALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1780  
Db 1741 ALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRV 1800  
QY 1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVVIKHLN 1840  
Db 1801 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVVIKHLN 1860  
QY 1841 KEAKEEALEAELEEMKTLSPQPHSPILGSPFLWPVGVEGPDSPSPKPGALHPAAHARS 1900

Db 1861 KEAKEEALEAELEEMKTLSPQPHSPILGSPFLWPVGVEGVDSPSPKPGAPHTTAHIGAA 1920  
QY 1901 SHFSLEHPTMQPHPTLP--GPDLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957  
Db 1921 SGFSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHG 1980  
QY 1958 WGLPKAQSGSVLSVHSPADTSYIQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQ 2017  
Db 1981 WGLPKAQSGSVLSVHSPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQ 2040  
QY 2018 PLRQAAIRTDSDVQGLGSRREDLLAEVSGSPPLARAYSFWGSSSTQAQHSRSHSKIS 2077  
Db 2041 PLRQAAIRTDSDVQGLGSRREDLLSEVSGSPCLTRSSSWGSSIQVQORSIGQSKVS 2100  
QY 2078 KHMTPPAPCPGPEPNWKGPPETRSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYS 2137  
Db 2101 KHIRLPAPCPGLEPSWAKDPPETRSLELDTLSWISGDL--PSSQEEPLSPRDLKKCYS 2159  
QY 2138 VEAQSCORRPTSWLDEQRRHSIAVCLDGSQPHLGTDPNSLGGQPLGGPSRPPKKLS 2197  
Db 2160 VETQSCRRRPGSWLDEQRRHSIAVCLDGSQPHLGTDPNSLGGQPLGGPSRPPKKLS 2219  
QY 2198 PSITIDPPESQGPRTPPSPGICLRRAPSSDSKOPLAGSPPDMAASPSPKOVLSLGL 2257  
Db 2220 PSISIDPPESQGSRRPPCSPGVCLRRAPASDSKOPSVSSPLDSTAASPSPKOTLSLGL 2279  
QY 2258 SSDPADLDP 2266  
Db 2280 SSDPTDMDP 2288

RESULT 4  
US-09-383-894-4  
; Sequence 4, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004.00191  
; CURRENT APPLICATION NUMBER: US/09/383,894  
; CURRENT FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: US 60/098,004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399  
; EARLIER FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 2425  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-383-894-4

Query Match 93.3%; Score 11111; DB 10; Length 2425;  
Best Local Similarity 93.3%; Pred. No. 0;  
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEEDGAGAEESGQPRSFMRNLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPV 60  
Db 52 MDEEEDGAGAEESGQPRSFMRNLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPV 111  
QY 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMRPCEDIACDSQRCRILQAF 120  
Db 112 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMRPCEDIACDSQRCRILQAF 171  
QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVLAGMLEYSLDLQNVFSFAVR 180  
Db 172 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVLAGMLEYSLDLQNVFSFAVR 231  
QY 181 TVRVLRPLRAINRVPSMRILVTLTLLDTLPMGLNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240  
Db 232 TVRVLRPLRAINRVPSMRILVTLTLLDTLPMGLNVLLLCFFVFFIFGIVGVQLWAGLLRNR 291



QY	241	CFLPENFSLPLSVDLERYQOTENEDESPFICSQPRENGMRCRSVPTLRGDCGGGPPCGL	300
Db	292	CFLPENFSLPLSVDLERYQOTENEDESPFICSQPRENGMRCRSVPTLRGDCGGGPPCGL	351
QY	301	DYEAYNSSNTTCVWNQYYTNCAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360
Db	352	DYETYNSSNTTCVWNQYYTNCAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	411
QY	361	YFVMDAHSFYNIYFILLIIVGSFEMINCLVVIATQFSETKQRESQOLMREQVRFLSNA	420
Db	412	YFVMDAHSFYNIYFILLIIVGSFEMINCLVVIATQFSETKQRESQOLMREQVRFLSNA	471
QY	421	STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAAGVRVCLLSSPAPLGGQETQPS	480
Db	472	STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAIGVRAGLLSSPVARSQGEQPSG	531
QY	481	SCSRSHRRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIQORDANGSRRLMLPPSTP	540
Db	532	SCTRSHRRLSVHHLVHHHHHHHHVHLGNGTLRVPRASPEIQORDANGSRRLMLPPSTP	591
QY	541	ALSGAPPGAESVHSFYHADCHLEPVRCOAPPPRSPSEASGRIVGSGKVYPTVHTSPPE	600
Db	592	TPSGGPPRGAESVHSFYHADCHLEPVRCOAPPPRCPSEASGRIVGSGKVYPTVHTSPPE	651
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACOSSCKISSPCLKADSG	660
Db	652	ILKDKALVEVAPSPGPPTLTSNIPPGPFSSMHKLLETQSTGACHSSCKISSPCKADSG	711
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSGLPD	719
Db	712	ACGPDSCPYCARTGAGEPESADHMPDSDSEAVYEFTQDAQHSDLRDPHSRRRRQRSGLPD	771
QY	720	AEPSVLAFWRLICDTRKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPEELTNALEISN	779
Db	772	AEPSVLAFWRLICDTRKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPEELTNALEISN	831
QY	780	IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGOQGGSLSVLRTFLM	839
Db	832	IVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGOQGGSLSVLRTFLM	891
QY	840	RVLKLVRFPLPALORQLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGT	899
Db	892	RVLKLVRFPLPALORQLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGT	951
QY	900	LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	959
Db	952	LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	1011
QY	960	VAILVEGFAOEIISKREDASGOLSCIQLPVDSSQGGDANKSESEPDFFPSLDGDRKKC	1019
Db	1012	VAILVEGFAOEIISKREDASGOLSCIQLPVNSQGGDATKSESEPDFFPSVDGDRKKR	1071
QY	1020	LALVSLGEHPLEIKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGA	1079
Db	1072	LALVALGEHAELKSLPLPIIHTAATPMSLPKSSSTGVEALGSGRRRTSSGSAEPGA	1131
QY	1080	A-HEMKSPPSARSPSPWSAASMTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1138
Db	1132	AHHEMKSPPSARSPSPWSAASMTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1191
QY	1139	SQDEEESSEERASPGSDHRRHRSLEAKSSFDLPDTLQVPLHRTASGRGSAEHQD	1198
Db	1192	SQDEEESSEEDRASPGSDHRRHRSLEAKSSFDLPDTLQVPLHRTASGRSSAEHQD	1251
QY	1199	CNGKSASGRLARLPDDPPLDGDADDENGLSKGERVRAWTRARLPACYLERSWSAYI	1258
Db	1252	CNGKSASGRLARTLRDPPQLDGDADDENGLSKGERIQAWVRSRLPACCRERDSWSAYI	1311
QY	1259	FPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFT	1318
Db	1312	FPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFT	1371

[illegible]

RESULT 5  
US-10-930-301-52  
; Sequence 52, Application US/10930301  
; Publication No. US20050026207A1

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; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/10/930,301
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/398,522
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
US-10-930-301-52

Query Match      53.1%; Score 6315.5; DB 17; Length 1207;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY 1 MDEEDGAGAEESGQPRSMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
Db 1 MDEEDGAGAEESGQPRSMRLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60

QY 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQSCRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQSCRILQAF 120

QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFIVIAQMLEYSLDLQNVFSAVR 180
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFIVIAQMLEYSLDLQNVFSAVR 180

QY 181 TVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

QY 241 CFLPENFSLPLSVDLERYQOTENEDESPFICSQPRENMRSCRSVPTLRGDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQOTENEDESPFICSQPRENMRSCRSVPTLRGDGGGPPCGL 300

QY 301 DYEAYNSSNTTCVNMNQYTYNCSAGEHNPFGAINFDNIGYAWIAFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTCVNMNQYTYNCSAGEHNPFGAINFDNIGYAWIAFQVITLEGWVDIM 360

QY 361 YFVMDAHSFYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLKYLVIYILRKAARLAQVSRAAGVRVGLLSSPAPLGQETQPS 480
Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARLAQVSRAAGVRVGLLSSPAPLGQETQPS 480

QY 481 SCSRSRRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSRSRRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTP 540

QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600

QY 601 TLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACOSSCKISSPCLKADSG 660
Db 601 TLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACOSSCKISSPCLKADSG 660

QY 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSILRDPHSRRQSLGDA 720
Db 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSILRDPHSRRQSLGDA 720

QY 721 EPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI 780
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Db 721 EPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI 780
QY 781 VFTSLFALEMLLKLIVYGPFGYIKPNYNIFDGVIVVIVSWEIVGQQGGISVLTFRLMR 840
Db 781 VFTSLFALEMLLKLIVYGPFGYIKPNYNIFDGVIVVIVSWEIVGQQGGISVLTFRLMR 840
QY 841 VLKLVRFALQRLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGTLL 900
Db 841 VLKLVRFALQRLVLMKTMNDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGTLL 900
QY 901 PDRKNFDSLLWAIYTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
Db 901 PDRKNFDSLLWAIYTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
QY 961 AILVEGFQAEISKREDASQLSCIQLPVDSSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020
Db 961 AILVEGFQAE-----GDANKSESEPDFFSPSLDGDGRKKCL 997
QY 1021 ALVSLGEHPELRKSLPPLIIHTAATPMSILPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080
Db 998 ALVSLGEHPELRKSLPPLIIHTAATPMSILPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1057
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGRRSLLSGEGQESQ 1140
Db 1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGRRSLLSGEGQESQ 1117
QY 1141 DEEESSEERASPGSDHRRHRSGLEREAKSFFDLPTLTQVPLHRTASGRGSASEHQDCN 1200
Db 1118 DEEESSEERASPGSDHRRHRSGLEREAKSFFDLPTLTQVPLHRTASGRGSASEHQDCN 1177
QY 1201 GKSASGRLARALRPDDPPLDGDADDDEGNL 1230
Db 1178 GKSASGRLARALRPDDPPLDGDADDDEGNL 1207
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```
RESULT 6
US-10-408-765A-1128
; Sequence 1128, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1128
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```
Query Match      52.2%; Score 6212; DB 16; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1366; Conservative 214; Mismatches 525; Indels 304; Gaps 61;

QY 7 GAGAEESGQP-RSFMRNLNDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVFFYLS 65
Db 27 GASPESPGAPGREAEARGSEL-GVSPSESP-AAERGAELGADEEQRPVYPALAATVFFCLG 84

QY 66 QDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEDIAQSCRILQAFDDFIF 125
Db 85 QTTRPRSWCLRLVCNPFWEHVSMVLMLNCVTLMFRPCEDVECGSERCNILEAFDAFIF 144

QY 126 AFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFIVIAQMLEYSLDLQNVFSAVRTRVL 185
```

Db 145 AFFAVEMVIMKVALGLFGQKCYLGDWTNRLDFFIVVAGMWEYSLDGHNVSLSAIRTVRVL 204  
QY 186 RPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVEFFIFGIVGVOLWAGLLRNCFLPE 245  
Db 205 RPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVEFFIFGIVGVOLWAGLLRNCFLDS 264  
QY 246 NFSPLSVD-LERYYQOTENEDESPFFICSOPRENGMRSRCSVP---TLRGDGGGPPCGLD 301  
Db 265 AFVRNNLTFLRPYYQTEEGEENPFICSSRRDNGMCKSHIPGRREL-----MPCTLG 318  
QY 302 YEAYN-----SSNTTCVNNQYYTNCISAGEHNPFGAINFDNIGYAWIAIFQVITLE 354  
Db 319 WEAYTQOAEVGAARNACINNNQYVNCVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE 378  
QY 355 GWVDIMYFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREORV 414  
Db 379 GWVDIMYVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREORA 438  
QY 415 RFLSNASTLASFSEPGSCYEELLYLVILRKAARRLAQVSRAGVRVGLSSPAPLGGQ 474  
Db 439 RHLSDNSTLASFSEPGSCYEELLYVGHIFRKVKRRSURLYARWQSRWRKVDPSAVOQG 498  
QY 475 ETQPSSSCSRSRRR-LSVHLV-HHHHHHHYHLGNLTIRAPRASPEIQDRDANGSRRLL 532  
Db 499 --GPGRQRRAGRHTASVHLVYHHHHHHHHYHFSHGSRPRPGPEPGACD-----TRLV 551  
QY 533 MLPPPSTPALSGAPPGAESVHSFYHADCHLE--PVRQOAPPPRSPSEASGR-TVGSGKV 589  
Db 552 RAGAPSPSPSGRPPDAESVHSIYHADCHIEGPOERARVAHAATAAASRLATGLGTM 611  
QY 590 -YPTV-----HTSP-----PPETLKEKALVEAASSGPPTLTSLNIPPGPY 629  
Db 612 NYPTILPSGVSGKSTSPGPKGWAGPPGT-----GGHGPLSLNS-----PDY 657  
QY 630 SSMHKLLETQSTGACQS-----SCKTSSPCLKADSGACGPDSCPYCARA-GAGEVELA 681  
Db 658 EKIPHVVEHGLGQAPGHLGSLVPCPLPSP--PAGTLTCELKSCPYCTRALEDPEGELS 715  
QY 682 DREMPDSDSEAVYFTQDAQHSDLRDP-----HSRRQSRSLGPDAPSSV 725  
Db 716 GSESGSDGRGVYFTQDVRHGDRWDPTREPRATDTPGPGPGSPQRAAQRAAPGEGWM 775  
QY 726 LAFWRLLICDTFRKIUDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNIVFTSL 785  
Db 776 GRWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGVEYHEQPELTNALEISNIVFTSM 835  
QY 786 FALEMLLKLIVYGPFGVIKNPNYIFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLV 845  
Db 836 FALEMLLKLACGLGYIRPNYIFDGIIVVISWEIVGQADGGLSVLRTFRLLRVLKLV 895  
QY 846 RFLPALQRQLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKFASERD-GDTLPDRK 904  
Db 896 RFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFISILGMHLFGCKFSLKTDGTDVDPDRK 955  
QY 905 NFDSSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILV 964  
Db 956 NFDSSLWAIWTVFQILTQEDWNVVLNGMASTSSWAALYFVALMTFGNYVLFNLLVAILV 1015  
QY 965 EGFOAEIISKREDASGQLSCIQLPVDVSQGGDANKSESEPDFFSPSLDGD-----GD 1015  
Db 1016 EGFOAE-----GDANRSDTDEDKTSVHFEEDFKHLRELQTE 1052  
QY 1016 RKKCLALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSA 1075  
Db 1053 LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMTPTKSSPFLDAAPSLPDSRRGSSSGD 1112  
QY 1076 EPGAHEMKSPSPSARSSPHSPWAASSWTSSRSSRSLGRAPSLKRRSPSGERRSLLSGE 1135  
Db 1113 PP--LGDQKPPASLRSSPCAPWPGSGAWSSRSSWSLGRAPSLKRRGQOCGERESLLSGE 1170  
QY 1136 GOESQDEESSEERASPA--GSDHRRHGRSLEREAKSSFDLPDTL-----QVPGLH--- 1184

Db 1171 GKGSTDDE--AEDGRAAPGPRATPLRRAESLDPRLPAPALPPTKCRDRDQGVVALPSDF 1228  
QY 1185 --RTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRA 1242  
Db 1229 FLRIDSHREDAAEALDDSEDSCLRLHKVLEPYK-----OWCRS 1268  
QY 1243 RLPACYLERDSWYIIFPPQSRFRLLCHRITTHKMFHDVVLVIFLNCITIAMERP KIDP 1302  
Db 1269 -----REAWALYLFSPQNRFRVSCQKVIITHKMFHDVVLVIFLNCVTIALERP KIDP 1320  
QY 1303 HSAERIFLTSNVIFTAVFLAEMTVKVVALGWCFGEQVLRSSWNVL DGLLVLSVIDIL 1362  
Db 1321 GSTERVFLSVSNYIFTAIFVAAEMVMKVVALGLLSGEHAYLQSSWNLLDGLLVLSVIDIV 1380  
QY 1363 VSMVSDSGTKILGMLRVLRLRLTLRPLRVISRAOGLKLVVETLMSLKPIGNIVVICCAF 1422  
Db 1381 VAMASAGGAKILGVLRLRLTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAF 1440  
QY 1423 FIIFGILGVOLFVKGFVFCQGEDTRNITNKSDCAEASVYVRHKYNFDNLGQALMSLFVL 1482  
Db 1441 FIIFGILGVOLFVKGFYCEGPDTRNISTKAQCAAHYRVRKYNFDNLGQALMSLFVL 1500  
QY 1483 ASKQGVVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIYVAFVFLNMFVGVVVENFHK 1542  
Db 1501 SSKDGWVIMYDGLDAVGVDQOQVQNHNPWMLLYFISFLLIYVAFVFLNMFVGVVVENFHK 1560  
QY 1543 CRQHQEEEEARRREKRLRLEKKRR-----KAQCKPYYSYDSRFRLLVHHLCTSHYLD 1596  
Db 1561 CRQHQEAEEARRREKRLRLERRRSTFPSPAQRPPYADYSPTRRSIHSLSCTSHYLD 1620  
QY 1597 LFTITVIGLNVVTMAHEHYQOQOILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDR 1656  
Db 1621 LFTITICVNVITMSMEHYNQPKSLDEALKICNYIFTVIFVFEAALKLVAFGFRFFQDR 1680  
QY 1657 WNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLD 1716  
Db 1681 WNQLDLAIVLLSIMGITLEEIEMSAALPINPTIIRIMRVLRIRARVLKLLKMATGMRALLD 1740  
QY 1717 TVMQALPQVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLT 1776  
Db 1741 TVVQALPQVGNLGLLFFLFFIYAALGVLEFGLECEDNCPCEGLSRHATFSNFGMAFLT 1800  
QY 1777 LFRVSTGDNWNGIMKDTLRDC--DQESTCVNTVISPFIYFVSFVLTAQFVLNVVIAVLM 1833  
Db 1801 LFRVSTGDNWNGIMKDTLRCSREDKHCLSYPALSPVYFVTFVLVAQFVLNVVIAVLM 1860  
QY 1834 KHLEESNKEAKEEALEAELEEMKTLSPQHPSPGLSGPFLWPVGVEGDPSP--DSPKPGA 1890  
Db 1861 KHLEESNKEAREDAELDAEIELEM-----AQGPGSARRVDADR-- 1899  
QY 1891 LHPAAHARSASHFSLEHPTMQPHTELPG-----PDLLTVRKSGVSRTHSLPNDSYMCRHG 1946  
Db 1900 -----PLQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV 1937  
QY 1947 STAEGP-----LHGRGWGLPKAQSGSVLSVHSOPADTSYIILQPKDAPHLLQPHSA 1997  
Db 1938 VPASAPHRPRLQEVEMETYGAGTP---LGSVASVHSPAESCASLQIP-----LAVSSPA 1989  
QY 1998 PTWGTIPKLPDPG--RSPLAQRPLRROAAIRTDSDLVQGLGSRREDLL--AEVSGPSP--P 2051  
Db 1990 RSGEPLHALSPRGRTARSPSLRLLCRQEAHVTDLSLEK-IDSPRDTLDPAEPEGKTPVRP 2048  
QY 2052 LARAYSFWG--QSSTQAQQHSHRSKISKHMTTPAP-CPGPEPNWGKGPPETRSSLELDT 2108  
Db 2049 VTQGGSLQSPSPRPPASVTRKHT-FGQHCVCSSRPAAPGGE-----EAEASDPADE 2099  
QY 2109 ELSWISGDLLP-----PGQEEPP---SPRDLKKCYVSAQSCQRRPTSWLDEQRHSI 2159  
Db 2100 EVSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGLDKP-GRADEQWRPSA 2158  
QY 2160 AVSCLDSGQPHLGTDPNLGGQPLGGPSRPPKKLSPSITIDPP-ESQGPRTPPSP-- 2216  
Db 2159 ELGSGEPGEAKAWGPE-----AEP--ALGARRKKQMSPPCISVEPPAEDEGSARPSAEG 2211





Db 1440 HTRLIHSMTSHYLDIFITFIICLVNVTMSLEHYNQPTSLETALKYCNMYFTTTFVLEA 1499  
QY 1641 VFKLVAFFRRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIAR 1700  
Db 1500 VLKLVAFGLRRFFKDRWNQDLAIVLLSVMGITLEEIEINAALPINPTIIRMRVLRIAR 1559  
QY 1701 VLKLLKMAVGMRAALLDTVMQALPQVGNLGLLFFMLFFIFAALGVLELFGDLECEDETHPCG 1760  
Db 1560 VLKLLKMATGMRAALLDTVVQALPQVGNLGLLFFMLFFIYAALGVLELFGKLVNDENPCG 1619  
QY 1761 LGRHATFRNFGMAFLTTLFRVSTGDNWNGIMKOTLRDC-DOESTCYNTV--ISPIYFVSFV 1817  
Db 1620 MSRHATFENFGMAFLTTLFQVSTGDNWNGIMKOTLRDCTHDERSCLSLQFVSPLYFVSFV 1679  
QY 1818 LTAQFVLNVVAVLMMKHEESKEAKEAEAELELEM-KTSLSPQSPHPLGSPFLWPG 1876  
Db 1680 LTAQFVLNVVAVLMMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGRLPTGSPGA-PG 1738  
QY 1877 VEGPDSPD-----SPKPGAL-----HPAAHA----- 1897  
Db 1739 -RPGGAGGGDEGLCRRCYSPAQDSLEGELTIIDNLGSGIFHHYSSPAGCKKCHDK 1797  
QY 1898 -----RSAS-----HFSLEHPTMQP-----HPTLPGPDLLTVRKSG-- 1929  
Db 1798 QEVQLAETAFLNSDRSSILLGDDLSLEDPACPPGRKDSKGELDPPEPMRVGDLGEC 1857  
QY 1930 ---VSRTHSLPN-DSYMCRRHGSTAEGPLGRGWGLPKAQSGSVLSVHSPADTSYILQLP 1985  
Db 1858 FFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSOAPSPFSPDASSPLPMP 1913  
QY 1986 KDAH-----LLQPHSAPTWTGTIPKLPPG-----RSPLAQRLRRQAAIRTSLDVQG 2034  
Db 1914 AEFFHFAVSAQKGPEKGTGTGLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLD--- 1970  
QY 2035 LGSREDLLAEVSGSPPLARAYSFWGQSSTQAOQHSRSHSKISKHMTTPPAPCPGPEPNWG 2094  
Db 1971 -----ASPSAGSLQTTLEDSTLSDSPRA-----LGPPAPAGPRAGLS 2012  
QY 2095 KGPPETRSSLELDTLSWISGDLPLPPGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDEQ 2154  
Db 2013 ---PAARRLSL-----RGRGLFSLRLGRA-----HQ 2036  
QY 2155 RRHSIAVCLDSGSOPLHTDSPN---LGQPLGPGSRPKKLSPPSIT---IDPPESQ 2208  
Db 2037 RSHSSGGS-TSPGCTHDSMDPDEEGRGGAGGGGAGSEHSETLSLSLTSFLCPPP--- 2092  
QY 2209 GPRTPPSPGICLRRRAPSSDS-----KPLASGPPDSMAASPSPKDVLSSLGSLSSDPADL 2264  
Db 2093 ---PPPAPGLTPARKFSTSSLAAPCRPHAAALAHGLARSPSWAAD-----RSKDPGPR 2143  
QY 2265 DP 2266  
Db 2144 AP 2145

RESULT 8  
US-10-425-800-2  
; Sequence 2, Application US/10425800  
; Publication No. US20030180886A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; FILE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/10/425,800  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US/09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2175

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-425-800-2  
Query Match 46.1%; Score 5492.5; DB 14; Length 2175;  
Best Local Similarity 51.3%; Pred. No. 0;  
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;  
QY 31 RPPGSAEKDPGSADSAEG---LPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERI 86  
Db 25 QPGRSPSPSPGLEEPLDGADPHVPHPLAPIAFFCLRTQTSRPNWCIVCNPFECV 84  
QY 87 SMLVILLNCVTILGMFRPCEDIACDSQRCRIIQAEDDFIFAFFAVEMVVMVALGIFGKKC 146  
Db 85 SMLVILLNCVTILGMYQPCDDMDCLSDRCKILQVEDDFIFIFFAMENVLKMVALGIFGKKC 144  
QY 147 YLGDTWNRDLFFIIVAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLED 206  
Db 145 YLGDTWNRDLFFIIVMAGMVEYSLDLQNLNLSAIRTVRLRPLKAINRVPSMRILVTLLED 204  
QY 207 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLPENFSLPLSVDLERYYQTEDE 266  
Db 205 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLEENFTIQGDVALPPYQPEEDE 264  
QY 267 SPFICSQPRENMRSCRVPFTRGDDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318  
Db 265 MPFICSLSGDNGIMGCHEIPPLEKEQ---GRECCLSKDDVDFGAGRQDLNASGLCVNWNR 321  
QY 319 YYTNCISAGEHNPFGAINFNDNIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYNIYFILL 378  
Db 322 YYNVCRGTGSANPHKGAINFNDNIGYAWIVIFQVITLEGVWEIMYVMDAHSFYNIYFILL 381  
QY 379 IIVGSFFMINCLVVIATQFSETKQRESQRLMREORVRFLSNASTLASFSEPGSCYEELLK 438  
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASAEPGDCYEEIFQ 440  
QY 439 YLVYILRKAARLAQVSRAGRVVGLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH 498  
Db 441 YVCHILRKAAR-----RALGLYQALQSRQALG----- 468  
QY 499 HHHHHVHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH 558  
Db 469 -----PEAPA--PAKPGP-----H 480  
QY 559 ADCHLEPVRCAQPPRSPSEASGRVTGSKVYPTVHTSPPTILKEKALVEVAASSGPPT 618  
Db 481 AK---EPRHYQLCPQHSPLDATPHTL-----VQIPATL----- 511  
QY 619 LTSNLNIPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672  
Db 512 -----ASDPACPCQCHEDGRRP 529  
QY 673 AGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRSLSGPDAPFSSVL----- 726  
Db 530 SGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSEDCGASSELGKEEEEEQADGAVWL 586  
QY 727 --AFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALISNIVFTS 784  
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFTS 646  
QY 785 LFALEMLLKLIVYGPFGYIKNPYNIPDGVIIVISVWEIVGQGGGLSVLRTFLMRVLKL 844  
Db 647 MFALEMILKLAAGLFDYLRNPYNIFDSIIIVISIWEIVGQADGGLSVLRTFLRLVLKL 706  
QY 845 VRFLPALQRLVVLKMTMDNVATFCMLMLFIFIFSILGMHLFGCKFASERD-GDTLPDR 903  
Db 707 VRFPALRRQLVVLKMTMDNVATFCMLMLFIFIFSILGMHIFGCKFSLRTDGTGTVDDR 766  
QY 904 KNFDSLLWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLVAIL 963  
Db 767 KNFDSLLWAIIVTVFQILTQEDWNVVLNGMASTSPWASLYFVALMTFGNYVLFNLVAIL 826  
QY 964 VEGFQABEISKREDASQQLSCIQLPVDSQGGDANKSESEPDFSPS-----LDGD 1013



Db 827 VEGFAE-----GDANRSYDEQSSNIEEFDKLEGLDSS 863  
Qy 1014 GDRKKCLALVSGEHPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRT----- 1069  
Db 864 GDPKLCPIPMTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRLSLQPD 906  
Qy 1070 -----SSGSAEPGAHEMKSPPSARSSPHSPWASAASWTSSRRSSNSLGRAPSLK 1120  
Db 907 PMLVALGSRKSSVSLGRMSYDQRLSSSRSSYYGPWGRSAWASRRSSWN-----SLK 960  
Qy 1121 RRSPPSGERRSLSGE-GQESQDEEESSE--ERASPAAGSDH-----RHRG 1162  
Db 961 HKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHHHHGHPLAHRHRHR 1020  
Qy 1163 SLEREAKSSFDPDLTQVPLGHRHTASGR--GSASEHQDCNGKSASGRLARALRPDDPPLD 1220  
Db 1021 TSLDNRDSVDLAELVPAVGAPRAAWRAAGPAPGHEDCNGRMPSTIAKDVFTKMGRDGR 1080  
Qy 1221 GDDADDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFPPQSRFRLLCHRIITHKMFEDH 1280  
Db 1081 GED-EEEDYTLCFVRVKMIDVYKPDWCNEVEDWSVYLFSPENRFRVLCQTIIAHKLFDY 1139  
Qy 1281 VVLVIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCGEQA 1340  
Db 1140 VVLAIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFGEMTLKWSLGLYFGEQA 1199  
Qy 1341 YLRSSWNVDGLVLISVIDILVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKL 1400  
Db 1200 YLRSSWNVDGLVVFVSIIDIVVSLASAGAKILGVLRLTLRPLRVISRAPGLKL 1259  
Qy 1401 VVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASV 1460  
Db 1260 VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTNRNITNRSDCMAANY 1319  
Qy 1461 RWVRHKYNFDNLQALMSLFLVASKDGVIMYDGLDAVGVDQOPIMHNPNWMLLYFISF 1520  
Db 1320 RWVHKYNFDNLQALMSLFLVASKDGVNIMYINGLDAVVDQOPVTNHNPNWMLLYFISF 1379  
Qy 1521 LLIVAFFVLNMFVGVVVENFHKCRHQHQBEEARRRREKRLRLEKKRRKAQCKPYSDYS 1580  
Db 1380 LLIVSFFVLNMFVGVVVENFHKCRHQHQBEEARRRREKRLRLEKKRRKAQRLPYATYC 1439  
Qy 1581 RFRLLVHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQOILDBALKICNYIFTVIFVLES 1640  
Db 1440 HTRLIIHSMCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLETALKYCNMYFTTVFVLEA 1499  
Qy 1641 VFKLVAFGFRFFODRWNLQDLAIVLISITMGITLIEIEVNASIPINPTIIRIMRVLRIAR 1700  
Db 1500 VLKLVAFGLRRFFKDRWNQDLAIVLLSVMGITLIEIEINAAALPINPTIIRIMRVLRIAR 1559  
Qy 1701 VLKLLKMAVGMRALLDTVMQALPOVGNLGLJFMLLFFIFAALGVLELFGDLECDETHPCEG 1760  
Db 1560 VLKLLKMATGMRALLDTVVQALPOVGNLGLJFMLLFFIYAALGVLELFGKLVNDENPCEG 1619  
Qy 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1817  
Db 1620 MSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDCTHDSRSLSSLQFVSPLYFVSFV 1679  
Qy 1818 LTAQFVLNVVAVLKMHLSESNKEABEALEAELELEM-KTILSPQPHSPLGSPFLWPG 1876  
Db 1680 LTAQFVLINVVAVLKMHLDDSNKEAQEDAEMDAELEMAHGLGPGPRLPTGSPGA-PG 1738  
Qy 1877 VEGPDSPD-----SPKPGAL-----HPAAHA----- 1897  
Db 1739 -RPGGAGGGGTGGLCRRCYSPAQDSLEGELTIIDNLSGSIFHYSSPAGCKKCHDX 1797  
Qy 1898 -----RSAS-----HFSLEHPTMQP-----HPTELPGPDLTLTVRKS-- 1929  
Db 1798 QEVQLAETAELSINSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGEC 1857  
Qy 1930 ---VSRTHSLPN-DSYMCRRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLP 1985

Db 1858 FFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPSPSPSPDASSPLLPMP 1913  
Qy 1986 KDAPH-----LLQPHSAPTWTGTPKLPPPG-----RSPLAQRPLRRQAARTDSDLVQG 2034  
Db 1914 AEFHHPAVSASQKGEKGTGTGTLPKIALQGSWASLRSRVNCTLLRQATGSDTSLD--- 1970  
Qy 2035 LGSREDLLAEVSGSPPLARAYSFWGOSSTQAQQHSRSHSKISKHMTTPPAPCPGPEPNWG 2094  
Db 1971 -----ASPSSAGSLQTTLEDSTLSDSPRA-----LGPPAPAPGPRAGLS 2012  
Qy 2095 KGPPETRSSLDELDTLSWISGDLPLPGQGEPPSPRDLKKCYVEAQSCQRRPTSWLDEQ 2154  
Db 2013 ---PAARRLSL-----RGRGLFSLRLRA-----HQ 2036  
Qy 2155 RRHSIAVSCLDGSGQPHLGTDPN---LGGQPLGGPGSRPKKGLSPPSIT---IDPPESQ 2208  
Db 2037 RSHSSGGS-TSPGCTHDSMDPSDEGRGGAGGGAGSEHSETLSSLSLTSLFCPPP--- 2092  
Qy 2209 GPRTPPSPGICLRRRAPSSDS---KDPASGPPDMSAASPSPKDVLVLSGLSSDPADL 2264  
Db 2093 ---PPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-----RSKDPGGR 2143  
Qy 2265 DP 2266  
Db 2144 AP 2145

RESULT 9  
US-09-935-541-4  
; Sequence 4, Application US/099335541  
; Patent No. US20020150911A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/935,541  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2188  
; TYPE: PRN  
; ORGANISM: Homo sapiens  
; US-09-935-541-4

Query Match 46.1%; Score 5484; DB 9; Length 2188;  
Best Local Similarity 51.1%; Pred. No. 0;  
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;  
Qy 31 RPPGSAEKDPGSADSEAG---LPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERI 86  
Db 25 QPGPRSPSPSPGLEEPLDGADPHVPHDLPAPIAFFCLRQTTSRPNWCIMVCNPFECV 84  
Qy 87 SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFAVEMVVMVALGIFGKCC 146  
Db 85 SMLVILLNCVTLGMYPQCDMDCLDRCKILQVDFDDFIFAFAMEMVLKMVALGIFGKCC 144  
Qy 147 YLGDTWNRLDFFIVAGMLEYSLDQNVFSFSAVRTVRLRPLRAINRVPSMRILVTLILD 206  
Db 145 YLGDTWNRLDFFIVMAGMVEYSLDQNLNLSAIRTVRLRPLKAINRVPSMRILVNLILD 204  
Qy 207 TPLMLGNVLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPLSVDLERYYQTENEDE 266  
Db 205 TPLMLGNVLLCFFVFFIFGIIIGVQLWAGLLNRNRCFLEENFTIQGDVALPPYYQPEEDE 264  
Qy 267 SPFICSQPRENGMRSRCSVPTRLRGDGGGPPCCGL-----DYEAYNSSNTT---CVNWNQ 318  
Db 265 MPFICSLSGDNGIMGCHEIPLPLEQ---GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR 321

QY 319 YYTNCAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYILL 378  
Db 322 YYNVCRGTSANPHKGAINDFNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYNFIFYILL 381  
QY 379 IIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFPSEPGSCYEEELK 438  
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASAEPGDCYEEIFQ 440  
QY 439 YLVYILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHH 498  
Db 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468  
QY 499 HHHHHYHLGNCTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYH 558  
Db 469 -----PEAPA--PAKPGP-----H 480  
QY 559 ADCHLEPVRCQAPPRSPSEASGRVTGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPT 618  
Db 481 AK---EPRHYQLCPQHSPLDATPHTL-----VOPIPATL----- 511  
QY 619 LTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672  
Db 512 -----ASDPASCPCQCHEDGRRP 529  
QY 673 AGAGEVELADREMPDSDSEAVYFTQQAQHSDLDRPHSRQRSLGPDAAEPSVL----- 726  
Db 530 SGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSSEDGASSELGKEEEEEQADGAVWL 586  
QY 727 --AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISNIVFTS 784  
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHQPEELTNIILEICNVVFTS 646  
QY 785 LFALEMLLKLVLVYGPFGYIKNPYINIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKL 844  
Db 647 MFALEMILKLAAGFLDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLRLVLKL 706  
QY 845 VRFLPALORQLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKFASERD-GDTLPDR 903  
Db 707 VRFPALRRQLVLMKTMNDNVATFCMLLMFLFIFISILGMHIFGCKFSLRTDTGDTVPR 766  
QY 904 KNFDSLLWAIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL 963  
Db 767 KNFDSLLWAIVTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL 826  
QY 964 VEGFOAEISKREDASGQLSCIQLPVDSSQGGDANKSESEPDFFSPS-----LDGD 1013  
Db 827 VEGFOAE-----GDANRSYDEQSSNIEEFDKLQEGLDSS 863  
QY 1014 GDRKKCLALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRT----- 1069  
Db 864 GDPKLCPIPMTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRLSLOPD 906  
QY 1070 -----SSSGSAEPGAHENKSPSPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLK 1120  
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYYGPWGRSAAWASRRSSWN-----SLK 960  
QY 1121 RRSPPSGERRSLSGE-GQESQDEEESSEE--ERASPGASDH-----RHRG 1162  
Db 961 HKPPSAEHESLLSAERGGGARVCEVADEGPPRAAPLTHFAHHIHHGPHLAHRHRHR 1020  
QY 1163 SLERAKSSFDLPDTLQVPLHRTASGR--GSASEHQCNKGSASGRLARALRPDDPPLD 1220  
Db 1021 TSLDNRDSVDLAELVPAVGAPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGDR 1080  
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFEDH 1280  
Db 1081 GED-EEEDYTLCFVRKMDIVYKPDWCEVREDWSVYLFSPENFRVLCQTIHAHKLFDY 1139  
QY 1281 VVLVIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFFEQA 1340  
Db 1140 VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGMTLKVVSGLYFFEQA 1199  
QY 1341 YLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLTLRPLRVISRAQGLKL 1400

RESULT 10

Db 1200 YLRSSWNVDGLFVFSIIDIWVSLASAGAKILGVRLVRLRLTLRPLRVISRAPGLKL 1259  
QY 1401 VVETLSSSLKPIGNIVVICCAFFIIFGILGVOLFKGFFVCQGEDTRNITNKSDCAEASY 1460  
Db 1260 VVETLSSSLKPIGNIVVICCAFFIIFGILGVOLFKGFFYHCLGVDTRNITNRSDCMAANY 1319  
QY 1461 RWVRHKYNFDNLGOALMSLFVLASKDGVWDIMYDGLDAVGDDQQPIMNHNPMWMLLYFISF 1520  
Db 1320 RWVHKYNFDNLGOALMSLFVLASKDGVWNIMYNGLDVAVDQQPVTNHNPMWMLLYFISF 1379  
QY 1521 LLIVAFFVLNMFVGVVVENFHKCRHQHEEEEEARRREKRLRLEKRRKCAQCKPYSDYS 1580  
Db 1380 LLIVSFFVLNMFVGVVVENFHKCRHQHEEEEEARRREKRLRLEKRRKCAQRLPYATYC 1439  
QY 1581 RFRLLVHLCCTSHYLDLFTITGVIGLNVVVTMAMEHYQOQILDEALKICNYIFTVIFVLES 1640  
Db 1440 HTRLIIHSMCTSHYLDIFITFIICLNVVVTMSLEHYNQPTSETALKYCNMYMETVTFVLEA 1499  
QY 1641 VFKLVAFGFRFFQDRWNQOLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIAR 1700  
Db 1500 VLKLVAFGLRFFFKDRWNQOLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLIAR 1559  
QY 1701 VLKLLKMAVGMRALLDTVMQALPOVGNLGLLMLFFIIPAAALGVLEFGDLECDETHPCEG 1760  
Db 1560 VLKLLKMATGMRALDVTWQALPOVGNLGLLMLFFIYAAALGVLEFGKLVCDENPCEG 1619  
QY 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKOTLRDC-DOESTCYNVTV--ISPIYFVSFV 1817  
Db 1620 MSRHATFENFGMAFLTFRVSTGDNWNGIMKOTLRDCTHDESLSSLOFVSPLFVSFV 1679  
QY 1818 LTAQFVLNVVVIIVLMKHEESKEAEAEAELELELEM-KTLSPOHSPHPLSGPFLWPG 1876  
Db 1680 LTAQFVLNVVVIIVLMKHLDDSNKEAQEDAEAELELEMAHGLGPGPRLPTGSPGA-PG 1738  
QY 1877 VEGPD-----SP-----DSPKPGALH-- 1892  
Db 1739 -RPGGAGGGDTEGGLCRRCYSPAQENLWLDVSLSIIKDSLEGELTIIDNLSGSIFHHY 1797  
QY 1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTLEP 1918  
Db 1798 SSPAGCKKCHDKQEVQLAETEAFLNSDRSSILLGDDLSELDPTACPPGRKOSKGELD 1857  
QY 1919 GPDLTLVRKSG-----VSRTHSLPN-DSYMRCHGSTAEGPLGHRGWGLPKAQSGSVLSVH 1972  
Db 1858 PPEPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSP 1913  
QY 1973 SQPADTSYILQLPKADPH-----LLQPHSAPTWGTIPKLPPPG-----RSPLAQRPLRR 2021  
Db 1914 FSPDASSPLLPMPAEFFHPAVSASQXGPEKGTGTGLPKIALQGSWASLRSRPNVCTLLR 1973  
QY 2022 QAAIRTSLDVQGLGSRREDLLAEVSGSPPLARAYSFQWQSSTQAAQHSRSHSKISKHMT 2081  
Db 1974 QATGSDTSLD-----ASPSSSAGSLQTTLEDSTLSDSPRA-----LG 2012  
QY 2082 PPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYVSAEQ 2141  
Db 2013 PPAPAPGPAGLS---PAARRRLSL-----RGRGLFSLRGLRA- 2047  
QY 2142 SCQRRPTSWLDEQRHRSIAVSCLDGSGSPHLGTDPSN---LGGQPLGGPSRPPKKLSPP 2198  
Db 2048 -----HQRSHSGGS-TSPGCTHDSMDPSPDEEGRGGAGGGAGGSEHSETLSSL 2095  
QY 2199 SIT---IDPPESQGPRTPPSPGICLRRRAPSSDS-----KDLASGPPDMSMAASPPKDV 2251  
Db 2096 SLTSLFCPPP-----PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD- 2148  
QY 2252 LSLGSLSSDPADLDP 2266  
Db 2149 -----RSKDPGGRAP 2158

US-10-425-800-4  
; Sequence 4, Application US/10425800  
; Publication No. US2003018086A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/10/425,800  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US/09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-425-800-4  
Query Match 46.1%; Score 5484; DB 14; Length 2188;  
Best Local Similarity 51.1%; Pred. No. 0;  
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;  
QY 31 RPPGSAEKDPCGADSEAG----LPYPALAPVVFYLSQSRPRRSWCLRTVCNPNPFI 86  
DB 25 QGPRSPSPSPGLEPLDGDAPHVPHDLAPIAFFCLRTQTSRPNWCIMKVCNPNPECV 84  
QY 87 SMLVILLNCVTLMFRPCEDIACDSQRCLQAFDDFIFAFPAVEMVVKMVALGIFGKKC 146  
DB 85 SMLVILLNCVTLMGVQPCDDMDCLSDRCKILQVDFDFIFIFPAMEMVLKQVALGIFGKKC 144  
QY 147 YLGDWTNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTL 206  
DB 145 YLGDWTNRLDFFVWAGVVEYSLDLQNINLSAIRTVRVLRPLKAINRVPSMRILVN 204  
QY 207 TPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDLERYQOTENE 266  
DB 205 TPLMLGNVLLLCFFVFFIFGIIQVQLWAGLLRNRCFLEENFTIQGDVALPPYQPE 264  
QY 267 SPFICSQPRENGMRSCRSVPTLRDGGGGPPCCGL-----DYEAYNSSNTT--CV 318  
DB 265 MPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKODVYDFGAGRQDLNASGLCV 321  
QY 319 YNTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILL 378  
DB 322 YNVVCRGTSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFIFILL 381  
QY 379 IIVGSFFMINCLVVIATQFSETKQRESQLMREQRVRFSLNASTLASFSEPGSCYBELLK 438  
DB 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS--SSTVASAEPGDCYEIFQ 440  
QY 439 YLVYILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRRLSVHHLVHH 498  
DB 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468  
QY 499 HHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH 558  
DB 469 -----PEAPA--PAKPGP-----H 480  
QY 559 ADCHLEPVRCQAPPRSPSEASGRITVSGKVYPTVHTSPPPETIKEKALVEAASSGPPT 618  
DB 481 AK---EPRHYQLCPQHSPLDATPHTL-----VQIPATL----- 511  
QY 619 LTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672  
DB 512 -----ASDPASCPCQCHEDGERP 529  
QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVL----- 726  
DB 530 SGLGSTD-SGQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEEEQADGAVWL 586

QY 727 --AFWRLICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 784  
DB 587 CGDVWRETRAKLRGIVDSKYFNRGINMAILVNTVSMGIEHHEQPEELTNIILEICNVFTS 646  
QY 785 LFALEMLKLIVYGPFGYIKNPYNIFDGVIVVVISVWEIVGQGGSLSVLRTFRLMRVLKL 844  
DB 647 MFALEMILKLAAGLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVLRTFRLLRVLKL 706  
QY 845 VRFLPALQROLVVLKMTMDNVATFCMLMLFIFIESILGMHLFGCKFASERD-GDTLPDR 903  
DB 707 VRFPALRRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKFSLRTDGTVPDR 766  
QY 904 KNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAAALYFIALMTFGNYVLFNLLVAIL 963  
DB 767 KNFDSLLWAIVTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL 826  
QY 964 VEGFOAEISKREDASGQLSCIQLPVDSSQGGDANKSESEPDFFSPS-----LDGD 1013  
DB 827 VEGFOAE-----GDANRSYDEDOSSSNIIEFDKLEGLDSS 863  
QY 1014 GDRKKCLALVSLGEHPELRKSLPPLIHTAATPMSLPKSTSTGLGEALGPASRRT---- 1069  
DB 864 GDPKLCPIPTPNHG-----LDP-----SLPLGGHLGPAGAAGPAPRLSLQPD 906  
QY 1070 -----SSGSAEPGAHEMKSPPSARSSPHSPWSAASWTSSRRSSRSLGRAPSLK 1120  
DB 907 PMLVALGSRKSSVMSLGRMSYDQSLSSSRSSYYGPWGRSAWASRRSSWN-----SLK 960  
QY 1121 RRSPPSGERRSLSGE-GQESQDEESSEE--ERASPAAGSDH-----RHRG 1162  
DB 961 HKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHHHHGHPLAHRHRHRR 1020  
QY 1163 SLERAKSSFDLPDTLQVPGHLRTASGR--GSAHEQDCKGKSASGRALARALRDPDPLD 1220  
DB 1021 TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAPGHEDCGRMPFIAKDVFTKMGDRGDR 1080  
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFFPQSRFRLLCHRIITHKMFH 1280  
DB 1081 GED-EEEIDYTLCFVRKMDIVVKPDWCEVREDWSVYLFSPENFRVLCTIIAHKLFY 1139  
QY 1281 VLVVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVALGWCFEQA 1340  
DB 1140 VLAFLIFLNCITIALERPOIEAGSTERIFLTVSNYIFTAIFVGMTLKVVSIGLYFGEQA 1199  
QY 1341 YLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLTLRPLRVISRAOGLKL 1400  
DB 1200 YLRSSWNVLDGELVFVSIIDIVVSLASAGGAKILGVLRLRLTLRPLRVISRAPGLKL 1259  
QY 1401 VVETLMSILKPIGNIVVICCAFFIIFGILGVQLFGKFFVCOGEDTRNITNKSDCAEASY 1460  
DB 1260 VVETLISLKPIGNIVLICCAFFIIFGILGVQLFGKFFYHCLGVLDTRNITNRSDCMAANY 1319  
QY 1461 RWVRHKYNFDNLGQALMSLVLASKDGWVDIMYDGLDAVGVDQPPIMNHNPMMLLYFISF 1520  
DB 1320 RWVHHKYNFDNLGQALMSLVLASKDGWVIMYNGLDADAVIDQPPVTNHNPMMLLYFISF 1379  
QY 1521 LLIVAFFVLNMFVGVVVENFHKRQHQEAEARRRREKRLRLEKKRRKAQCKPYVSDYS 1580  
DB 1380 LLIVSFFVLNMFVGVVVENFHKRQHQEAEARRRREKRLRLEKKRRKAQRLPYVATYC 1439  
QY 1581 RFRLLVHHLCTSHYLDLDFITGVIGLVNVTVMAMEHYQQPQILDEALKICNYIFTVIFVLES 1640  
DB 1440 HTRLLIHSMTCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLTALKYCNMYFTTVFVLEA 1499  
QY 1641 VFKLVAFGERRFFQDRWNQDLDAIVLLSIMGITLEEIEVNASLPINPNTIIRIMRVLRIAR 1700  
DB 1500 VLKLVAFGLRRFFKDRWNQDLDAIVLLSVMGITLEEIEINAAALPINPTIIRIMRVLRIAR 1559  
QY 1701 VLKLLKMAVGMRALDVTVMQALPQVGNLGLLMLLFFIFAALGVELFGDLECEHPCEG 1760  
DB 1560 VLKLLKMAVGMRALDVTVMQALPQVGNLGLLMLLFFIFAALGVELFGKLVNDENPCEG 1619  
QY 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1817

Db 1620 MSRHATFENFGMAFLJTLFOVSTGDNWNGIMKDTLRDCTHDERSCUSSLOQFVSPLYFVSFV 1679

QY 1818 LTAQFVLNVVIAVLMKHLSESNKEAKEAELEAELELEM-KTSLSPQSPHSPGLSPFLWPG 1876

Db 1680 LTAQFVLNVVIAVLMKHLSDSNKEAQEDAEMDAELEMAHGLGPGRLPTGSPGA-PG 1738

QY 1877 VEGPD-----SP-----DSPKPGALH-- 1892

Db 1739 -RPGGAGGGGDEGLCRRCYSPAQENLWLDVSLLIKDSLEGELTIIDNLGSIFFHY 1797

QY 1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTPLP 1918

Db 1798 SSPAGCKKCHHDKQEVQLAETEAFSLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELD 1857

QY 1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVH 1972

Db 1858 PPEPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSP 1913

QY 1973 SQPADTSYILQPKDAPH-----LLQPHSAPTWTGTIPKLPPLPG-----RSPLAQRLRR 2021

Db 1914 FSPDASSPLLPMAEFHFAVASAQGPEKGTGTGLPKIALQGSWASLRSPRVNCTLLR 1973

QY 2022 QAAIRTDSDVQGLGSRDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKSKHMT 2081

Db 1974 QATGSDTSLD-----ASPSSAGSLQTTLEDLSLSDSPRA-----LG 2012

QY 2082 PPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDLPLPGGQHEPPSPRDLKKCYVSEAQ 2141

Db 2013 PPAPAGPFRAGLS---PAARRLSL-----RGRGLFSLRGLRA- 2047

QY 2142 SCQRRTSWLDEQRHSIAVSCLDGSGSQPHLGTDPN---LGGQPLGGPGSRPKKLSPP 2198

Db 2048 -----HQRSHSGGS-TSPGCTHDSMDPSDEEGRGAGGGGAGSEHSETLSSL 2095

QY 2199 SIT---IDPPESQGRTPPPSPGICLRRRAPSDS-----KDPLASGPPDSMAASPSPKKDV 2251

Db 2096 SLTSLFCPPP-----PPAPGLTPARKFSTSSLAAPGRPHAAALAHGLARSPSWAAD- 2148

QY 2252 LSLGLSSDPADLDP 2266

Db 2149 -----RSKDPGGRAP 2158

RESULT 11

US-09-935-541-5

; Sequence 5, Application US/09935541

; Patent No. US20020150911A1

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-935-541-5

Query Match 45.1%; Score 5366; DB 9; Length 1835;

Best Local Similarity 56.8%; Pred. No. 0;

Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;

QY 83 FERISMLVILLNCVTLMGMRPCEDIACDSQRCRILQAFDDFIFFAFVAVMVVWVWALGIF 142

Db 79 FECVSMVLVILLNCVTLMGYQPCDDMECLSDRCKILQVDFDDFIFFAFVAVMVVWVWALGIF 138

QY 143 GKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRRAINRVPSMRILVT 202

Db 139 GKCYLGDWTNRLLDFFIVMAGMVEYSLDLQNLNSAIRTVRVRPLKAINRVPSMRILVN 198

QY 203 LLLDTPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLFLENFSLVSDLERYYQTE 262

Db 199 LLLDTPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLFLENFTIQGDVALPPYYQPE 258

QY 263 NEDESPFICSQPRENGMRSRCSVPVTLRGDGGGPPCGL-----DYEAYNSSNTT--CV 314

Db 259 EDEMPFICSLTGDNGIMGCHBIPLKEQ---GRECLSKDDVYDFGAGRQDLNASGLCV 315

QY 315 NNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYI 374

Db 316 NNRYYNVCRGTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYYVMDAHSFYNFYI 375

QY 375 FILLIIVGSFFMINCLVVIATOFSETKQESQMRBORVFLSNASTLASFSEPGSCYE 434

Db 376 FILLIIVGSFFMINCLVVIATOFSETKQESQMRBORVFLSNASTLASFSEPGSCYE 434

QY 435 ELLKYLVIILKKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHL 494

Db 435 EIFQYVCHILKAKRRALGLYQALQNR----- 461

QY 495 VHHHHHHHHVHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVH 554

Db 462 -----RQAMG-----PGTPA--PAKPGP----- 477

QY 555 SFYHADCHLEPVRQAPPPSPSEASGRVGVSGKVYPTVHTSPPPETLKEKALVEVAASS 614

Db 478 ---HAK---EPHCKLCPHSPLD-----PTPHTLVQP----- 504

QY 615 GPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-- 672

Db 505 -----ISAILASD-----PSSCPHCOHEA 523

QY 673 ---AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLGDAEPSSVLA- 727

Db 524 GRRPSGLGSTD-SGQEGSGSGSAEAEANGDG---LQSSDGVSSDLGKEEEQEDGAAR 578

QY 728 ---FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIYEHQEPBELTNALEISNIVFT 783

Db 579 LCGDVWRETRKRLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQEPBELTNILEICNVVFT 638

QY 784 SLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISWVEIVGQGGGLSVLRTFRLMRVLK 843

Db 639 SMFALEMILKLAAGFLFDYLRNPYNIFDSIIIVISIWEIVGADGGLSVLRTFRLLRVLK 698

QY 844 LVRFLPALORQLVVLMTMDNVATFCMLLMLFIFIFISILGMHLFGCKFASERD-GDTLPD 902

Db 699 LVRFMPALRRQLVVLMTMDNVATFCMLLMLFIFIFISILGMHLFGCKFSLRTDGTVPD 758

QY 903 RKNFDSLILWAIWTVFOILTQEDWNKVLNGMASTSSWAALYFIALMTFGNVVLFNLLVAI 962

Db 759 RKNFDSLILWAIWTVFOILTQEDWNVVLNGMASTTPWASLYFVALMTFGNVVLFNLLVAI 818

QY 963 LVEGFQAEIISKREDASQLSCILQLPVDSQGGDANKSESEPDFFSPS-----LDG 1012

Db 819 LVEGFQAE-----GDANRSCDEDDQSSSNLEEFDKLPEGLDN 855

QY 1013 DGDRKKCLALVSLGEHPELKRSLPLPLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071

Db 856 SRDLKLCPIPMTPNGH-----LDP-----SLP-----LGAHLGPAGTGTAP 892

QY 1072 SGSAEPG-----AAHEMKSPPSARSSPHSPWSAASSWTSRRSRNSL 1113

Db 893 RLSLQPDVPLVALDSRKSSVMSLGRMSYDQRLSSSRSSYYCPGWRSGTWSRRSSWN-- 950



QY 1114 GRAPSLKRRSPGERRSLLSGEGQESQDEE-ESSEEE---RASPGSDH----- 1158  
Db 951 -----SLKHKPPSABHESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAHAGHGHILA 1006  
QY 1159 ----RHRGSLEREAKSSFDLPDTLQVPGHLHTAS--GRGSASEHDCNGKSASRLARAL 1212  
Db 1007 HRRHRRRTSLDTRDSVDLGELVPVVGHAHRAAWRGAGQAPGHEDCNGRMPNIAKDVT 1066  
QY 1213 RPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI 1272  
Db 1067 KMDDRRDRGED-EEEDYTLCFVRVKMIDVYKPDWCVEVDWVSYLEFSPENKFRILCOTI 1125  
QY 1273 ITHKMFEDHVVLVILFNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1332  
Db 1126 IAHKLFYVVLAFIFLNCITIALERPOIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVS 1185  
QY 1333 GWCFGQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLLRLLRPLRVI 1392  
Db 1186 GLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSVASAGGAKILGVLRVLRLLRPLRVI 1245  
QY 1393 SRAOGLKLVETIMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNITNK 1452  
Db 1246 SRAPGLKLVETLSSSLKPIGNIVVICCAFFIIFGILGVQLFKGFYHCLGVDTNRITNR 1305  
QY 1453 SDCAEASRWVRHKYNFNDLGOALMSFLVLASKDGVVDIMYDGLDVGVDQOPIMNHPW 1512  
Db 1306 SDCVAANYRWVHKYNFNDLGOALMSFLVLASKDGVNIMVNGLDVAVDQOQVTVNHPW 1365  
QY 1513 MLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHOOEAEARRRLEKRRKAQC 1572  
Db 1366 MLLYFISFLLIIVSFVLMFVGVVVENFHKCRHQHOOEAEARRRLEKRRKAQR 1425  
QY 1573 KPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQOPQILDEALKICNYIF 1632  
Db 1426 LPYATYCPTRLIHSMTCTSHYLDIFITFICLVNVTMSLEHYNQPTSETALKYCNMF 1485  
QY 1633 TVIFVLESVKLVAFGRFRFFQDRWNQDLAIVLLSIMGITLLEIEVNASLPINPTIIRI 1692  
Db 1486 TTVFVLEAVLKVAFGLRFRFFKORWNQDLAIVLLSVMGITLLEIEINAALPINPTIIRI 1545  
QY 1693 MRVLRIARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLEC 1752  
Db 1546 MRVLRIARVLKLLKMATGMRALDVTVMQALPQVGNLGLLFMLFFIYAALGVLEFGKIVC 1605  
QY 1753 DETHPCEGLRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS 1809  
Db 1606 NDENPCEGMSRATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCSSLOFVS 1665  
QY 1810 PIYFVSFVLTAQFVLNVVIAVLKMLEESNKEAKEEAELEAELELEM-KTLSPOPHSPL 1868  
Db 1666 PLYFVSFVLTAQFVLINVVAVLKMHLDDSNKEAQEDAEMDAIELEMAHGLGPCP---- 1721  
QY 1869 GSPFLWPGVEGSDSPSPKPGALHPAAHARSASHFSLEHPTMQPHPTLPDPLLTV--- 1925  
Db 1722 -----GPCPG-----PCPCPCPCPCAGPRLPTSSPG 1747  
QY 1926 ---RKSGVSRTHSLPNDSYMCRH 1945  
Db 1748 APGRSGGAGAGG-DTESHLCH 1769

RESULT 12

US-10-425-800-5  
; Sequence 5, Application US/10425800  
; Publication No. US20030180886A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/10/425,800  
; CURRENT FILING DATE: 2003-04-29

; PRIOR APPLICATION NUMBER: US/09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1835  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-425-800-5  
  
Query Match 45.1%; Score 5366; DB 14; Length 1835;  
Best Local Similarity 56.8%; Pred.No. 0;  
Matches 1138; Conservative, 183; Mismatches 346; Indels 336; Gaps 38;  
  
QY 27 GAGGRPGGSAEKDPGSADSEAE-----LPYPALAPVVFVYLSQDSRPRSWCLRTVCNPW 82  
Db 19 GITEQPGPRSPPPSPGLEELEGNTDPVPHDLAPVAFCLRQTTSRPNWCIMKVCNPW 78  
QY 83 FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIAFFAVEMVVMKVALGIF 142  
Db 79 FECVSMVLILLNCVTLGMYPQCDMECLSDCKILQVFDDFIFIFFAMEMVLKVALGIF 138  
QY 143 GKCYLGDWTNRLDFFIVIAAGMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVPSMRILVT 202  
Db 139 GKCYLGDWTNRLDFFIVMAGMVEYSLDLQNLNSAIRTVRLRPLKAINRVPSMRILVN 198  
QY 203 LLLDTPMLGNVLLLCFFVFFIFGIVGVQVLWAGLLNRNRCFLPENFSLPLSVDLERYIQTE 262  
Db 199 LLLDTPMLGNVLLLCFFVFFIFGIVGVQVLWAGLLNRNRCFLPENFTIQGDVALPPYQPE 258  
QY 263 NEDESPFICSPQPRENMRSCRSVPTLRGDGGGPPCGL-----DYEAYNSSNTT--CV 314  
Db 259 EDEMPFICSLTGDNGIMGCHETPPLKEQ---GRECCLSKDDVDYDFGAGRODLNASGLCV 315  
QY 315 NWNQYTNCSAGEHNPFKGAINFNDNIGYAMIAIFQVITLEGWVDIMYFVMDAHSFYNYFI 374  
Db 316 NWNRYNVCRGTGNANPHKGAINFNDNIGYAGIVIFQVITLEGWVEIMYVMDAHSFYNYFI 375  
QY 375 FILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNASTLASFSEPGSCYE 434  
Db 376 FILLIIVGSFFMINCLVVIATQFSETKQEHRLMLEQRQYLS-SSTVASAEPGDCYE 434  
QY 435 ELLKYLVTILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHL 494  
Db 435 EIFQVCHILRKAKRRALGLYQALQNR----- 461  
QY 495 VHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVH 554  
Db 462 -----RQAMG-----PGTPA--PAKPGP----- 477  
QY 555 SFYHADCHLEPVRCAOPPRSPSEASGRTVSGKVYPTVHTSPPETLKEKALVEVAASS 614  
Db 478 ---HAK---EPSHCKLCPRHSPLD-----PTPHTLVQP----- 504  
QY 615 GPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-- 672  
Db 505 -----ISAILASD-----PSSCPHCQHEA 523  
QY 673 ----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRSLGPDAPSSVLA- 727  
Db 524 GRRPSGLGSTD-SQOEGSGSGSAEAEANGDG----LOSSEDGVSSDLGKEEEDGAAR 578  
QY 728 ----FWRLICDTFRKIVDSKYFGRGIMIAAILVNTLSMGIBYHEQPEELTNALEISNIVFT 783  
Db 579 LCGDVWRERTRKKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFT 638  
QY 784 SLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLK 843  
Db 639 SMFALEMILKLAAGFLDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLMRVLK 698  
QY 844 LVRFPLALQRLVLMKTMNDNVATFCMLLMFLIFISILGMHLFGCKFASERD-GDTLPD 902  
Db 699 LVRFMPALRRQLVLMKTMNDNVATFCMLLMFLIFIFISILGMHIFGCKFSRLRTDGTVPD 758



QY 903 RKNFDSLLWAIIVTFQILTOEDWNVLYNGMASTSSWAALYFIALMTFGNYVLENLIVAI 962  
Db 759 RKNFDSLLWAIIVTFQILTOEDWNVLYNGMASTTPWASLYFVALMTFGNYVLENLIVAI 818  
QY 963 LVEGFOAEHISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS-----LDG 1012  
Db 819 LVEGFOAE-----GDANRSCSDEQSSSLEEFDKLPEGLDN 855  
QY 1013 DGDRKKCLALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071  
Db 856 SRDLKLCPIPMTPNGH-----LDP-----SLP-----LGAHLGPAAGTMGTAP 892  
QY 1072 SGSAEPG-----AAHEMKSPPSARSSPHSPWSAASWTSRRSSRNSL 1113  
Db 893 RLSLQPDPLVALDSRKSSVMSLGRMSYDQRLSSSRSSYYGPWGRSGTWASRRSSWN-- 950  
QY 1114 GRAPSLKRRSPSGERRSLLSGEGQESQDEE-ESSEEE---RASPAGSDH----- 1158  
Db 951 ----SLKHKPPSAEHESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAHHAHGHPLA 1006  
QY 1159 ----RHRSGLEREAKSSFDLPDTLQVPLHRTAS--GRGSASEHQCNGKSASGRLARAL 1212  
Db 1007 HRHRHRRRTLSLDRSDVDLGELVPVVGHAHRAAWRGAGAPGHEDCNGRMENIAKDVFT 1066  
QY 1213 RPDDPPLDGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRPRLCHRI 1272  
Db 1067 KMDDRRDRGED-EEEDYTLCFVRKMDIVKPDWCVEVREDWSVYLFSPENKPRILCQTI 1125  
QY 1273 ITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLNVIYFTAVFLAEMTVKVVAL 1332  
Db 1126 IAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMLKVVSL 1185  
QY 1333 GWCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTRPLRVI 1392  
Db 1186 GLYFGEQAYLRSSWNVDGLFLVFSIIDIVSVASAGGAKILGLVLRVLRLLRTRPLRVI 1245  
QY 1393 SRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK 1452  
Db 1246 SRAPGLKLVVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGFYHCLGVDTRNITNR 1305  
QY 1453 SDCAEASVVRVHRKYNFNDLQALMSLFLVLASKDGVVDIMYDGLDAVGVDQOPIMHNFW 1512  
Db 1306 SDCVAANYRWVHHKYNFNDLQALMSLFLVLASKDGVNIMYNGLDVAVDQOQPVTHNFW 1365  
QY 1513 MLLYFISFLLIIVAFFVLNMFVGVVVENFHKRQHQBEEEEARRREEKRLRLEKRRKAQC 1572  
Db 1366 MLLYFISFLLIIVFFVLNMFVGVVVENFHKRQHQBAAEARRREEKRLRLEKRRKAQR 1425  
QY 1573 KPYYSYSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQOQLDEALKICNYIF 1632  
Db 1426 LPYATYCTPRLLIHSMCTSHYLDIFITFIIICLVNVTMSLEHYNQPTSLTALKYCNMF 1485  
QY 1633 TVIFVLESVFKLVAFGRFRFFQDRWNQLDLAIVLLSINGITLEEIEVNASLPINPTIIRI 1692  
Db 1486 TTVEVLEAVLKVAFGLRFRFFKDRWNQLDLAIVLLSINGITLEEIEINAAIPINPTIIRI 1545  
QY 1693 MRVLRIRVLRKLVKMAVGMRRALLDTVMQALPQVGNLGLLFFLFFIFAALGVELFGDLEC 1752  
Db 1546 MRVLRIRVLRKLVKMATGMRRALLDTVVQALPQVGNLGLLFFLFFIYAALGVELFGKLV 1605  
QY 1753 DETHPCGLGRHATFENFGMAFLTLFRVSTGDNWNGIMKDTLDC-DQESTCVNTV--IS 1809  
Db 1606 NDENPCGMSRHAFTENFGMAFLTLFVSTGDNWNGIMKDTLDCDTHDERTCLSSLOFVS 1665  
QY 1810 PIYFVSFVLTAQFVLNVVVIIVLVMKHEESNKEAEAELEAELELEM-KTLPQPHSPL 1868  
Db 1666 PIYFVSFVLTAQFVLNVVVIIVLVMKHLDSNKEAQEDAEMDAIELEMAHGLGPCP---- 1721  
QY 1869 GSPFLWPGVEGPDSPDSKPKGALHPAAHARSASHFSLEHPTMQPHPTLPDPDLTV--- 1925  
Db 1722 -----GPCFG-----PCPCPCPCPCAGPRLPTSSPG 1747

QY 1926 ---RKSGVSRTHSLPNDSYMCRH 1945  
Db 1748 APGRSGGAGAGG-DTESHLCRH 1769  
RESULT 13  
US-09-030-482B-19  
; Sequence 19, Application US/09030482B  
; Patent No. US2002009772A1  
; GENERAL INFORMATION:  
; APPLICANT: Snutch, Terry  
; APPLICANT: NeuroMed Technologies, Inc.  
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED  
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS  
; FILE REFERENCE: 38109-20007.00  
; CURRENT APPLICATION NUMBER: US/09/030,482B  
; CURRENT FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: US 60/039,204  
; PRIOR FILING DATE: 1997-02-28  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 1853  
; TYPE: PRT  
; ORGANISM: Human  
US-09-030-482B-19  
Query Match 33.3%; Score 3959.5; DB 9; Length 1853;  
Best Local Similarity 46.8%; Pred. No. 4e-241;  
Matches 908; Conservative 158; Mismatches 361; Indels 515; Gaps 42;  
QY 27 GAGGRPG-----PGSAEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSCLRTVC 79  
Db 76 GTGHTGTFOGABEPGSSQHPAQATYTAGCTPAPTGDPTCCFVLD-----LVC 124  
QY 80 NPWFERISMLVILNVCVTGLMFRPCEDIACDSQRCRILQAEDDFIFAFFAVEMVVKVAL 139  
Db 125 T-WFECVSMVLILNVCVTGLMYQPCDDMDCLSDRCKILQVFDDEFIFFFAMEMVLKVAL 183  
QY 140 GIFGKKCYLGDWTNRLDFFIIVIAQMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRI 199  
Db 184 GIFGKKCYLGDWTNRLDFFIIVAG-----NINLSAIRTVRLRPLKAINRVPSMRI 234  
QY 200 LVTLILLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERY 259  
Db 235 LVNLLDTPMLGNVLLLCFFVFFIFGIIIGVQLWAGLLRNRCFLEENFTIQGDVALPPY 294  
QY 260 QTENEDESPFICSPRENGMRSCRSVPTLRGCGGGPPCGL-----DYEAYNSSNTT- 312  
Db 295 QPEEDDEMPFICSLSGDNGIMGCHEIPLKEQ--GRECCLSKDDVYDFGAGRQDLNASG 351  
QY 313 -CVWNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN 371  
Db 352 LCVWNRYNVVCRGTSANPHKGAINFNDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYN 411  
QY 372 FIYFILLII----- 380  
Db 412 FIYFILLIISELHLVMPDCSFSTAQSPKCQGDLSLPGVAAESLLLRDSSSVITDEAAM 471  
QY 381 ----- 380  
Db 472 ENLLAGTSKGDESILLRAGSQVHSQAQOQMLGRGLGPESLETGETEHPHSWSPRATRRWDPO 531  
QY 381 -----VGSFFMINLCLVVIATQFSETKQESQLMREQVRFLSNASTLAS 425  
Db 532 CQPQQLPLHFMOAQVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVAS 590  
QY 426 FSEPGSCYEELLYLVILRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRS 485  
Db 591 YAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQALQSRQALGPEAPAKP----- 640  
QY 486 HRRLSVHHLVHHHHHHHHHHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGA 545

Db 641 -----GPHAKEPRHYPLTVWESILGRQAECTLRAA-----AHPSSGAS 679

Qy 546 PPG-GAESVHSFYHADCHLEPVRCAQAPPRSPSEASGRITVSGKVYPTVHTSPPPETLKE 604

Db 680 HPGVGSEEA-----PELC---PQHSPLDATPHTL-----VQPIPATL-- 713

Qy 605 KALVEVAASSGPPTLTSNLNPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGP 664

Db 714 -----ASDP 717

Qy 665 DSCPYPAR-----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGP 718

Db 718 ASCPCCQHEDGRPPSGLSTD-SGQEGSGSGSAGGE--DEADGDGARSSSEDGASSELGK 774

Qy 719 DAEPSSVL-----AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPE- 769

Db 775 EEEEEQADGAVMLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQASA 834

Qy 770 -----ELTNALE-----ISNIV----- 781

Db 835 AQGRACGRGQNPDLCTMKAPCLCHNVSPSPGGVLSHPVTPHTAPWRMETGKQHGCE 894

Qy 782 -----FTSLFALEMLLKLLVYGPFGYIKPNYNIFDGVIVVLSVWEIVGQGGGLSVLRT 835

Db 895 EGPQRSSDMFALEMILKLAAGFLDYLRNPYNIFDSIIIVISWEIVGADGGLSVLRT 954

Qy 836 FRLMRVLKLVRELPAQRLQVLVLMKTMNDVATFCMLLMFLIFISILGMHLFGCKFASER 895

Db 955 FRLLRVLKLVRFMPALRRQLVLMKTMNDVATFCMLLMFLIFISILGMHIFGCKFSLRT 1014

Qy 896 D-GDTLPDRKNFDSLLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNVY 954

Db 1015 DTGDTVPRKNFDSLLWAIIVTFQILTOEDWNKVLYNGMASTSPWASLYFVALMTFGNVY 1074

Qy 955 LFNLLVAILVEGFAE-EISKREDA-----SGQLSCIQLP 988

Db 1075 LFNLLVAILVEGFAEVTVLAEEAPPQGLRKTGRGRGLDGGGLQFKLLAGNLS-LKEG 1133

Qy 989 VDSQGGDANKSESEPDPFFSPS-----LDGDGRKKCLALVSLGEHPELRKSILLPP 1038

Db 1134 VADEVGDANRSYDEDDQSSNIEEFDKIQEGLDSSGDPKLCPTPMTPNGH-----LDP 1186

Qy 1039 LIHTAATPMSLPKSTSTGLGEALGPA-----SRRTS----- 1070

Db 1187 -----SLPLGCHLGPAGAGAPAPRLSLQDPMLVALGSRKSSVMSLGRMSYDQRS 1236

Qy 1071 -----SSGSAPFGAAHEMKSP-----PSARSSPHSPWSAASSWTSRRSS 1109

Db 1237 LVGGLRATAGVQAAGHLVPPQVWVCLWGADPNNGNSFQSSSRSSSYGPGWGRSAAWASRRSS 1296

Qy 1110 RNSLGRAPSLKRSPSGERRSLLSGE-GQESQDEEESSEE--ERASPPAGSDH----- 1158

Db 1297 WN-----SLKHKPPSAEHESLLSAERGGGARVCEVADEGPRAAPLHTPHAHVHHGP 1350

Qy 1159 -----RHRGSLEREAKSSFDLPDTLQVPLHRTASGR--GSASEHQDCNGKSASGRLA 1209

Db 1351 HLAHRHRHRRRTLSLDRDSVDLAELVPAVGAPRAAWRAAGPAPGHEDCNGRMPSTAKD 1410

Qy 1210 RALRPDDPPLDGDADD-----EGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260

Db 1411 VFTKMGDRGDRGDEDEEIDYVSGGGAEGDLTLCFRVRKMDIVYKPDWCEVREDWSVLF 1470

Qy 1261 PQSRFR-----LLC-----HRIITHKMFHDVVLVIFLNCITAME 1296

Db 1471 PENRLRDLGWVSLCQKGVGDVVVYVQRRQRQTIIAHKLFYDVVLAFLFNLNCITALE 1530

Qy 1297 RPKIDPHSAERIPLTLSNYIFTAVFLAEMTVKVVALGWCFCGEAYLRSSWNVLGLVLVI 1356

Db 1531 RPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVWSLGLYFGGEAYLRSSWNVLGDGLFEV 1590

Qy 1357 SVIDILVMSVDSGTKILGMLRVLRRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIV 1416

Db 1591 SIIDIVVSLASAGAKILGVLRLRLTLRPLRVISRAPGLKLVVETLISLKPIGNIV 1650

Qy 1417 VICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCABASYRWVRHKYNFDNLGOAL 1476

Db 1651 LICCAFFIIFGILGVQLFKGKFFYHCLGVDTNRNITRSDCMAANYRWVHHKYNFDNLGOAL 1710

Qy 1477 MSLFVLASKDGVVDIMYDGLDAVGVDQOQPIMNHNPMMLLYFISFLLIIVAFVFLNMFVGV 1536

Db 1711 MSLFVLASKDGVNIMYNGLDVAVDQOQPVTNHNPMMLLYFISFLLIIVSFFVLNMFVGV 1770

Qy 1537 VENFHKCRHQHEEEARRREERKRRLRLEKRRKAQCKPKYSDYSRFRLLVHHLCTSHYLD 1596

Db 1771 VENFHKCRHQHEAEARRREERKRRLRLEKRRKAQRLPYATYCHTRLLIHSMTCTSHYLD 1830

Qy 1597 LFITGVIGLNVVVTMAHEHYQQP 1618

Db 1831 IFITFIICLNVVVTMSLEHYNQP 1852

RESULT 14

US-10-369-493-6836

; Sequence 6836, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6836

; LENGTH: 1657

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6836

Query Match 29.9%; Score 3564.5; DB 15; Length 1657;

Best Local Similarity 42.2%; Pred. No. 3.3e-216;

Matches 822; Conservative 231; Mismatches 430; Indels 465; Gaps 50;

Qy 15 QPRSFMRNLDSGAGGRPG-----PGSAEKDPG-----SADSEA 48

Db 56 QSQSTRHEDVEALGSIEGSKETLQSEHGRLLASSSEASPSRWEGRIEWGNEEQIEEES 115

Qy 49 EGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLMFRPCED-I 107

Db 116 E-LPYPGFAEPALRCFYQARPPRKWALQVMVSPWFDRITMAVIMINCVTLGMYRPCEDGP 174

Qy 108 ACDSQRCRIIQAFFDDFIFAFFAVEMVVMVALGIFGKCYLGDWTNRDLDFIIVAGMLEY 167

Db 175 DCDTYRCQILDIIDNCIFVYFAFEMVIKIMALGFYGPAAVMSDTWNRLDFFIVMAGIAEF 234

Qy 168 SLDLQ---NVSFSAVRTVRVLRPLRAINRVPSMRILVTLILLDTLPMGLNVLLLCFFVFFI 224

Db 235 VLHEYLGGINLTAIRTVRVRPLRAVNRIPSMRILVLLNLLDTLPMGLNVLLLCFFVFFI 294

Qy 225 FGIVGVQLWAGLLNRCPF--LPENFS-----LPLSVDLERYQTENEDESPFICSQPREN 277

Db 295 FGIVGVQLWAGLLNRRCVINLPKTISENQSALENVNVKLTFRYPE-DTSLEYICSQPDAN 353

Qy 278 GMRSCRSVPTLRGDGGGPPCGLDYEAYNSSNTTTCVNNQYNTNCAG----- 326

Db 354 GLHTCSNLPPTYVD---GVKCNLTLDDEYDKVTNDSCINWNIIYNECQVNIYPSLMTIAIS 410

Qy 327 -----EHNPFKGAINFNDNIGYAWITAFQVITLEGWVDIMYFVMDAHSFYNFYILLI 380

Db 411 CFIKVMQRNPFQGSVSFDNIGFAWVAIFLVISLEGWTDIMYVYQDAHSFNNWYFVLLIV 470

QY 381 VGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNASTLASFSEPG-----S 431  
Db 471 IGAFMINCLVVIATQFAETKRRETERMLQERKMLNRDSISCTGSEIGGASSKEEGDT 530  
QY 432 CYEELLKVLVYLKKAARRLAQVSRAGVRVGLLSPAPLGGQETQPSSSCSRRLRSV 491  
Db 531 VYAAFVRFIGHTFRR-TKRAAKKYTAYMEE----- 560  
QY 492 HHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAE 551  
Db 561 -----RAERKSSERQOR-----RKSCLDDMAT--LS----- 584  
QY 552 SVHSFYHADCHLEFVRQAPPPRSPSEASGRTVGSGKYPTVHTSPPPETLKEKALVEVA 611  
Db 585 -----RIEKAED----- 593  
QY 612 ASSGPPTLTSLNPPGPYSSMHKLELTQSTGACQSSCKI-SSPCLKADSGACGPDSCPYC 670  
Db 594 --EDETITREN-----GDDQIEQNGDGVRIKRVKIEEPPKIKIGN---GNSNGPHY 640  
QY 671 ARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRSRQSLGPDAPSSVLAFWR 730  
Db 641 KHSSDSE-----ESDEGEEDQVYDGEAAKKS-----TPSKJL--WW- 675  
QY 731 LICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEM 790  
Db 676 -FREKIQKVICDHFTRGILVAILVNTLSMGVEYHQPEILTVILEYSNLFFTALFALEM 734  
QY 791 LLKLLVYGPFGYIKPNYNIQDGVIVISVWEIVGQGGGLSVLRTFRLMRVLKLVFLPA 850  
Db 735 LLKIITASGLFGLADGFNLFDGGIVALSVLLEFQEGKGLSVLRTFRLRLILKLVFMPPA 794  
QY 851 LQQLVVLMTMDNVATFCMLMLFIFIFISILGNHILFGCKFASERD---GDTLP--DRKN 905  
Db 795 LRYQLVVMRLTMDNVTVFFGLVLVIFIFISILGNHILFGCKFCKVEKFLGGLAKKCKRN 854  
QY 906 FDSLLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNVVFNLLVAILVE 965  
Db 855 FDTLLWALITVFQILTQEDWNVLFNGMAQTNPWAALYFVALMTFGNVVFNLLVAILVE 914  
QY 966 GFQAEIEISKEDASGOLSCIQLPVDSSQGDANKSESEPDFFPSLDGDKRKKCLALVSL 1025  
Db 915 GFQE--SKEEE-----KROLEEDARKQAVEEEDERKRELELI-- 949  
QY 1026 GEHPELRKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAHEMKS 1085  
Db 950 -----IAKTTSPAFNNGVAPA-----ECTCORPSSPEESPS 980  
QY 1086 PPSARSSPHSPWGAASWTSRRSRNSLGRAPSLKRSPSG-----ERRSLLSGEQESQ 1140  
Db 981 PRLLSANYH-----PSPERKHSANLDAIIDKRLVL----- 1010  
QY 1141 DEEESSEERASPAQSDHRRHGSRLEREAKSSFDLPDTLQVPGLHRTASGRGSASEHODCN 1200  
Db 1011 --RNSAPFDR-SPV-SEGRDDSRNLNHA--SLVLPVANGVP-----YRRQRVH 1052  
QY 1201 GXSASGLARALRPDDPLDGDADDDEGNLSKGE-RVRANTRARL-PACYLERDSWSAYI 1258  
Db 1053 SWKASQELKQAL-----AEEE---KRNEAKQNTFVRKLLKKTCLNHRTEFSLFL 1098  
QY 1259 FPPQSRFRLLCHRIITHKMFHDHVLVLIIFNLCTITAMERPDKIDPHSAERIFLTLSNIYFT 1318  
Db 1099 MGPKNPLRIKCLQTTQKKWFDYTVLFFIGINCITLAMERPSIPDPSFERQFHLISGYFT 1158  
QY 1319 AVFLAEMTVKVVALGCFCGQAYLRSSWNVLNLDGLLVLSVIDILVSMVSDSGTKILGMLR 1378  
Db 1159 VIFTGEMMK----- 1168  
QY 1379 VLRLRLRPLRVLVISRAQGLKLVVETLMSLLKPIGNIVWICCAFFIIFGILGVQLFKGF 1438  
Db 1169 -----VSHRIPTLKPIGNIVLICCTFFIIFGILGVQLFKGMW 1205

QY 1439 FVQGEDTRNITNKSDCAEASYSR--WVRHKYNFDNLGQALMSLFLVASKDGVWDIMYDGL 1496  
Db 1206 YHCIGPEVGNVTTKADCIIE-DYRNKWNHRYNFDNLGQALMSLFLVSSKDGWVSIMYQGI 1264  
QY 1497 DAVGVDDQOPIMNHNPMWLLYFISFLLIYAFVFLNMFVGVVFNHFKCRQHQQHEEEARRRE 1556  
Db 1265 DAVGVDDQPIENYNEWRMIYFISFLLLVGFVFLNMFVGVVFNHFKCKEALKEKEMREKEK 1324  
QY 1557 EKRLRLEK-----KRRKAQC-----KPYSDYSRFRLLVHHL 1590  
Db 1325 EKRLRKLKQKFEESMAGKRKNRIVWAGSAIKSIFSVERNYPYHYDYGHTRLFLHGIV 1384  
QY 1591 TSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFLKLVAFGR 1650  
Db 1385 TSKYFDLAIAAVIGINVISMAEFYMPMPGLKYVLKALNYFFTAFTLEAAMKLIAGFK 1444  
QY 1651 RFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVG 1710  
Db 1445 RFFIEKWNRLDMFIVILSIAGIIFEEFEA-LELPINPTIIRVMRVLRIARVLKLLKMAK 1503  
QY 1711 MRALLDTVMQALPOVGNLGLLFLMLFFIFAALGVLEFGDCEDETHPCBGLGRHATFRNF 1770  
Db 1504 IRSLLDTVGEALPOVGNLGLSFLFFIFAALGVLEFGKLECEDHPCDGLGEHAHFKNF 1563  
QY 1771 GMAFLTFRVSTGDNWNGIMKDTLR-DCD-----QESTCYNTVISPIYFVSFVLTAQFVL 1824  
Db 1564 GMAFLTFRATGDNWNGIMKDALRDDCDSSDHCEITNCCVDPILAPCFFVIFVLISQFVL 1623  
QY 1825 VNVVIAVLMKHLEESNKEAKEEAELEAE 1852  
Db 1624 VNVVAVLMKHLEESN---KRDAEGPAB 1648  
RESULT 15  
US-10-627-370-2  
; Sequence 2, Application US/10627370  
; Publication No. US20040081988A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Jason M.  
; APPLICANT: Castle, John C.  
; APPLICANT: Armour, Christopher D.  
; TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B  
; FILE REFERENCE: RS0202Y  
; CURRENT APPLICATION NUMBER: US/10/627,370  
; CURRENT FILING DATE: 2003-07-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 2264  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-627-370-2  
Query Match 14.7%; Score 1753; DB 15; Length 2264;  
Best Local Similarity 24.8%; Pred. No. 2.1e-101;  
Matches 637; Conservative 358; Mismatches 830; Indels 744; Gaps 85;  
QY 27 GAGGRPGGSAEKDPGSADSEAEGLPYPALAPVVF-----FYLSDSRP 70  
Db 25 GAGGAGGPGGGLQPGQORVLYKQIAQARTMALYNPIPVKQNCFTVNRSLFVSEDNVV 84  
QY 71 RSWCLRTVCNPNWFERISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAFDD---FIFAF 127  
Db 85 RKYAKRITWPPPEYMIATIIANCIVLAL-----EQHLPDGDKTPMSERLDDTPEYFIGI 140  
QY 128 FAVEMVVMVALG-IFGKKCYLGDWNRLDFFVIAGMLEYS---LDLQNVSPSAVRTVR 183  
Db 141 FCFEAGIKIIALGFFVHKGSYLRNGWNVMDFVVVLTGILATAGTDFDLR-----TLRAVR 195  
QY 184 VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCF 243  
Db 196 VLRPLKLVSGIPSLQVVVLSIMKAMVPLLIQIGLLFFAILMFAIGLEFYMGKFKACF- 254

QY 244 PENFSLPLSVLERYQ TENEDESPFFICSPRENGMRCRSVPTRLRGDGGGPPCGLDYE 303  
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273  
QY 304 AYNSSNTTCVNMNOYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363  
Db 274 ARLCEGDTEC---REYWP-----GPNFGITNFDNILFAILTVQCITMEGWTDLINYT 323  
QY 364 MD-AHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRVF 416  
Db 324 NDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENPRAFLKLRQQQIE- 382  
QY 417 LSNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET 476  
Db 383 -----RELNGYLEWIFKAEEVMLAEEDRNA-----BEK 410  
QY 477 QPSSSCSRSHRRLSVHHLVHHHHHHYHLGNGTLRAPRASPEIQORDANGSRRLMLPP 536  
Db 411 SPLDVLKRAATKXSRNDLIH-----AEEGEDRFAD-----440  
QY 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRVCQAPPPRSPSEASGRVTGSKVPTVHTS 596  
Db 441 -----440  
QY 597 PPETLKEALVEVAASSGPPTLTSLNIPGPYSSMHKLTETQSTGACQSSCKISSPCLK 656  
Db 441 -----LCAVGSPFAR 450  
QY 657 ADGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSL 716  
Db 451 ASLSKGTESSYFR-----KEKMF-----473  
QY 717 GPDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALE 776  
Db 474 -----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLY 515  
QY 777 ISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISWEIVGQ-----QGGLS 831  
Db 516 FAEFVLGLFLEMTSLKMYGLGPRSYFRSFCDFGVIVGSEVVEVWAAIKPGSSFGIS 575  
QY 832 VLRTFRLMRVLKLVRFPLPALQRLVVLMTDNVATFCMLMLFIFIFSILGMHLFGCKF 891  
Db 576 VLRALRLRIFKVTKYWSSLRNLVSLNSMKSIISLLFLFLFIVV FALLGMQLFGGQF 635  
QY 892 ASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIA 946  
Db 636 NFQDETPT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV 691  
QY 947 LMTFGNYVFLNLLVAAILVEGF-QAEEISK-----REDASGQ-----LSCIQ 986  
Db 692 LTLFGNYTLNVLFAIAVDNLANAQELTKDEEEMEEAANQKALQAKAEVAEVS PMSAAN 751  
QY 987 LPVDSQGGDANKSESEPDFFSPSLDGDGRKKCLALVSLGE-----HPELRK 1033  
Db 752 ISIAARQONSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTTRHLRPMKT 811  
QY 1034 SLLPPLIIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSSG-----1073  
Db 812 HLDRLPLVVELGRDARGPVGGKARPEAAEAPGVDPRRRHHRRDKDTPAAGDQDRAEA 871  
QY 1074 ----SAEPGA-----AHEMKSPPSARS-----SPH-----SPWSAASSW 1103  
Db 872 PKAESGEPGAREERPRPHRSHSKEAAGPEARSERGRGPGPEGRRHRRGSP EEAARE 931  
QY 1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSE-----ERASP- 1153  
Db 932 PRHRAHRH---QDPSKECAGAKGERRARHRRGGPRAGPREAESGEEPARRHRARHKAQPA 988  
QY 1154 -----AGSDHHRGSLEREA KSSFDLPDTLQVPLHRTASGRG 1191  
Db 989 HEAVEKETTEKEATEKEAEIIVEADKEBLRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048  
QY 1192 SASEHQDCNGKSASGRALARALRPDDP-----PLDGDADDEGNL-----SKGE 1234

Db 1049 QKVEEQPEDADNQNRNVTMRGSOQPPDPNTTIVHIPVMLTGPLGEATVVPSGNVLDLESQAEGK 1108  
QY 1235 R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIF 1287  
Db 1109 KEVEADDVMRSGRPPIVPYS-----SMFCLSPNTLLRRFCHYIVTMRYFEVWILVIA 1161  
QY 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347  
Db 1162 LSSIALAAEDP-VRTDSPRNNAKLYDYIFTGVFTFEMVIKIMIDGLLLHPGAYFRDLWN 1220  
QY 1348 VLDGLLVLSVIDILVSMV-SDSGTKILGMLRLVRLRLTLRPLRVLSRAQGLKLVVETLM 1406  
Db 1221 ILD----FIVVSGALVAFASGSGKGDINTIKSLRVLRLPLTKIKRLPKLKAVFDCVV 1276  
QY 1407 SSLKPIGNIVVICCAFFIIFGILGVQLPKGFFVCQGE-----DTRN---ITNKSDCAEA 1458  
Db 1277 NSLKNVLNILIVMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYLDYEKEEVEA 1336  
QY 1459 SYR-WVRHKYNFDNLGOALMSLFLVASKDGWVDIMYDGLDAVGVDQOQPIMNHNPMWMLLYF 1517  
Db 1337 QPRQWKYDFHYDNVLMALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIFY 1396  
QY 1518 ISFLLIIVAFVLMFVGVVVENFHKCRQHQEEEEARRREKRRLREKKRKA-----QC 1572  
Db 1397 VYFVVFPPFFVNI FVALIITF-----QEQDKVMSE-----CSLEKNERACIDFAISA 1446  
QY 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLVNVTWAMEHYQQPQILDEALKIC 1628  
Db 1447 KPLTRYMPQNRQSFQYKWTWTFVVSPPPEYFIMAMIALNTVLMKMFYDAPYEYELMLKCL 1506  
QY 1629 NYIFTVIFVLESVFKLVAFGFRFFQDRWNQLDLAIVLLSIMGITLEEI-EVNASLPINP 1687  
Db 1507 NIVFTSMFSMECVLKIIAFGLVNYFRDANWVDFVTVLGSIITDILVEIAETN-----NF 1561  
QY 1688 TIIRIMRVLRIRARVLKLLKMAVGMRALLDVTMOALPOVGNLGLLPMLLFFIFAALGVLELF 1747  
Db 1562 INLSFLRLFRAARLIKLLRQGYTIRILLWTQSFKALPYVCLLIAMLFFIYAIIGMOVF 1621  
QY 1748 GDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE--STC 1803  
Db 1622 GNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678  
QY 1804 YNTVISPIYFVSFVLTAQFV-----LVNVVIAVLMKHLE-----ESNK 1841  
Db 1679 CGSDFAYFYFVSFIFLCSFLRLVRMNMPI SNEDMTVHTSTLMALIRTALEIKLAPAGTK 1738  
QY 1842 EAKEEAELEAELEEMKTLSPQPHSLGSPFLPWGVEGDPSPSPKPGALHPA-----1894  
Db 1739 QHQCDAELRKEISVWVANL-PQKTLDLLVP-----PHKPDENTVGKVAALMIFDFY 1789  
QY 1895 -----AHARSASHFSLEHPTM---QPHPTELPGDILLTVRKSGVSRTHSL 1936  
Db 1790 KONKTTTRDQMQQAPGGLSQMGVPVSLFHLPLKATLEQTQPAVLRCARVFLRKQSSSTLSN-- 1847  
QY 1937 PNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQP-- 1994  
Db 1848 -----GGAIONQESGIKESV-----SWCTQRTQDAPHEARPPL 1880  
QY 1995 ---HSAPTWTGTPKLP PPPGRSPLAQRPLRRQAIR-----TDSL DVQGLGSREDLLAE 2044  
Db 1881 ERGHSTEI-----PVGRSGALAVDVQMOSITRRRPGDGPQGLSQGRAASMPRLAA 1932  
QY 2045 VSGP---SPPLARAYSFWGQSSTQAQHSRSHSKISKHMTPPAPCPG-----2088  
Db 1933 ETQPVTDASPMKRSI-----STLAQPRGTHLCST---TPDRPPPSQASSHHHHHRCHR 1983  
QY 2089 ----PEPNWKGPPETRSLSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCYSVEAQSCQ 2144  
Db 1984 RRDRKQRSLEKGP---SLSADMDGAPSSAVGPGLPFG--EGPTCRRERERRQERGRSQE 2038  
QY 2145 RR-PTSWLDEQRRHSIAVSCLD SG-----SQPHLGTDP-----SNLGG 2181

Mon Apr 18 12:41:44 2005

Db 2039 RROPSSSSSEKQRF---YSCDRFGGREPPKPKPSLSHPTSPTAGQEPGHPQGGSVNG 2095  
QY 2182 QPL-----GGPGRPKKKLSP-PSITI-----DPPESQGPRT--PP-SPG----- 2217  
Db 2096 SPLLSTSGASTPGRGRRQLPQTPLTPRPSITYKYKTANSSPHFAGAQTSLPAPFSPGRLSR 2155  
QY 2218 -----ICLRRRAPSSDSKDPPLASGPPDSDMAASPSPKKDVLSLGLSSDP 2261  
Db 2156 GLSEHNALLQORDPLS---QPLAPG-----SRIGSDP 2183

Search completed: April 13, 2005, 16:55:25  
Job time : 242 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:23:47 ; Search time 41 Seconds  
(without alignments)  
5317.736 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKKDVLSLGSLSSDPADLDP 2266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	10945	91.9	2254	T09053	low voltage-activa
2	3564.5	29.9	1657	T15838	hypothetical prote
3	1746.5	14.7	2339	A42566	omega-conotoxin-se
4	1741	14.6	2237	T45115	N-type calcium cha
5	1711	14.4	2336	A45386	omega-conotoxin-se
6	1706	14.3	2288	S41080	calcium channel al
7	1697	14.3	2259	S29236	calcium channel pr
8	1689	14.2	1810	T31092	probable voltage-g
9	1681	14.1	2178	S29237	calcium channel pr
10	1681	14.1	2272	C54972	voltage-dependent
11	1665	14.0	2270	A54972	voltage-dependent
12	1664.5	14.0	1891	T43262	calcium channel al
13	1663.5	14.0	2251	B54972	voltage-dependent
14	1656	13.9	2223	A47447	calcium channel pr
15	1651.5	13.9	2222	A37490	voltage-dependent
16	1633	13.7	1911	T43048	calcium channel al
17	1632	13.7	1873	A30063	dihydropyridine re
18	1626	13.7	1993	T30902	sodium channel sca
19	1625.5	13.7	1852	A37860	calcium channel pr
20	1612	13.5	2143	JH0427	voltage-dependent
21	1602.5	13.5	2139	A44467	voltage-dependent
22	1597.5	13.4	1559	T30535	calcium channel al
23	1596.5	13.4	2166	S11339	calcium channel pr
24	1591	13.4	2019	A33996	sodium channel pro
25	1590	13.4	1783	T37258	probable voltage-d
26	1586	13.3	2016	A38195	sodium channel pro
27	1583.5	13.3	1873	A55645	calcium channel, v
28	1583	13.3	1977	S54771	sodium channel alp
29	1581.5	13.3	2171	S05054	calcium channel al

30 1578 13.3 1917 2 C88728 protein C48A7.1 [i  
31 1573.5 13.2 1983 2 A60054 sodium channel pro  
32 1572.5 13.2 2212 2 A41098 calcium channel pr  
33 1568.5 13.2 1687 2 S41742 calcium channel al  
34 1566.5 13.2 2203 2 T42742 voltage-dependent  
35 1565.5 13.2 1951 2 S00320 sodium channel pro  
36 1564.5 13.1 2181 2 A38198 calcium channel al  
37 1561 13.1 2326 2 B47447 calcium channel pr  
38 1560.5 13.1 1610 2 A46227 voltage-dependent  
39 1557.5 13.1 2161 2 JH0564 calcium channel al  
40 1555 13.1 2220 2 A45290 calcium channel pr  
41 1554 13.1 2262 2 T30890 calcium channel al  
42 1553.5 13.1 2005 2 A46269 sodium channel alp  
43 1550 13.0 1957 2 S68453 sodium channel pro  
44 1549.5 13.0 2009 2 A25019 sodium channel pro  
45 1549 13.0 1646 2 JH0422 voltage-dependent

ALIGNMENTS

RESULT 1

T09053 low voltage-activated, T-type calcium channel alpha chain - rat

C;Species: Rattus norvegicus (Norway rat)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: T09053  
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox

Nature 391, 896, 1998  
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium

A;Reference number: Z16538; MUID:98154730; PMID:9495342  
A;Accession: T09053

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA

A;Residues: 1-2254 <PER>  
A;Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3

A;Experimental source: strain Sprague-Dawley; brain  
C;Genetics:

A;Map position: 17  
A;Note: CACNA1G

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C;Keywords: calcium channel; voltage-gated ion channel

Query Match 91.9%; Score 10945; DB 2; Length 2254;  
Best Local Similarity 92.5%; Pred. No. 0;  
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;

Qy 1 MDEEDGAGAEESGQPRSFMRNLDSGAGRPGSGAEKDPGSADSEAEGLPYPALAPVV 60

Db 1 MDEEDGAGAEESGQPRSFMTQLNDLSGAGRQGPSTGKDPGSADSEAEGLPYPALAPVV 60

Qy 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120

Qy 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLLDFIVIAGMLEYSLDLQNVFSAVR 180

Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLLDFIVIAGMLEYSLDLQNVFSAVR 180

Qy 181 TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Db 181 TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Qy 241 CFLPENFSLPSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Db 241 CFLPENFSLPSVDLEPYQTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL 300

Qy 301 DYEAYNSSNTTCVWNQYTYNCISAGEHNPFGKAINFDNICYAWIAIFQVITLEGWVDIM 360

Db 301 DYEAYNSSNTTCVWNQYTYNCISAGEHNPFGKAINFDNICYAWIAIFQVITLEGWVDIM 360

Qy 361 YFVMDAHSPYNFIFYILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

QY 421 STLASFEPGSCYEELLKYLIVILRKAARRLAQVSRAGVRVGLSSPAPLGGQETQPS 480

Db 421 STLASFEPGSCYEELLKYLIVILRKAARRLAQVSRAGVRVGLSSPVARSGQEPQSG 480

QY 481 SCSRSHRRLSVHLLVHHHHHHHHYHLGNGTILRAPRASPEIQDRDANGSRRLMLPPSTP 540

Db 481 SCTRSHRRLSVHLLVHHHHHHHHYHLGNGTILRAPRASPEIQDRDANGSRRLMLPPSTP 540

QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKYPTVHTSPPE 600

Db 541 TPGGPPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKYPTVHTSPPE 600

QY 601 TLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADSG 660

Db 601 ILKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLLLETQSTGACHSSCKISSPCLKADSG 660

QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQSLGPD 719

Db 661 ACPDSCPCYCARAGAGEPEADHVPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720

QY 720 AEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779

Db 721 AEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780

QY 780 IVFTSLFALEMLKLLVYGPFGYIKNPYINIFDGVIVVLSWEIVGOQGGGLSVLRTFLM 839

Db 781 IVFTSLFALEMLKLLVYGPFGYIKNPYINIFDGVIVVLSWEIVGOQGGGLSVLRTFLM 840

QY 840 RVLKLVRFALQQLVVLMTMDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGD 899

Db 841 RVLKLVRFALQQLVVLMTMDNVATFCMLLMFIFIFISILGMHLFGCKFASERDGD 900

QY 900 LPDRKNFDSLWAIIVTFQILTOEDWNKVLNGMASTSSWAAALYFIALMTFGNVVLFNLL 959

Db 901 LPDRKNFDSLWAIIVTFQILTOEDWNKVLNGMASTSSWAAALYFIALMTFGNVVLFNLL 960

QY 960 VAILVEGFQAEIISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKC 1019

Db 961 VAILVEGFQAEIISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKC 997

QY 1020 LALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079

Db 998 LALVALGEHAELRKSLLPLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGA 1057

QY 1080 A-HEMKSPPSARSSPHSPMSAASSWTSSRRSRNSLGRAPSLKRSPSGERRSLLSGEQE 1138

Db 1058 AHHEMKPPSARSSPHSPMSAASSWTSSRRSRNSLGRAPSLKRSPSGERRSLLSGEQE 1117

QY 1139 SQDEEESSEERASAPGSDHRHSGSLEREAKSFDLPDTLQVPLHRTASGRGSASEHQD 1198

Db 1118 SQDEEESSEEDRASAPGSDHRHSGSLEREAKSFDLPDTLQVPLHRTASGRSSASEHQD 1177

QY 1199 CNGKSASGRILARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258

Db 1178 CNGKSASGRILARTLRTDDPQLDGDNDDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1237

QY 1259 FPPQSRFRLLCHRIITHKMFHDVVLVLIIFLNCITTIAMERPKIDPHSAERIFLTLSNYIFT 1318

Db 1238 FPPQSRFRLLCHRIITHKMFHDVVLVLIIFLNCITTIAMERPKIDPHSAERIFLTLSNYIFT 1297

QY 1319 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1378

Db 1298 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1357

QY 1379 VLRLRLTRLRPLRVISRAQGLKVVEITLMSLLKPIGNIWVICCAFFIIFGILGVQLFKGKF 1438

Db 1358 VLRLRLTRLRPLRVISRAQGLKVVEITLMSLLKPIGNIWVICCAFFIIFGILGVQLFKGKF 1417

QY 1439 FVCQGEDTRNITNKSDCAEASYSRWVRHKYNFNDNLGQALMSLFLVLASKDGVIMYDGLDA 1498

Db 1418 FVCQGEDTRNITNKSDCAEASYSRWVRHKYNFNDNLGQALMSLFLVLASKDGVIMYDGLDA 1477

QY 1499 VGVDQOQPIMNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKRQHQEEEEARRREK 1558

Db 1478 VGVDQOQPIMNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKRQHQEEEEARRREK 1537

QY 1559 RLRLLEKKRR-----KAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTITVIGLNVVTMA 1611

Db 1538 RLRLLEKKRRSKEQMAEAAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTITVIGLNVVTMA 1597

QY 1612 MEHYQOQIILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMG 1671

Db 1598 MEHYQOQIILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMG 1657

QY 1672 ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDVTVMQALPQVGNLGLL 1731

Db 1658 ITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDVTVMQALPQVGNLGLL 1717

QY 1732 FMLLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMK 1791

Db 1718 FMLLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMK 1777

QY 1792 DTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEAELEA 1851

Db 1778 DTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEAELEA 1837

QY 1852 ELELEMTLSPQPHSPGLSGPFVPGVEGDPSPSPKPGALHPAAHARSASHFSLEHPTMQ 1911

Db 1838 ELELEMTLSPQPHSPGLSGPFVPGVEGDNSTSPKPGAPHTTAHIGAAASGFSLEHPTMV 1897

QY 1912 PHPTPLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSV 1968

Db 1898 PHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHARGWGLPKAQSGSI 1957

QY 1969 LSVHSQPADTSYILQPKDAPHLLOPHSAPTWTGTPKLPDPGRSPLAQRPLRQAARTD 2028

Db 1958 LSVHSQPADTSYILQPKDVHYLLQPHGAPTGAIPKLPDPGRSPLAQRPLRQAARTD 2017

QY 2029 SLDVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKI SKHMTTPPAPCPG 2088

Db 2018 SLDVQGLGSRREDLLSEVSGSPCLTRSSSFVWGSSIQVQORSGIQSKVSKHIRLPAPCPG 2077

QY 2089 PEPNWKGPPETRSLELDTLSWISGDLTPPGQEEPPSPRDLKKCYSVAEQAQCORRPT 2148

Db 2078 LEPSWAKDPPETRSLELDTLSWISGDLTPSSQEEPLFRDLKKCYSVETQSCRPPG 2136

QY 2149 SWLDEQRRHSIAVSCLDGSGQPHLGTDPNLGGQPLGGPGSRPKKLSPPSITIDPPESQ 2208

Db 2137 FWLDEQRRHSIAVSCLDGSGQPLRCPSPSLGGQPLGGPGSRPKKLSPPSISIDPPESQ 2196

QY 2209 GPRTPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLISLGLSSDPADLDP 2266

Db 2197 GSRPPCSPGVCLRRRAPASDSKDPSSVSPDSTAASPSPKDVLISLGLSSDPTDMDP 2254

RESULT 2

T15838  
hypothetical protein C54D2.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Mar-2000  
C;Accession: T15838  
R;Minx, P.  
submitted to the EMBL Data Library, October 1995  
A;Description: The sequence of C. elegans cosmid C54D2.  
A;Reference number: Z18415  
A;Accession: T15838  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1657 <MIN>  
A;Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D2  
C;Genetics:  
A;Gene: CESP:C54D2.5  
A;Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 513/3  
C;Superfamily: sodium channel protein

Query Match		29.9%;	Score 3564.5;	DB 2;	Length 1657;
Best Local Similarity		42.2%;	Pred. No. 6.5e-210;		
Matches 822;		Conservative 231;	Mismatches 430;	Indels 465;	Gaps 50;
Qy	15	QPRSFMRNLNDSGAGRPG-----PGSAEKDPG-----SADSEA	48		
Dd	56	QSQSTRRHEDVEALGSIEGSKETQLQSEHGRLASSEASPSRWEGRIEWGNEEQIEEES	115		
Qy	49	EGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERRISMLVILLNCVTLMFPCED-I	107		
Dd	116	E-LPYPGFAEPALRCFYQARPPRKWALQVMWSPWFDRTIMAVIMINCVTLGMVRPCEDGP	174		
Qy	108	ACDSQRCRILOAFDDFIEAFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFIVIAGMLEY	167		
Dd	175	DCDITYRCQILDIDNCIFVYFAFEMVIKIMALGFYGPAAYSMTWNRLDFFIVMAGIAEF	234		
Qy	168	SLDLQ---NVSPSAVRTVRVLRPLRAINRVPSMRILVTLLLDTPLMGNVLLLCFFVFFI	224		
Dd	235	VLHEYLGGINLTAIRTVRVLRLRAVNRIPSMRILVNLLDTPMLGNVLLLCFFVFFI	294		
Qy	225	FGIVGVQLWAGLLNRCF--LPENFS-----LPLSVDLERYQTENEDESPFCSQPREN	277		
Dd	295	FGIVGVQLWAGLLNRCSVINLPKTISENQSALENNVVKLTFRYIPE-DTSLEYICSQPDAN	353		
Qy	278	GMRSCRSVPTLRGDGGGPPCGLDYEAYNSSNTTCVNNNQYTYNCSAG-----	326		
Dd	354	GLHTCSNLPPTYVD--GVKCNLTLDYDKVTNDSCINWNIYNECQVNIYPSLMTIAIS	410		
Qy	327	-----EHNPFKAINEDNIGYATIAIQVITLEGWVDIMYFVMDAHSFYNFIFILLII	380		
Dd	411	CFIKVMQRNPFQGSVFDNIGFAWVAIFLVISLEGWTDIMYVQDAHSFNNWIVFVLIV	470		
Qy	381	VGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPG-----S	431		
Dd	471	IGAFFMINCLVVIATQFAETKRRETERMLOERKMLLNRDSISCTGSEIGGASSKEEGDT	530		
Qy	432	CYEELLKYLVIILKAARRLAQVSRAGVRVGLLSSPAPLGQETQPSSSCSRSHRRLSV	491		
Dd	531	VYAAFVRFIGHTFRR-TKRAAKKKYTAYMEE-----	560		
Qy	492	HHLVHHHHHHHHYHLNGTTLRAPASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAE	551		
Dd	561	-----RAERKSSERQOR-----RKSCLDDMAT--LS-----	584		
Qy	552	SVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVA	611		
Dd	585	-----RIEKEADE--	593		
Qy	612	ASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKI-SSPCLKADSGACGPDSCPYC	670		
Dd	594	--EDETTIEN-----GDDQIEQNGDGVRIKRVKIEEPKIKIGN--GNSNGPHY	640		
Qy	671	ARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDDLDPHSRRQRSGLPDAEPSVLAFWR	730		
Dd	641	KHSSSDE-----ESDEGEEDQVYDGEAAKKKS-----TPSKL--WW-	675		
Qy	731	LICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEM	790		
Dd	676	-FREKIQKVICDHFTRGILVAILVNTLSMGVEYHQQPEILTVILEYSNLFFTALFALEM	734		
Qy	791	LLKLLVYGPFYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMRVLKLVRFPLPA	850		
Dd	735	LLKIIASGLFGYLADGNLFDGGIVALSVLELFQEGKGLSVLRTFRLLRILKLVRFMPA	794		
Qy	851	LQQLVVLKMTMDNVATFCMLLMLFIFISILGMHLFGCKFASERD---GDTLP--DRKN	905		
Dd	795	LRQLVVMRLTMDNVTVFFGLLVLFIFISILGMNLFQCKECKVEKFLGGLAKCKERKN	854		
Qy	906	FDSLLWAIVTVFQILTQEDWNKVLVNGMASTSSWAALYFTIALTMTFGNYVLFNLLVAILVE	965		
Dd	855	FDTLWALITVFQILTQEDWNMVLFNMGMAQTNPWAALYFVALMTFGNYVLFNLLVAILVE	914		

Qy	966	GFQAEIEISKREDASQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSL	1025
Dd	915	GFQE---SKEEE-----KRQLEEDARKQAVEEEDERKRELELI--	949
Qy	1026	GEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAHEMKS	1085
Dd	950	-----IAKTSPAFNNGVAPA-----ECTQRPSSPEESPS	980
Qy	1086	PPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLLSGEGQESQ	1140
Dd	981	PRLLSANYH-----PSPERKHSANLDAIIDKRLVL-----	1010
Qy	1141	DEEESSEERASPAGSDHRHRGSLEREAKSSFDPDLPTLQVPLGHLRTASGRGSASEHQDCN	1200
Dd	1011	--RNSAPFDR-SPV-SEGRDSDRLNRHA--SLVLPVANGVP-----YRRQRVH	1052
Qy	1201	GKSASGRLARALRPDDPPLDGDADDEGNLSKGE-RVRAWIRARL-PACYLERDSWSAYI	1258
Dd	1053	SWKASQELKQAL-----AEEE---KRNEAKQNTFVRKLLKTKTCLHNRTEFSLFL	1098
Qy	1259	FPQSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFT	1318
Dd	1099	MGPKNPLRIKCLQTQTKWFDTYTLFFIGINCITLAMERPSIPDPSFERQFLHISGYIFT	1158
Qy	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLR	1378
Dd	1159	VIFTGEMMK-----	1168
Qy	1379	VLRLRLRLRLRVISRAOGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGP	1438
Dd	1169	-----VSHRIPTLKPIGNIVLICCTFFIIFGILGVQLFKGMM	1205
Qy	1439	FVCQGEDTRNITNKS DCAEASVR--WVRHKYNFDNLGALMSLFLVASKDGVIMYDGL	1496
Dd	1206	YHCIGPEVGNVTTKADCIE-DYRNKWNHRYNFDNLGALMSLFLVSSKDGWVSIMYQGI	1264
Qy	1497	DAVGVDQOPIMNHNPMMLLYFISFLLIYAFFVLNMFVGVVVENFHKCRQHQEEEEARRRE	1556
Dd	1265	DAVGVDVQPIENYNEWRMIIYFISFLLLVGFVLNMFVGVVVENFHKCKEALKEKEMREKEK	1324
Qy	1557	EKRLRLLEK-----KRKAQC-----KPYYS DYSRFRLLVHHLC	1590
Dd	1325	EKRLKRLKQKFEESMAGRKKNRIVWAGSAIKSIFSVERNYPYHYDGHTRFLFLHGIV	1384
Qy	1591	TSHYLDLFIITGVIGLNVVTNAMEHYQQOQILDEALKICNYIFTVIFVLESVFKLVAFGFR	1650
Dd	1385	TSKYFDLAIAAVIGINVISMANEBFYMPMGLKYVLKALNYFFTAFTTLEAAMKLIAGFK	1444
Qy	1651	RFFQDRWNQLDLAIIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLLKXAVG	1710
Dd	1445	RFFIEKNRLLDMFIVILSIAGIIFEEFEA-LELPINPTIIRVMRVLRARVLKLLKXAKG	1503
Qy	1711	MRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNF	1770
Dd	1504	IRSLDVTVEALPQVGNLGLSFLFLFFIFAALGVLEFGLECEDHPCDGLGEHAFKMF	1563
Qy	1771	GMAFTLFRVSTGDNWNGIMKDTLR-DCD-----QESTCVNTVISPIYFVSFVLTAQFVL	1824
Dd	1564	GMAFTLFRATGDNWNGIMKDARDDCDSSDHCTNCCVDPILAPCFFVIFVLISQFVL	1623
Qy	1825	VNVVIAVLMKHLSESNKEAEAEAEAE	1852
Dd	1624	VNVVAVLMKHLSESN---KRDAEGPAE	1648

RESULT 3  
A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively spliced)  
C;Species: Homo sapiens (man)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Sep-1998  
C;Accession: A42566  
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC  
Science 257, 389-395, 1992

A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type  
A;Reference number: A42566; MUID:92335886; PMID:1321501

A;Accession: A42566

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-2339 <WIL>

A;Experimental source: IMR32, hippocampus

A;Note: sequence extracted from NCBI backbone (NCBIP:109168)

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.7%; Score 1746.5; DB 2; Length 2339;

Best Local Similarity 24.2%; Pred. No. 2.2e-98;

Matches 641; Conservative 361; Mismatches 823; Indels 819; Gaps 86;

QY	27	GAGGRPGGSAEKDPGSADSEAGLPYPALAPVVF-----FYLQDSRP 70	
DB	25	GAGGAGGPGGGLQPGQORVLYKQSIARARTMALNPIPVKQNCFTVNRSLSLFVSEDNVV 84	
QY	71	RSWCLRTVCNPFWRISMLVILNCVTLMFRPCEDIACDSQRCRILOAFDD---FIFAF 127	
DB	85	RKYAKRITETWPPREYMITATIANCIIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI 140	
QY	128	FAVMVVKVVALG-IFGKCKYLGDWTNRLLDFFIVIAQMLEYS---LDLQNVSFSAVRTVR 183	
DB	141	FCFEAGIKIIALGFVFKGSLRNGWNVMDVVVLTGILATAGTDFDLR-----TLRAVR 195	
QY	184	VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFIFIGVGVQLWAGLLNRCLF 243	
DB	196	VLRPLKLVSGIPSLQVVLKSIKMAVPLLIQIGLLFFAILMFAIIGLEFFYMGKFHKACF- 254	
QY	244	PENFSLPLSVDLERYVYQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGGPPCGLDYE 303	
DB	255	-----PNSTDAE-----PV-----GDFPCQKEAP 273	
QY	304	AYNSSNTTCVNNQYVYTNCSAGEHNPFGKAINFDNIGYAWTAIFQVITLEGWVIMYFV 363	
DB	274	ARLCEGTEC---REYWP-----GPNFGITNFDNILFAITVFCITMEGTIDILYNT 323	
QY	364	MD-AHSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKQES-----QLMREORVRF 416	
DB	324	NDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERENRRAFLKLRRQOQIE- 382	
QY	417	LSNASTILASFSEPGSCYEELKLVLYILRKAARRLAQVSRAAGVRVGLLSSPAPLGQET 476	
DB	383	-----RELNGYLEWIFKAEVMLAEEDRNA-----EEK 410	
QY	477	QPSSSCSRRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPP 536	
DB	411	SPLDLVKRAATKSRNDLIH-----AEEGEDRFAD-----440	
QY	537	PSTPALSGAPPGAESVHSFYHADCHLEPVRCQAPPSPSEASGRVTGSGKVPTVHTS 596	
DB	441	-----440	
QY	597	PPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKILETQSTGACQSSCKISSPCLK 656	
DB	441	-----LCAVGSPPAR 450	
QY	657	ADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRS 716	
DB	451	ASLSKSGKTESSESYFR-----KEKMPFR-----473	
QY	717	GPDAEPSSVLAFWRLICDTFRKI VDSKYVGRGIMIAILVNTLSMGIEYHEQPEELTNALE 776	
DB	474	-----FIRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTY 515	
QY	777	ISNIVFTSLFALEMLLKLIVGPGFYIKNPYNI FDGVIIVISVWEIVG---QGGG--GLS 831	
DB	516	FAEFVELGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGVSFEVWAAIKPGSGSFGIS 575	
QY	832	VLRTFRLMRVLKLVRLPALORQLVLMKTMNDNVATFCMLLMFLFIFISILGHLFGCKF 891	
DB	576	VLRALRLRLRIFKVTKYWSSLRNLVSVLSNMSKSIISLLFLFLFIVV FALLGMQLFGGQF 635	

QY	892	ASERDGDITLPRKNFDSLLWAIIVTVFQILTQEDWNKVLNMG-----ASTSSWAAALYFIA 946	
DB	636	NFQDETPT-----TNFDTFPAAILTVFQILTGEDWNAVVMYHGIESQGVSKGMFSFYFIV 691	
QY	947	LMTFGNYVLFNLLVAILVEGF-QAEEISK-----REDASGQ-----LSCIQ 986	
DB	692	LTLFGNYTLLNVFLATAVDNLANAQELTKDEEMEEAANQKALQAKAKEVAEVSMPMAAN 751	
QY	987	LPVDSQGDANKSESEDFPSLDGDKKCLALVSLGE-----HPELRK 1033	
DB	752	ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRLRLPDMKT 811	
QY	1034	SLLPPLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSSG-----1073	
DB	812	HLDRPLVVELGRDGARGPVGCKARPEAAEAEPEGVDPPRRHHRHRDKKTPAAGDQDRAEA 871	
QY	1074	-----SAEPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW 1103	
DB	872	PKAESGEPGAREERPRPHRSKSEAAGPPEARSGRGPPEGGRHRRHRRGSPEEAERE 931	
QY	1104	TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEEESSE-----ERASP- 1153	
DB	932	PRRHRAHRH---QDPKCEKAGAKGERRARHRRGGPRAGPREAESGEEPARHRARHKAQPA 988	
QY	1154	-----AGSDHHRHRSLEERAKSSFDLPDITLQVPLHRTASRG 1191	
DB	989	HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTIVTVPMTLTPSTCL 1048	
QY	1192	SASEHQDCNGKSASGLARALRPDDP-----PLDGGDDADDEGNL---SKGER- 1235	
DB	1049	QKVEEQPEDADNQNVTRMGSPDPDNTIVHIPVMLTGLGEATVVPVSGNVLDLESQAEQK 1108	
QY	1236	-----VRAMIRARLPACYLERDSWSAYIFPPQSRFLLCRRIITHKMFHDHVLVLIIF 1287	
DB	1109	KEVEADDVMSRGPPIVPYS-----SMFCLSPTNLLRRFCHYIVTMYRFEVVLVIA 1161	
QY	1288	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347	
DB	1162	LSSIALAAEDP-VRTDSPRNNAKYLDYIFTGVFTFEMVIKMDLGLLLHPGAYFRDLWN 1220	
QY	1348	VLDGLLVLSVIDILVSMV-SDSGTKILGLMLRVLRLRLRLRPLRVLISRAOGLKLVVETLM 1406	
DB	1221	ILD-----FIVVSGALVAFAFSGSKGDKINTIKSLRVLRLPLKTIKRLPKLKAFCVW 1276	
QY	1407	SSLKPIGNIVVICAPFIIFGILGVQFKGFFVCCQE-----DTRN---ITNKSDCAEA 1458	
DB	1277	NSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGGYLDYEKEVEA 1336	
QY	1459	SYR-WVRHKYNFDNLGOALMSLFLVASKDGWVDIMYDGLDVGVDQOQIPIMNHNPMWLLYF 1517	
DB	1337	QPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSGYRMELSIFY 1396	
QY	1518	ISFLLI VAFVFLNMFVGVVVENFHKCRQHQBEEBARRRREKRLRLLEKKRKA-----QC 1572	
DB	1397	VVYFVFPFFVNFIVFVALIITF-----QEOGDKVMSE-----CSLEKNERACIDFAISA 1446	
QY	1573	KPY--YSDYSR--FRLLVHLLCTSHYLDLFIITGVIGLNVVTMAMEHYQOPQILDEALKIC 1628	
DB	1447	KPLTRYMPQNRQSFQYKTTWTFVSPFPFYMAMIALNTVLMKFDAPYELMLKCL 1506	
QY	1629	NYIFTVIFVLESVKLVAFGFRFFQDRWNQDLALVLLSIMGITLEEI-EVNASLPINP 1687	
DB	1507	NIVFTSMFSMECVLKIIAAGVNLNFRDANNVDFVTVLGSIITDILVTEIAETN-----NF 1561	
QY	1688	TIIRIMRVLRIARVLKLLKMAVGNRALLDTVMQALPQVGNLGLLFLMLFFIFAALGVLEF 1747	
DB	1562	INLSFLRLFRARLKLRLRQGYTIRILLNTFVQSFKALPVYVCLLIAMLFFIYAIIGMQVF 1621	
QY	1748	GDLECDETHPCGLGRHATFRNFGNAFLTFRVSTGDNWNGIMKDTLRD--CDQE--STC 1803	
DB	1622	GNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678	



QY 1804 YNTVISPIYFVFLTAQFVLNVNVIIVLM-----KHLEE----- 1838  
Db 1679 CGSDFAYFYFVSIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHDEFIRVWAEYDP 1738  
QY 1839 ----- 1838  
Db 1739 AACGRISYNDMFEMLKHMSPPGLGKKCPARVAYKRLVRNMMPISNEDMTVHTFTLMAL 1798  
QY 1839 -----SNKEAKEAELEAELEMKTLSPQPHSPGLSPFLWPVGVEGDSPPDSP 1886  
Db 1799 IRTALEIKLAPQTKQHQCDAELRKEISVWVANL-PQKTLDLLVP-----PHKPEM 1849  
QY 1887 KPGALHPA-----AHARSASHESLEHPTM-----QPHPTLPGPD 1921  
Db 1850 TVGKYAALMIFDYKQNKTTTRDQMQQAPGGLSQMGFVSLFHLKATLEQTQPAVLRGAR 1909  
QY 1922 LLTVRKSGVSRTHSLPNDSYMCRRHGSAEGPLHGRGWGLPKAQSGSVLSVHSQPADTSYI 1981  
Db 1910 VFLRQKSTSLSN-----GGAIQNESGIKESV-----SWQ 1940  
QY 1982 LQPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRLRRQAAIRTDSDLVQGLGSR-- 2039  
Db 1941 TORTQDAPHEAR-----PPLERGHSTEIPVGRSGALAVD-VQMOSITRRQPD 1986  
QY 2040 -----DLAEVSGSPPLARAYFWQSQSTQAQQHRSRSHSKISK-----HM---TPPAPC 2086  
Db 1987 QEPQGLSQQRAASMPRLAAET---QPVTDA SPMKRSISTLAQPRGTHLCSTTPDRPP 2043  
QY 2087 PG-----PEPNWKGPPETRRSSLELDTLSWISGDLPLPPGQEEPPSP 2129  
Db 2044 PSQASSHHHHCHRRRRDRKQRSLEKGP---SLSADMGAPSSAVGGLPPG--EQPTQC 2098  
QY 2130 RDLKKCYVEAQSCQRR-PTSWLDEQRRHSIAVCLDSG-----SQPHLG 2173  
Db 2099 RRERERQERGRSQERRQPSSSSEKQRF---YSCDRFGREPPKPKPSLSSHTSPTAG 2155  
QY 2174 TDP-----SNLGGQPL-----GGPGSR---PKKLLSP-PSITIDPPES-----Q 2208  
Db 2156 QEPGPHPOGSGSVNGSPLLSTSGASTPGRGRRQLPOTPLTPRPSITYKTANSPIHFAQ 2215  
QY 2209 GPRTPP--SPG-----ICLRRRAPSSDSKOPLASGPPDSMAASPSPKDVLSSLGL 2257  
Db 2216 AQTSLPAPSPGRLSRLSEHNALLQDPLS---QPLAPG-----SRI 2254  
QY 2258 SSDP 2261  
Db 2255 GSDP 2258

RESULT 4  
T45115  
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T45115  
R:Williams, M.E.; Bruet, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McQ  
Science 257, 389-395, 1992  
A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type  
A:Reference number: A42566; MUID:92335886; PMID:1321501  
A:Accession: T45115  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2237 <WIL>  
A:Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g1797  
A:Experimental source: cell line IMR32; neuroblastoma  
C:Genetics:  
A>Note: CCHL1A2  
C:Function:  
A:Description: calcium influx  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
Query Match 14.6%; Score 1741; DB 2; Length 2237;  
Best Local Similarity 24.1%; Pred. No. 4.6e-98;

Matches 629; Conservative 361; Mismatches 836; Indels 780; Gaps 80;  
QY 27 GAGGRPGPSAEKDPGSADSEAGLPYPALAPVF-----FYLQDSRP 70  
Db 25 GAGGAGPGGLQPGQRLYKQSIARARTMALYNPIVKQNCFTVNRSLFVSESDNVV 84  
QY 71 RSWCLRTVCNPWFERISMLVILLNCVTLGMFPCEDIACDSQRCRILQAFDD---FIFAF 127  
Db 85 RYAKRITWPPPEYMILATIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI 140  
QY 128 FAVEMVVMVALG-IFGKKCYLGDWTNRDLDFVFIAGMLEYS---LDLQNVSFSAVRTVR 183  
Db 141 FCFEAGIKIILALGFVFKGSLRNGWNVDFVVVLTGILATAGTDFDLR-----TLRAVR 195  
QY 184 VLRPLRAINRVPSMRILVTLDDTLPLMGNVLLCCFFVFFIFIGIVGVQLWAGLLNRNCF 243  
Db 196 VLRPLKLVSGIPSLQVVLKSIKAMVPLLIQIGLLFFAILMFAIIGLEFYMGKFHKACF- 254  
QY 244 PENFSLPLSVDLERYYYQTENEDESPPFICSPRENGMRSRCSVPTLRGDGGGPPCGLDYE 303  
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273  
QY 304 AYNSSNTTCVNNQYYTNCSEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363  
Db 274 ARLCEGDETC---REYWP-----GPNFGITNFDNIFAILTVFQCITMEGTDLIYNT 323  
QY 364 MD-AHSEFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRES-----QLMREQRVRF 416  
Db 324 NDAAGTNWNLWYFIPLIIIGSFPMNLNLVLGVLGSEPAKERERVENRRAFLKLRQOQIE- 382  
QY 417 LSNASTLASFPSEPGSCYEELLYVILRKAARRLAQVSRRAAGVRVGLLSSPAPLGGQET 476  
Db 383 -----RELNGYLEWIFKAEVVMLEEDRNA-----EEK 410  
QY 477 QPSSSCSRSHRRRLSVHLLVHHHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPP 536  
Db 411 SPLDVLKRAATKKSRLDIH-----AEEGEDRFAD----- 440  
QY 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTS 596  
Db 441 ----- 440  
QY 597 PPTETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK 656  
Db 441 -----LCVCSPPAR 450  
QY 657 ADGACGDDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSL 716  
Db 451 ASLKSCKTESSESYFRR-----KEKMFRE----- 473  
QY 717 GPDAEPSSVLAFWRLICDTPRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPEELTNALB 776  
Db 474 -----FIRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTY 515  
QY 777 ISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGLS 831  
Db 516 FAEFVFLGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGSVFEVWAAIKPGSSFGIS 575  
QY 832 VLRTRFLMRVLKVRFLPALQRLVVLMTMDNVATFCMLMLLFIFFISILGMHLFGCKF 891  
Db 576 VLRALRLLRIFKVTKYWSSLRNLVSVLLNSMKSIISLLFLFLFVIVFALLGMQLFGGQF 635  
QY 892 ASERDGTLPDRKNFDSLLVAIVTVFOILTQEDWNKVLNGM-----ASTSSWAAALYFIA 946  
Db 636 NFQDETPT---TNFDTFPAILTVFOILTGEDWNAVMYHGIESQGGVSKGMFSFYFIV 691  
QY 947 LMTFGNYVLFNLLVAILVEGF-QAEEISK---REDASQ-----LSCIQ 986  
Db 692 LTLFGNYTLNVLFAIVDNLANAQELTKDEEEMEEAANQKALQKAKEVAEVSPPMSAAN 751  
QY 987 LPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGE-----HPELRK 1033  
Db 752 ISIAARQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDEPEERLRFATTHLRPDMKT 811



QY	1887	KPGALHPA-----AHARSASHFSLEHPTM---QPHTELP	1921
Db	1850	TVGKYAALMIFDYKONKTTTRDQMOQAPGGLSQMGVSLFHPKATLEQTQPAVLRGAR	1909
QY	1922	LLTVRKSGVSRTHSLPNDSYMCRHSGTAEGPLGHRGWLKPAQSGSVLSVHQSQADTSYI	1981
Db	1910	VFLRQKSSSTLSN-----GGAIQNESGIKESV-----SWG	1940
QY	1982	LQLPKADAPHLQP-----HSAPTWTGTIPKLPPLPPGRSPLAQRPLRQAIR-----TDS	2029
Db	1941	TQRTQDAPHEARPPLERGHSTEI-----PVGRSGALAVDVQMOSITRRRPGDGEPOPG	1992
QY	2030	LDVQGLGSREDLLAEVSGP---SPPLARAYFWGQSSTQAQOHSRSHSKISKHMTTPAPC	2086
Db	1993	LESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPRGTHLCST---TPDRPP	2043
QY	2087	PG-----PEPNWGKGPPEPTRSSLELDTLSWISGDLPLPPGGQEEPPSP	2129
Db	2044	PSQASSHHHHRCHRRDRDKQRSLEKGP---SLSDMDGAPSSAVGPGPLPG---EGPTGC	2098
QY	2130	RDLKKCYVEAQSCORR-PTSWLDEQRRHSIAVSCLDSGS-----QPHLGTDPN--LG	2180
Db	2099	RRERERRQGRSQERRQPSSSSEKQRF---YSCDRFGGREPKPKPSLSHPTSTAG	2155
QY	2181	GQPLGGSGSRPKKLSPSITIDPPESQGRTPPSP-----GIC	2219
Db	2156	QEP---GHPQAGSAVGFPNTT---PCCRETPSASPWPLALELALTWTGWSVWTVRPLSTPC	2211
QY	2220	LRRRAPSSDSKDPLASGPPDSMAASP	2245
Db	2212	LRTRSLRRLWPPTRAAPPGLPTCPP	2237
RESULT 5			
A45386			
omega-conotoxin-sensitive calcium channel alpha-1 subunit rBb-I - rat			
C:Species: Rattus norvegicus (Norway rat)			
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004			
C:Accession: A45386			
R:Dubel, S.J.; Starr, T.V.; Hell, J.; Ahljanian, M.K.; Enyeart, J.J.; Catterall, W.A.; -			
Proc. Natl. Acad. Sci. U.S.A. 89, 5058-5062, 1992			
A:Title: Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensitive calcium			
A:Reference number: A45386; MUID:92279265; PMID:1317580			
A:Accession: A45386			
A>Status: preliminary; not compared with conceptual translation			
A:Molecule type: nucleic acid			
A:Residues: 1-2336 <DUB>			
A:Cross-references: UNIPROT:089089			
A:Experimental source: brain			
A>Note: sequence extracted from NCBI backbone (NCBIP:104355)			
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
Query Match 14.4%; Score 1711; DB 2; Length 2336;			
Best Local Similarity 24.0%; Pred. No. 3.3e-96;			
Matches 644; Conservative 365; Mismatches 810; Indels 860; Gaps 93;			
QY	27	GAGGRPGSGSAEKOPGSAADSEAEGLPYPALAPVVF-----FYLSDSRP	70
Db	25	GAGGAGGPGGGGLPPGQGVLYKQSIQAQARTMALYNPIPVKQNCFTVNRSLFVSEDNVV	84
QY	71	RSWCLRTVCNPNWFERISMLVILLNCVTLGMFRPCEDIAQSCRILOAFDD---FIFAF	127
Db	85	RKYAKRITETWPPPEYFMYLTIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI	140
QY	128	FAVEMVVMVALG-IFGKKCYLGDWTNRLDFFIVIAMLEYS---LDLQNVSFSAVRTVR	183
Db	141	FCFEAGIKIILGTFVFKGSYLRNGWNVDMFVVVLTEILATAGTDFDLR-----TLRAVR	195
QY	184	VLRPLRAINRVPSMRILVTLTLLDPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCF	243
Db	196	VLRPLKLVSGIPSLQVWLKSIKAMVPLLIQIGLLFFAILMFAIIGLEFYMKGFKACF-	254
QY	244	PENFSLPLSVDLERYVYQTENEDESPFICSPRENGMRCRSVPTLRGDGGGGPPCGLDYE	303

QY	1034	SLPLPLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSSG-----	1073
Db	812	HLDRPLVVELGRDARGPVGKARPEAAEAPGVDPRRHHRDKDKTTPAAGQDQRAEA	871
QY	1074	-----SAEPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW	1103
Db	872	PKAESGEPGAREERPRPHRSKSEAAGPPPEARSERGRPGPEGGRHRRGSPPEAAERE	931
QY	1104	TSR-RSRNSLGRAPSLKRRSPSGERRSLLSGGQESQDEESEE-----ERASP-	1153
Db	932	PRHRAHRH---QDPSKECAGAKGERRARRHRRGGPRAGPREAESGEEPARRHRAHKAQPA	988
QY	1154	-----AGSDHRRHRSGLEREAKSSFDPDLTVLPVGLHRTASGRG	1191
Db	989	HEAVEKETTEKEATEKEAEIVAEADKEKELRNHOPREPHCDLETSGTVTVGPMHTLPSTCL	1048
QY	1192	SASEHQDNCCKSASGLRALALRPDDP-----PLDGGDDADDEGNL-----SKGE	1234
Db	1049	QKVEQPEDADNQNRNVTMRMGSPQDPDNTIVHIPVMLTGPLGEATVVPVSGNVLDLESQAEKG	1108
QY	1235	R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHVVLVIF	1287
Db	1109	KEVEADVMRSGRPPIVPS-----SMFCLSPNLLRRFCHYIVTMRYFEWILVIA	1161
QY	1288	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN	1347
Db	1162	LSSIALAAEDP-VRTDSPRNNAKLYLDYIFTGVFTFEMVIKIDGLLLHHPGAYFRDLWN	1220
QY	1348	VLDGLLVLSVIDILVSMV-SDSGTKILGMLRVLRLRLRLPLRVRISRAOGLKLVVETLM	1406
Db	1221	ILD-----FIVSGALVAFAPSGSGKGDINTIKSLRVLRLPLKTIKRLPKLKAADFV	1276
QY	1407	SSLKPIGNIVVICAPFIIFGILGVQLFKGKFFVCQGE-----DTRN--ITNKSDCAEA	1458
Db	1277	NSLKNVLNIIIVMLFMFIFAVIAVQLFKGFFYCTDESKELERDCRGQYLDYEKEVEEA	1336
QY	1459	SYR-WVRHKYNFNDLGOALMSFLVLSKDGWVDIMYDGLDAVGVDQQPIMNHNFWMLLYF	1517
Db	1337	QPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATVEEQGSPGYRMELSIFY	1396
QY	1518	ISFLIVAFVFLNMFVGVVVENFHKCRHQHEEARRREKRLRLEKKRKA-----QC	1572
Db	1397	VVYFVVPFFVNFVLIITF-----QEGDKVMSE-----CSLEKNERACIDFAISA	1446
QY	1573	KPY--YSDYSR--FRLLVHLLCTSHYLDLFTGVIGLNVVTMAHEHYQQPQILDEALKIC	1628
Db	1447	KPLTRYMPQNRQSFQYKWTWTFVVPFPFEYFIMAMIALNTVLMKMFYDAPYEYELMLKCL	1506
QY	1629	NYIFTVIFVLESVFKLVAFGFRFRFFQDRWNQLDLAIVLLSIMGITLEEI-EVNASLPINP	1687
Db	1507	NIVFTSMESMECVLKIIAFGVNLVYFRDAWNVDFVTVLGSITDILVTEIAETN-----NF	1561
QY	1688	TIIRIMRVLRIARVLKLLKMAVGMRAALLDTVMQALPQVGNLGLLFFLFFIFAALGVLELF	1747
Db	1562	INLSFLRLFRAARLIKLLRQGYTIRILLWTVQSFKALPYVCLLIAMLFFIYAIIGMQVF	1621
QY	1748	GDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE--STC	1803
Db	1622	GNIALDDD---TSINRHNHNFRTFLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE	1678
QY	1804	YNTVISPIYFVSFVLTAQFVLNVNVIIVLM-----KHLEE-----	1838
Db	1679	CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDREIRVWAEYDP	1738
QY	1839	-----	1838
Db	1739	AACGRISYNDMFEMLKHMSPPGLGKGPARGVAYKRLVRNMNPI SNEDMTVHTSTLMAL	1798
QY	1839	-----SNKEAKEEALEAELEMLKTLSPQPHSPGSPPLWPGVEGDPSPDSP	1886
Db	1799	IRTALEIKLAPAGTKHQCDAELRKEISVVWANL-PQKTLDLLVP-----PHKPDEM	1849









QY	1729	GLLFMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATERNFGMAFLTLFRVSTGDNWN	1787
Db	1601	CLLIAMLFFIYAIIGMQVFGNIRLDEESH-----INRHNFRSFFGSLMLLFRSATGEAWQ	1656
QY	1788	GIMKDTL--RDCD-----QESTCYNTVISPFIYFVFLTAQFVLNVVIAVLKHL	1836
Db	1657	EIMLSCLGEKCEPDTTAPSGQESERCCTDLAYVYFVSIFFCFLMLNLFVAVIMDNF	1716
QY	1837	EESNKEAK-----EBAELEAELE-----LEMKTLSPQPHSPGLSPFLWPG	1876
Db	1717	EYLTRDSSILGPHHLDEFVRVWAEYDRAACGRHITYEMYELTM-----SPPLGLG	1768
QY	1877	VEGPDSPDPKPGALHPAAHARSASHFSLHPTMQPHPTLPDPDLTVRKSGVSRTHSL	1936
Db	1769	KRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD-----IKIAKGGADRQQL-	1821
QY	1937	PNDSYMCRHGSTAEGPLGHRGWL-----PKAQSGSVLSVHSQPADTSYI-----	1981
Db	1822	--DSELQKETLAIWPHLSQKMLDILLVMPKASDLTVGKIYAAMIMDYKQSKVKQRQ	1879
QY	1982	LQLPKDAP--HLLQPHSAP-----TWGTIPKLPP-----PGRSPLAQRPLRRQ	2022
Db	1880	LEEQKNAFMFORMEPSSLPQEIIANAKALPCLPQGPAGLGGRSGCPAMSPSPQIFQLT	1939
QY	2023	AAIRTD-----SLDVQGLGSRREDLLAEVSGPSPPLARAYSF-----GQSSTQ	2065
Db	1940	CMDPADDDGQFQEQRSLVVTPDQSMRRSFSTIRD-----KRSSSWLEEFMSERSDNTY	1994
QY	2066	AQQHSRSHS--KISKHMTPPAPCPGPEPNWGKGPETRSLSLELDTLSWISGDLPPGGQ	2123
Db	1995	KRRRSYHSSLRLSAHRL-----NDSGHKSDTHRS-----GGR	2028
QY	2124	EEPPSPR-----DLKKCYVEA-----QSCORRPTSWLDEQRRHSIAVSCLDGSGQP	2170
Db	2029	ERGRSKEREHLISADVSRCSSEERGAQADWDSPERHPSRSPSEGRSQS-----	2076
QY	2171	HLGTDPSNLGGPLGGPSRPPKKSPPSITIDPPES--QGPRTPPSPGICLRRRAPSSD	2228
Db	2077	-----PSR-----QGTGSLSESSIPSVSDTSTPRHSRRQLPPVPKPRPLL---SYSSL	2122
QY	2229	SKDPLASGPP-----DSMAASPSPKDVLSSLGLSSDP	2261
Db	2123	KQPSNFSPPADGSGGSLLASPALESAQVGLPESDSDP	2161
RESULT 8			
T31092			
probable voltage-gated sodium channel - Aiptasia pallida			
C;Species: Aiptasia pallida			
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004			
C;Accession: T31092			
R;White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.			
submitted to the EMBL Data Library, January 1998			
A;Description: Structure of a putative sodium channel from the sea anemone Aiptasia palli			
A;Reference number: Z20975			
A;Accession: T31092			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-1810 <WHI>			
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AAB9;			
C;Genetics:			
A;Gene: Na1			
C;Superfamily: sodium channel protein			
Query Match			
Best Local Similarity			
Matches			
Query			
Db			
QY			

QY	826	QGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDVATFCMLMLFIFISILGMH	885
Db	564	TSFGISVLRALRLRIKTIKYWASLRNLVSLMSMKSIISLLPLFLFIVV FALLGMQ	623
QY	886	LFGCKFASERDGTLPDRKNPDSLLWAI VTVFOILTQEDWNKVLYNM-----ASTSSWA	940
Db	624	LFGGRF--NFNDG--TPSANFDTFPAAIMTVFOILTGEDWNEVMYNGIRSGGVSSGWS	679
QY	941	ALYFIALMTFGNYVFLNLLVAILVEGF-QAEISK-----REDASGLSCIQLPVD SQGD	995
Db	680	AVYFIVLTIFGNYTLLNVFLATAVDNLANAQELTKDEQEEEA FNQHALQAKEV-----	735
QY	996	ANKSESEPDPFSPSLDGDGDRKKCLAL-----VSL	1025
Db	736	--SPMSAPNV--PSIERDRRRRHMSMWEPSSHLRERRRRHHMSVMEQTSQLRRHMOM	791
QY	1026	GEHPELRKSLPLPLIHTAATPMS-----LPKSTSTGLGEALGPASRRRTSSS	1072
Db	792	SSQEALNKEEAPPNPNPLNPLNPLNAHPSLYRRPRPME-GLALGLEKCEEEHVSR	850
QY	1073	GSAEPGAHEMKSPPS-ARSSPHSPWSA-----ASSWT-----SRRS	1108
Db	851	GGSLKALDCORSPLSLGRREP--PWLARPCHGNCEPALQETAGGETVTVTFEDRARHRQS	908
QY	1109	SRNSLGRAPSLKRSPSGERRSLLSGEGQESQDEEESSEERASPA GSDHRRGS-----	1163
Db	909	QRRSRHRRVRTEAKESSASRS-RSVQSERSLDEGASTEGER-----DHEARGSHGKE	961
QY	1164	---LEREAKSFDLPTLQVP-----GLHRTAS-----GRGSASEHQDCNGKS	1203
Db	962	PTIHEEERAQDLRRTDLSLMVPGKGLAGGLDEAGTFLVSSPEGVKEAAPTEQHADGSG	1021
QY	1204	ASGRL-----ARALR-----PDDPPL-----	1219
Db	1022	EPALLGHVQLDVGRAISQSEPDLSCTVATTDKVTTESTDVTVAIPDAEPLVDSTVVHIGN	1081
QY	1220	--DGD-----DADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRRL	1267
Db	1082	KTDGEASPFOEAEMKEAQETEKQKKERPASGKAMVPHS-----SMFIFSTSNPIRR	1134
QY	1268	LCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTV	1327
Db	1135	ACHYVNVNLYFEMCILLVIAASSIALAAEDPVLTNSENRV-LRYFDYVFTGVFTFEMVI	1193
QY	1328	KVALGWFGEQAYLRSSWNVDGLLVLSVIDI-LVSMVSDSGTKILGMLRLVRLRLTL	1386
Db	1194	KMIDQGLILQDGSYFRDLWNILDVWVGALVAFALANALGTNKGRIKTIKSLRVLRL	1253
QY	1387	RPLRVISRAQGLKLVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC--QGE	1444
Db	1254	RPLKTIKRLPKLKA VDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYCTDSK	1313
QY	1445	DTRN-----ITNKSDCAEASVR-WVRHKYNFDNLGQALMSLFLVLSKDGWVDIMYDGLD	1497
Db	1314	DTEKECIGNVVDHEKNMEVKGRWKREHFHYDNIWALLTLFTVSTGEGWPQVLQHSVD	1373
QY	1498	AVGVDOQPIMNHPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREE	1557
Db	1374	VTEEDRGPSNRNMEMSIFVYVVFVFPFFVFVNFVFIITF-----QEQDKMEE	1426
QY	1558	KRLRLLEKRRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVGLNVV	1608
Db	1427	---CSLEKNERACIDFAISAKPLTRYPQNRHTFQYRVWHFVVSFYEYTIMAMIALNTV	1483
QY	1609	TMAMEHYQQPQILDEALKICNIYIFTVFLVESVFKLVAFGRFRFFQDRWNQDLAIVLLS	1668
Db	1484	VLMKYSAPCTVELALKYLNIAFTWVFSLECVLKVIAFGVNYFRDWTNIFDFITVIGS	1543
QY	1669	IMGITLEEIEVNASLPINPTIIRIMRVLRIRVLRKLLKMAVGMRALLDVTMQALPQVGNL	1728
Db	1544	ITEIVLTDKLVNTTGFNMSFLKLFRA---ARLIKLRQGYTIRILLTWTFFVQSPKALPYV	1600



Db 156 IAKGLVMHEYAYLRDPWNWLDFFVVVILGYVTLVPNVANL--SGIRIFRVLRALRTISAVE 213  
Qy 196 SMRILVTLTLLDTPMLGNVLLLCFFVFIFIGVQVWAGLNRNRCFLPENFSLSDVL 255  
Db 214 GLKTMVNALLKSMQWLSVLTLTFFLCVFAVGMQLFVGLRNKCVLKPLPLNTTIDYDS 273  
Qy 256 ----ERYQTENEDESPFICSQPRENGMRSCRSVPTLRDGGGGPPCGLDYEAYNSSNT 311  
Db 274 FVTNESHWHYHPDTPITC-----GNSTAGPCPLNY----- 306  
Qy 312 TCNVNWNQYTNCSAGEHNPFGKAINFDNIGYAMIAIFQVITLGGWVDIMYFVMDAHSFYN 371  
Db 307 TCL-----ANIG-NNPNYGYTNLDNFGWAVITAFQLVTLDYWENVYNYVLSSMGSWY 357  
Qy 372 FIYFILLIIVGSPFMINCLVVIATOFSETKQRESQLMREQVRFLSNASTLAS-FSEPG 430  
Db 358 IFYFFMWIFEGSFYLLNLVLAVVAVSY-----QOEVLALQDRENYNNLKGVASLYSPHG 412  
Qy 431 SCYEEELLKYLVIILKAARRLAQVSRAGVRVGLLSSPAPLGGQETQTPSSSCSRSHRRLS 490  
Db 413 CVVPKLLRN-----SKSKTKSLASKCK-----MSFCVPCFSIGKQPE----- 449  
Qy 491 VHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGA 550  
Db 450 -HSNGHASDNESHASTG-GTIRVDSTAEMK-----MLNDKNEVRTNG----- 491  
Qy 551 ESVHSFYHADCHLEPVRQCAPPSPSEASGRTVGSGKVYPTVHTSPPPETLK--EKALV 608  
Db 492 ---HSL-----PEPKTSFFSVSSDINSIHRMNSSTEVMPTQTSKFDNILT 534  
Qy 609 EVAASSGPPTLTSLNIPPGPYSSMHKLETSQSTGACQSSCKISSPCLKADSGACGPDSCP 668  
Db 535 K-----TLDVKSFLRLKLSAISEQSSTGDVDNENINN-----TQPKSVS 575  
Qy 669 YCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDHSHRRQRSLSGPDAPSSVL-- 726  
Db 576 FIARVLTPRGSLA-----RQTSTGSATHKTIKQ 605  
Qy 727 -AFWRLLICTFRKIVDSKYFGRGIMTIALVNTLSMGIEYHQPHEELTNALEISNIVFTSL 785  
Db 606 DTKWNRIRRMISKIVLHGMDTFTFCTMVNTLFLSLEYHNDSNYLMVLEIGNKVFTMV 665  
Qy 786 FALEMLLKLIVYGFPGYIKPNYINFDGVIWVISWE-----IVGQGGGLSVLRTFRLMR 840  
Db 666 FLEMLIKITAFGFGYIKSRWNIFDGFIVWISMDVLMVELLDHSDGLSVLRTFRLLR 725  
Qy 841 VLKVRFLPALQRLVLMKTMNDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGTLL 900  
Db 726 VFKLAQSWQTMNMLLSTIARSVGQLGNLTIVLGIVIYMLAVGVQLFDQYTTKNGVDV 785  
Qy 901 PDRKNFDSLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLV 960  
Db 786 P-RWNFTDFWHSFMMIFRVLCE-WIEPLYDCMRASTSWATLFFLTTLVIGNFLVNLFL 843  
Qy 961 AILVEGFOAEIISKREDASGQLSCIQLPVDQSOGGDANKSESEPDFFPSLDGDGRKKCL 1020  
Db 844 ALLNAPARESLEQ-----EAKKTKPKSKFAQGVSKLSRALRFR 883  
Qy 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080  
Db 884 STVS-----KTTQVLPTIRVHD-----GE-----NATDGDKAPTQV 914  
Qy 1081 HEMKSPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGE-----RRSLLSG 1134  
Db 915 NGLESKTS-----SAIS--TSSNASAMISAVTAFQGNKKGKLNDRDTRRLSLAI 964  
Qy 1135 EGQESQDEEESSEERASPAGSDHRHGRGSLEREAKSSFDPDTLQVPLHRTASGRGSAS 1194  
Db 965 E-----TANSDSNTSNVLAASST-----SIT 987  
Qy 1195 EHQDCNGKSASGRALARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACVLERDSW 1254

Db 988 GRQD-HGTS-----DPPDPP-----MTEVDECCPCWCMKMTGCGITR--W 1024  
Qy 1255 SAYI-FPQOSRFRLLCHRIITHKMFHDHVVLVIIFLNCITIAE-----RPKIDPHSAER 1307  
Db 1025 KASDGYRSWRNLR LAVKKFVEHKYFEWITLAIIMASSIALTFEDINLPSRPKL-----K 1078  
Qy 1308 IFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDLGLLVLSVIDILVSMVS 1367  
Db 1079 EYLQYLNIFFAVTFSEIFLLKVLGL-----GVVSYFRNCWNCILDVIVFVPV-----SSVIA 1130  
Qy 1368 DSGTK--ILGMLRVLRLRLTLRPLRVISRAOGLKLVETLMSLLKPIGNIVVICCAFFII 1425  
Db 1131 DSSNQDSSLSSRLSLRTLRLALRPLRAISRWEGRVNVVNSLLPAIPGIGNVLLVCMVFWLI 1190  
Qy 1426 FGILGVQLFKGKPFVCCGEDTRN-----ITNKSDCAEASVRWVRHRYNEDNLGQALMSLF 1480  
Db 1191 FSIIMGVQFPGGRFFKCDVNNKERLPISIVQNRSECIQGYRWVNSDINFNLSNGFMALF 1250  
Qy 1481 VLASKDGVVDIMYDGLDAVGVDQOPIMNHNPMWLLYFISFLIIVAFVFLNMFVGVVENF 1540  
Db 1251 QVATFEGWIEWMRDAVDAREVDQOPSDGYNFSAYAFVVFVFIIVGSFFTLNLFIGVIIDNF 1310  
Qy 1541 HKCRQHQB-----EARRRREKRLRR-LEKRRRKAQCKPYYSYDSYRRLLVHHLCT 1591  
Db 1311 NRLKKQVEDFGALDVLTLTPSORAWFGTIRKAATKKPKKVISRPENS-----FMAWLFDVH 1366  
Qy 1592 SHYDLFITGVIGLVNVTMAHEHYQQPQILDEALKICNYIFTVIVLESVFKLVAFGFR 1651  
Db 1367 SSRFETLIMFFICLNILVMMIQHYGQKPAVEQALMIINLVFTGLFTLEAILRIVVLRL-H 1425  
Qy 1652 FFQDRWNQDLALVLLSIMGITLSEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGM 1711  
Db 1426 YFREPNVDFVIVVLSILGIILEHLEYELFITPSPF---VARVFRIGRLLRFRYKGAKGI 1482  
Qy 1712 RALLDTVMQALPQVGNLGLLMLLFFIFAALGVLFGLDECDETHPCGLGRHATFRNPG 1771  
Db 1483 RRLLFALIISLPALLNIGALLFLIMFIYAIIGMSSFGYVK-----KTGALDSVVNFETFG 1537  
Qy 1772 MAFLTFRVSTGDNWNGIMKDTL--RDCDQE-----STCYNTVISPIYFVSFVLTAF 1822  
Db 1538 NSMLLLFRLSTAGWNDVLKPLLIKPPDCDKLWCIPNGCSTPWLAVVYFTTILFTFL 1597  
Qy 1823 VLVNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSPQSPHSPGLSPFPLWPGVEGPD 1882  
Db 1598 IINMYIAILENLSQAH-EQEEVGVTDDDLDMFY-----YHWERF----- 1638  
Qy 1883 PDSKPGALHPAAHARSASHF--SLEHPTMQPHPTLPTELPGEDLLTVRKSGVSRTHSLPND 1940  
Db 1639 -----PGATQYIPHS-ALSDFVDGLDHLPLRIPQPNKFACINLNIPIKQG-DRVHCDFVMQ 1691  
Qy 1941 YMCRH--GSTAEGPLHGRWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAP 1998  
Db 1692 ALVRRVLGDIEEDGLG-----SSSV-----AYTLMKSKMEQHCI----- 1725  
Qy 1999 TWGTIPKLPPPPGRSPLAQRLRRQAARTDSL 2030  
Db 1726 --STFPK--RHRTKTESTTLKRTQEVRAATI 1752

RESULT 9

S29237

calcium channel protein BII-2, brain - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S29237

R;Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.

FEBS Lett. 308, 7-13, 1992

A;Title: Molecular cloning and characterization of a novel calcium channel from rabbit

A;Reference number: S29236; MUID:9235472; PMID:1379552

A;Accession: S29237

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2178 <Nil>



Db 1717 EYLTRDSSILGPHHLDHFVRVWAEYDRAACGRHITYEMYMLTLM-----SPPLGLG 1768

Qy 1877 VEGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQPHTELPGPDLLTVRKSGVSRTHSL 1936

Db 1769 KRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD---IKIAGGADRQQL- 1821

Qy 1937 PNDSYMCRHGSTABGPLGHRGWGL-----PKAQSGSVLSVHSPADTSYI----- 1981

Db 1822 --DSELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMIMDYKQSKVKQRQ 1879

Qy 1982 LQLPKDAP--HLQPHSAP-----TWGTIPKLP--PPGRSPLAQRLRQAAIRTDSDLV 2032

Db 1880 LEEQKNAPMFORMEPSSLPQEIIANAKALPCLPQGPFA----- 1917

Qy 2033 QGLGSRREDLLAEVSGPSPPLARAYSFWGQSSTQAQOHSRSHSKIKHMTTPAP-----C 2086

Db 1918 -GLGRRSGCPA-----MSPLSPQIFQLTC 1940

Qy 2087 PGPEPNWKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSAEQSCQR 2146

Db 1941 MDPADDDGQF-QEQRSLVVTD-----PGSMRRSFSTIRD--KRS 1976

Qy 2147 PTSWLDE-----QRRHSIAVSC-----LDGSGPHLGTDPNSNLGGQPLGG\*2186

Db 1977 SSSWLEEFMSERSDNTYKSRRRSYHSSRLSAHRLNSDSGHK---SDTHRSRGRERG- 2031

Qy 2187 PGSRPKKLSPPSITIDPPESQ-----PRTPPSPGICLRRRAPSSDSKDPLAS 2235

Db 2032 -RSKEREHLLSADVSRCSSEERGAQADWDSPERHPSRSPSEG---RSQSPSRQGTCSLSE 2087

Qy 2236 GPPDSMAASPSPKK 2249

Db 2088 SSIPSVSDTSTPRQ 2101

RESULT 10

C54972

voltage-dependent calcium channel alpha 1E - mouse

C;Species: Mus musculus (house mouse)

C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004

C;Accession: C54972

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A;Reference number: A54972; MUID:94350992; PMID:8071363

A;Accession: C54972

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA

A;Residues: 1-2272 <WIL>

A;Cross-references: UNIPROT:Q61290; GB:129346; NID:G522330; PIDN:AAA59206.1; PID:G522331

A;Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.1%; Score 1681; DB 2; Length 2272;

Best local Similarity 23.7%; Pred. No. 2.2e-94;

Matches 607; Conservative 375; Mismatches 844; Indels 740; Gaps 82;

Qy 30 GRPGGSAEKDPGSADSEAEGLPYPALAPV----- 60

Db 11 GRPGSGDGSD---QSRNRQGTVPFASGPAAAYKQKAQARTMALYNPIPVRCQFTVN 67

Qy 61 --FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMR--PCEDIAQSCRCRI 116

Db 68 RSLFIFGEDNIVRYAKKLIDWPPPEYMIATIANCIVLALEQHLPEDDKTPMSRR--- 124

Qy 117 LQAFDDFIFAFPAVEMVVKWALG-IFGKKCYLGDWTNRLDFFIVIAGMLEYSLDLQN-- 173

Db 125 LEKTEPYFIGFCFEAGIKIVALGFIFHKSYLRNGWNVMDFIVLSGILATAGTFNTH 184

Qy 174 VSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLW 233

Db 185 VDLRALRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLIQIGLLLFFAILMFAIGLEFY 244

Qy 234 AGLLRNRCFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGG 293

Db 245 SGKLRACFMNNGIL-----EGFDP-----PHPCGVQGC----- 274

Qy 294 GGPPCGLDYBAYNSSNTTTCVNMNQYTNCSAGEHNPFKGAINEDNIGYAWIAIFQVITL 353

Db 275 ---PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITM 309

Qy 354 EGWVDIMYFVMDA-HSFYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQ 412

Db 310 EGWTTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVGLSGEFAKERERV-----EN 364

Qy 413 RVRFLSNASTLASFPSEPGSCYEELLKYVILRKAARRLAQVSRRAAGVRVGLLSSPAPLG 472

Db 365 RRAFMK-----LRRQQQI----- 377

Qy 473 GOETQPSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRL 532

Db 378 -----ERELNGYRAW 387

Qy 533 MLPPSTPALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPT 592

Db 388 I----- 388

Qy 593 VHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMMKLLTQSTGACQSSCKISS 652

Db 389 -----DKAEVMLAEENKNGSTSALEVLRRATIKRSRTAMTRDSSDEHCVDISSVGT 441

Qy 653 PCLKADSGACGPDSCPYPARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRR 712

Db 442 PLARASIKSTKVDGASY-----FRHKE----- 463

Qy 713 ORSLGPDAEPSSVLAFWRLLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELT 772

Db 464 -----RLLRISIRHMVKSQVIFYWLVSVVALNTACVAIVHVNQPOWLT 506

Qy 773 NALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QG 827

Db 507 HLLYYAEFLFLGLLLEMSLMYGMGPRLYFHSSFCDFGVTVGSIFEVWVAIFRPGTS 566

Qy 828 GGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDVATFCMLLMFLFIFISILGMHLF 887

Db 567 FGISVLRALRLRIFKITKYWASLRNLVSVLSMSSMKSIISLLFLFLFIVFVALLGMQLF 626

Qy 888 GCKFASERDGDTLDPDRKNFDSLWAIIVTVFOILTQEDWNKVLYNGM-----ASTSSWAAL 942

Db 627 GGRF-NFNDG---TPSANFDTPFAIMTVFOILTGEDNWEVMYNGIRSQGGVSSGMWSAI 682

Qy 943 YFIALMTFGNYVLFNLLVAILVEGF-QAEEISK---REDASGQLSCIQLPVDSQGDAN 997

Db 683 YFIVLTFGNYTLNLVFLAIVDNLANAQELTKDEEBEAFNQKHALQAKEV----- 736

Qy 998 KSESEPDFFPSLDGDGDRKKCLAL-----VSLGE 1027

Db 737 SPMSAPNM--PSIERDRRRRRHMSMWEPSSHLRERRRRHHMSVWEQRTSLRRHMQMSS 794

Qy 1028 HPBLRKSLLPPLIHTAATPMS--LPKSTSTGL-----GEALGPA-----SRTSSS 1072

Db 795 QEALNKEEAPPNPNPLNPLNPLNPLNAHPSLYRRPPRIEGLALGLLEKCEERISRG 854

Qy 1073 GSAE-----PGAAHEMKSPPS-ARSSPHSPWSAASWTS----- 1105

Db 855 GSKGDIGGLTSALDNQRSPLSLGKREP--PWLPRSCHNCNDPIQOEAGGETVVTFEDR 912

Qy 1106 ---RRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEERASPAQSDHRRHG 1162

Db 913 ARHRQSORRRSRHRRVTRTEGKDSASASRS-RSASQERSLDEGVSVEGEKEHEPHSHRSKB 971

Qy 1163 SLEREAKSSFDL--PDTLQVP--GL-----HRTASGRGSASEHQDCNGK 1202

Db 972 PTIHEBERTQDLRRTNSLMVPRGSLVGALDEAETPLVQPQPELVGKDAALTEQAEGS 1031

Qy 1203 SAS-----GRLARALRPD-----DPPLD----- 1220

Db 1032 SEQALLGDVQLDVGRGISQSEPDLSMTANMDKATTESTSVTVAIPDVLVDSTVVNIS 1091  
QY 1221 -----GDDADDEGNLSKGER-----VRAWIRARLPACYLERDSWSAYIFPPQSR 1264  
Db 1092 NKTDGEASPLKEAETKEEEEEVEKKKQKKEKRETKAMVPHS-----SMFIFSTTNP 1144  
QY 1265 FRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNVIFTAVFLAE 1324  
Db 1145 IRRACHYIVNRYFEMCILLVIAASSIALAAEDPVTNSERNKV-LRYFDYVFTGVTFTE 1203  
QY 1325 MTVKVVALGWCGEQAYLRSSWNVDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRL 1383  
Db 1204 MVIKMIDQGLILQDGSYFRDLWNILDFVVVGALVAFALANALGTMKGRDIKTIKSLRVL 1263  
QY 1384 RTLRPLRVISRAQGLKLVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC-- 1441  
Db 1264 RVLRLPKTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFCYCTD 1323  
QY 1442 QGEDTRN-----ITNKSDCAEASYSR-WVRHKYNFDNLGQALMSLVFLASKDGVVDIMYD 1494  
Db 1324 SSKOTEKECIGNYVDHEKNKMEVKGREWKREHFHYDNI I WALLTLFTVSTGEGWPQVLQH 1383  
QY 1495 GLDAVGVDQOQPMNHNPMWMLLYFISPLLIVAFVLMFVGVVVENFHKCRQHOREEEARR 1554  
Db 1384 SVDVTEEDRGSRNRMEMSIYFVYVFWVFPFFVFNIFVALIITF-----QEQGDKM 1436  
QY 1555 REEXRLRLEKKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGL 1605  
Db 1437 MEE---CSLEKNERACIDFAISAKPLTRYMPQNRHTFOYRVWHFVVSFEXTIMAMIAL 1493  
QY 1606 NVVTMAMEHYQQOILDEALKICNYIFTVFVLESVKLVAFGRFRFFQDRWNQDLDAIV 1665  
Db 1494 NTVVLMKYYTAPCTYELALKYLNIAFTVFSLECVLKVIAPGFLNYFRDWTNIFDFITV 1553  
QY 1666 LLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLMKMAVGMRALLDTVMQALPQV 1725  
Db 1554 IGSITEIILTDSKLVNTSGFNMSFLKLFR--ARLIKLRQGYTIRILLWTFFVQSFKAL 1610  
QY 1726 GNIGLLFMLLFFIFAALGVELFGDLECD-ETHPCEGLGRHATFRNFGMAFLTFRVSTGD 1784  
Db 1611 PYVCLLIAMLFFIYAIIGMOVFGNIKLDDESH---INRHNFRSFFGSLMLLFRSATGE 1666  
QY 1785 NWNIGIMKDTL--RDCQESTC-----YNTVISPIYFVSFVLTAQFVLNVNVI AVL M 1833  
Db 1667 AWQEIMLSCLGKGCBEPTTAPSGQNESERCGTDLAYVYFVSFIFCSFLMLNLFAVIM 1726  
QY 1834 KHEESNKEAK-----EEAELEAELE-----LEMKTLSPQPHSLGSPFL 1873  
Db 1727 DNPYLTRDSSILGPHHDLDFVRVWAEYDRAACGRHYHTEMVEMLTLM-----SPPL 1778  
QY 1874 WPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHTELPDGLLTVRKSGVSRT 1933  
Db 1779 GLGKRCPKSVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD----IKIAGGADRQ 1832  
QY 1934 HSLPNDSYMCRHSGTAEGPLHGRGWGL-----PKAQSGSVLSVHSPADTSYI----- 1981  
Db 1833 QL---DSELQKETLAIWPHLSQKMLDLLVPMKASDLTVGKIYAAMMIMDYKQKVKKQ 1889  
QY 1982 ---LQLPKDAP--HLLQPHSAP-----TWGTIPKLP-----PGRSPLAQRL 2019  
Db 1890 RQLEEQKNAPMFORMEPSLIPQEI I ANAKALPYLQDDPVSGLSGRSGYPSPMSPLSQEI 1949  
QY 2020 -----RRQAAIRTDSDVQGLGR-----EDLLAEVSGSPPLA 2053  
Db 1950 FQLACMDPADGQFQEQQSLVYVDPSSMRRSFSTIRDKRSNSSLWLEEFMSERSSENTYKS 2009  
QY 2054 RAYSFWSQSSTOAQOH-----SRSHSKI SKHMTTP----- 2083  
Db 2010 RRRSY--HSSLRLSAHRLNSDGHKSDTHRSGGRERGRSKERKHLSPDVSRCNSEERGT 2067  
QY 2084 -APCPGPEPNWGKGPPETRS-----SLE-----LDTELSWISGDLPLPPGQKEEP 2126

Db 2068 QADWESPERRQSRSPSEGRSQTPNRQGTGSLSESSIPSISDTSTPRRRRRQLPP-----VP 2123  
QY 2127 PPSRDLKKCYSEVAQSCQRRPTSWLDEQRRHSIAVSCLDGSGOPHLGTDPSNLGGQPLGG 2186  
Db 2124 PKPRPLLSYSSL-----MRHTGGISPPPDGSE-----GGSPLAS 2157  
QY 2187 PGSRPKKK-LSPPSITIDPPESQQRTP---PSPGICLRRRAPSSD 2228  
Db 2158 QALESNSACLTSSNSLHPQOQHPSPOHYISEPYLALHEDSHASD 2203  
RESULT 11  
A54972  
voltage-dependent calcium channel alpha 1E-3 - human  
C;Species: Homo sapiens (man)  
C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: A54972  
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil  
J. Biol. Chem. 269, 22347-22357, 1994  
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel  
A;Reference number: A54972; MUID:94350992; PMID:8071363  
A;Accession: A54972  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2270 <WIL>  
A;Cross-references: UNIPROT:Q15878; GB:L29385; NID:9495869; PIDN:AA59205.1; PID:9495870  
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
Query Match 14.0%; Score 1665; DB 2; Length 2270;  
Best Local Similarity 24.2%; Pred. No. 2.1e-93;  
Matches 620; Conservative 386; Mismatches 814; Indels 744; Gaps 90;  
QY 31 RPPGSAEKDPGSADSEAEGLPYPALA-----PV----- 59  
Db 11 RPSGSDGSDS---QSRNRQGTVPVPSAGQAAAYKQTKAQRARTMALYNPIPVQRNCFVNR 67  
QY 60 VPFYLSQDSRPRSRNCLRTVCNPFERISMLVILLNCVTLGMFR--PCEDIACDSQRCRIL 117  
Db 68 SLFIFGEDNIVRYAKKLIDWPPFEYMITATIANCIVLALEOHLPEDDKTPMSRR---L 124  
QY 118 QAFDDPFIFAFFAVEMVVKMVALG-IFGKKCYLGDWTNRLLDFFIVIAGMLEYSLDLQN--V 174  
Db 125 EKTPEYFIGIFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFNTHV 184  
QY 175 SFSAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWA 234  
Db 185 DLRTLRVVRVLRPLKLVSGIPSLQIVLKSINKAMVPLLQIGLLLPFAILMFAIIGLEFYS 244  
QY 235 GLLNRNCFLPENFSLPLSVDLERYYYQTENEDESPFCISQPRENGMRSCRSVPTLRGDGG 294  
Db 245 GKLHRACFMNNSGIL-----EGFDP-----PHPCGVQGC----- 273  
QY 295 GPPCGLDYEAYNSSSTNTTCVNWNYTNCNCSAGEHNPFKGAINFNIGYAWIAIFQVITLE 354  
Db 274 --PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITWE 309  
QY 355 GWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKORES-----Q 407  
Db 310 GWTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVLGVLGSEFAKERERVENRRAFMK 369  
QY 408 LMREQRVRFVLSNASTLASFSEPGSCYEELLKYLVLIRKAARRLAQVSRAGVRVGLLSS 467  
Db 370 LRRQQQIE-----RELNGYRAWIDKAEVMLAEENKNAG----- 403  
QY 468 PAPLGGQETPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTILRAPRASPEIQDRDAN 527  
Db 404 -----TSALEVLRRATI-----KRSTEAMTRDS- 427  
QY 528 GSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTGSG 587  
Db 428 -----SDEH----- 431  
QY 588 KVIPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACQSS 647









C>Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 24-Sep-1999  
C;Accession: B54972  
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil  
J. Biol. Chem. 269, 22347-22357, 1994  
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel  
A;Reference number: A54972; MUID:94350992; PMID:8071363  
A;Accession: B54972  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-2251 <WIL>  
A;Cross-references: GB:129384; NID:9495867; PIDN:AAA59204.1; PID:9495868  
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1663.5; DB 2; Length 2251;  
Best Local Similarity 24.2%; Pred. No. 2.6e-93;  
Matches 617; Conservative 383; Mismatches 815; Indels 735; Gaps 89;

QY 31 RPPGSAEKDPGSADSEAGLPYPALA-----PV----- 59  
Db 11 RPPSGDGDSD--QSRNRQCTVPASGQAAYKQTKAQRARTMALYNPIPVQRQCFTVNR 67

QY 60 VFFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTLMFR--PCEDIAQSQRCLIL 117  
Db 68 SLFIFGEDNIVRKYAKKLIDWPPPEYMILATIIANCIVLALAEQHLPEDDKTPMSRR--L 124

QY 118 QAFDDFIFAPFAVEMVVMVALG-IFGKKCYLGDWTNRLLDFVIAGMLEYSLDLQN--V 174  
Db 125 EKTEPYFIGFCEAGIKIVALGFPHKGSYLNRGNWVNDPIVLSGILATAGTHFNTHV 184

QY 175 SFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGQLWA 234  
Db 185 DLRTLRVLRPLKLVGIPSLQIVLKSIMKAMVPLLGILLFFAILMFAIIGLEFYS 244

QY 235 GLLRNRCFLPENFSLPLSVDLERYVQTENEDESPFICSPRENGMRSCRSVPTLRGDGG 294  
Db 245 GKLHRACFMNSGIL-----EGFDP-----PHPCGVQGC----- 273

QY 295 GPPCGLDYEAYNSSNTTCVNWNYQYTNCSAGEHNPFGAINFDNIGYAWIAIPIQVITLE 354  
Db 274 --PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITME 309

QY 355 GWVDIMYFVMDA-HSFYNFYIFILLIIVGSFFMINLCLVVIATQFSETKORES-----Q 407  
Db 310 GWTTVLYNTDAGATWNWLYFIPLIIGSFFVLNLVLGVLGSEFAKERERVENRRAFMK 369

QY 408 LMREQVRFLSNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAAGVRVGLLSS 467  
Db 370 LRRQQQIE-----RELNGYRAWIDKAEVMLAEENKNAG----- 403

QY 468 PAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIQDRDAN 527  
Db 404 -----TSALEVLRRATI-----KRSRTEAMTRDS- 427

QY 528 GSRRMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVCQAPPPRSPSEASGRVTGSG 587  
Db 428 -----SDEH----- 431

QY 588 KVPYTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLTQSTGACQSS 647  
Db 432 -----CVDI 435

QY 648 CKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHDLRD 707  
Db 436 SSVGTPLARASIKSAKVDGVSY-----FRHKE--- 462

QY 708 PHRRQRSLSGDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQ 767  
Db 463 -----RLLRISIRHMVKSQVFWIVLSLVALNTACVAIVHHNQ 500

QY 768 PEELTNALEISNIVFTSLFALEMLKLVYGPFGYIKNPYNIFDGVIVIVISVWEIVGQ-- 825  
Db 501 POWLTHLLYYABFLFLGLFLLMSLKMVGMPRLYFHSFNCDFDGVTVGSIFEVVAIF 560

QY 826 --QGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFLFIFISIL 882  
Db 561 RPGTSFGISVLRALRLRIFKITKYWASLRNLVSLSMSSMKSIISLLFLFLFIVVFALL 620

QY 883 GMHLFGCKPASERDGTLPDRKNFDSLLWAVTVVFQILTQEDWNKVLYNGM-----ASTS 937  
Db 621 GMQLFGGRF-NFNDG--TPSANEDTFPAAMTVFQILTGEDWNEVMYNGIRSQGGVSSG 676

QY 938 SWAALYFIALMTFGNYVLFNLVAILVEGF-QAEEISK-----REDASQOLSCIQLPVDSQ 992  
Db 677 MWSAIYFIVLTFLFGNYTLNVLAVDNLANAQELTKDEQEEEEAFNQKHALQAKEV- 735

QY 993 GGDANKSESEPDFFPSPLDGDGRKKCLAL-----VSLGHEPELRK----- 1033  
Db 736 -----SPMSAPNM--PSIERERRRRHHMSVWEQRTSQLRKHQMSSQEALNREEAPTNNP 788

QY 1034 -----SLLPPLIIHTAATPMSLPKSTSTGLGEALGPA-----SRRTSSSGS-----AE 1076  
Db 789 LNPLNPLSSLNPLNAHP-----SLYRRPRAIEGLALGLEKFEERISRGSLKGDGD 843

QY 1077 PGAAHEMKSPPSARSSPHSPWSA-----ASSWTSRRSSR 1110  
Db 844 RSSALDNQRTPLSLGQREPPWLPARPCHGNCDPTQOEAGGSAVVTFEDRARHRQSRSR 903

QY 1111 NSLGR-----APSLKRRSPSGERRSL--LSGEGQESQD-----EESSESEERASPA 1155  
Db 904 HRRVTEGKESSSASRSRSASQERSLDEAMPTGEKDHRLGNHGAKEPTIQEERA---- 959

QY 1156 SDHRHRSGLEREAKSSF-----DLPDTLOVPLHRTASGRGSAHEQDCNGKSAS--- 1205  
Db 960 QDLRRTNSLMVSRGSLAGLDEADTPLVLPHELE---VGKHVVLTQEPEGSSEQALL 1016

QY 1206 -----GRLARALRPD-----DPPLDG----- 1221  
Db 1017 GNVQDMGRVISQSEPDLSCTANTDKATTESTSVTVVAVDPDPLVDSTVVHISNKTGDE 1076

QY 1222 -----DDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCH 1270  
Db 1077 ASPLKEABIREDEEEVEKKQKKEK-RETGKAMVPHS-----SMFIFSTTNPIRRACH 1128

QY 1271 RIITHKMFHDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKV 1330  
Db 1129 YIVNLRVEMCILLVIAASSIALAAEDPVLTNSEKRV-LRYFDYVFTGVFTFEMVIMKI 1187

QY 1331 ALGWCFCGEQAYLRSSWNVDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLRLRPL 1389  
Db 1188 DQGLIQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGKRDIKTKSLRVLRLRPL 1247

QY 1390 RVISRAQGLKLVAVETLMSLSKPIGNIVVICCAFFIIFGLGVQLFKGKFFVC--QGEDTR 1447  
Db 1248 KTIKRLPKLKAADFVCTVTSLNKVNFIIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDE 1307

QY 1448 N-----ITNKSDCAEASYR-WVRHKYNFDNLQALMSLFVLASKDGVVDIMYDGLDAVG 1500  
Db 1308 KECIGNYVDHEKNKMEVKGREWKREHFYDNIWALLTLFTVSTGEGWPQVLQHSVDVTE 1367

QY 1501 VDQQPIMNHNPMWMLLYFISFLIIVAFVFLNMFVGVVVENFHKCRQHQQEERARRRERKRL 1560  
Db 1368 EDRGPRSRNRMEMSIFYVVVYVFPFVFFVNFVALIITF-----QEQDKMMES--- 1417

QY 1561 RRLEKKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVLNVVTMA 1611  
Db 1418 CSLEKNERACIDFAISAKPLTRYMPQNRHTFQYRVVHVVVSPSFYEYTIMAMIALNTVVL 1477

QY 1612 MEHYQQOILDEALKICNYIFTVIVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMG 1671  
Db 1478 MKYISAPCTYELALKYLNIAFTMVFSLECVLKVIAFGLNFRDFTWNIFDITVIGSITE 1537

QY 1672 ITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLL 1731  
Db 1538 IILTDSKLVNTSGFNMSFLKLFRA--ARLIKLRQGYTIRILLTWTVQSFKALPYVCLL 1594

QY 1732 FMLLFFIFAALGVLEFGDLECD-ETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIM 1790

Db 1595 IAMLFYIAYIGMQVFGNIKLDDESH-----INRHNFRSFFGSLMLLFRSATGEAWQEIIM 1650

QY 1791 KDTL--RDCDQESTC-----YNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEES 1839

Db 1651 LSCIGKEGCEPDTTAPSGQENENERCGTDLAYVYFVSFFFCFSLMLNLFVAVIMDNFEYL 1710

QY 1840 NKEAK-----EEAELEAELE-----LEMTLSPQSPHSPGLSPFLWPVEG 1879

Db 1711 TRDSSILGPHHLDDEFVRVWAEVDRAACGRIHVTEMYEMLTLM-----SPPLGLGKRC 1762

QY 1880 PDSPPSKPGALHPAAHARSASHFSLEHPTMQPHPTLPGLDPTLVKRGVSVRTHSLPND 1939

Db 1763 PSKVAYKRLVLMNMPVAEDMTVHT--STLMALIRTALD-----IKIAGGADRQQL---D 1813

QY 1940 SYMCRHGSTAEGPLHGRWGGL-----PKAQSGSVLSVHSQPADTSYI-----LQL 1984

Db 1814 SELQKETLAIWPHLSQKMLDLLVMPKASDLTVGKIYAAMMIMDYKQSKVKKQROQLEE 1873

QY 1985 PKDAP--HLQPHSAP-----TWGTIPKLPP-----PGRSPLAQRLRRQAAI 2025

Db 1874 QKNAPMFQMEPSSLPOEIIANAKALPYLQDPVSGLSGRSGYPSMSPLSPQDIFQLACM 1933

QY 2026 RTDSLQVQGLGREDLLAEVSGSPPLARAYS-----FWGQSSTQAQQHSR 2071

Db 1934 --DPADDGQFQEROSLV--VTDPS--SMRERSFTIRDKRNSWLEEFMSERSSENTYKSR 1988

QY 2072 SHSKISKHMTPPAPCGPEPNWGKPPETRSSLELDT--ELSWISG--DILLPPGGQEEPP 2127

Db 1989 RRS-----YHSSLRLSAHRLNSDSGHKSDTHPSGGRERR 2023

QY 2128 SPR-----DLKKCVSVEAQSCORRPTSWLDQORRHSIAVCLDSGSPHLGTDPSNLG 2180

Db 2024 SKERKHLSPDVSRNCSEE--RGTQADWESPERRORSRPS--EGRSQ-----TPNR-- 2070

QY 2181 GQPLGGPSRPPKKLSPSITIDPPES--QGPRTPPSPGICLR-----RRAPS----- 2226

Db 2071 ----QGTGSLSESSIPSVSDTSTPRRRRRQLPVPKPRPLLSYSSLIHAGSISPPADG 2126

QY 2227 SDSKDPLASGPPDSMAA-----SPSPKK 2249

Db 2127 SEEGSPLTSQALESNNAWLTSSNSPHPQQ 2156

RESULT 14

A47447

calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)

C;Species: Discopyge ommata

C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A47447

R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.

Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993

A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Discopyge ommata

A;Reference number: A47447; PMID:93248175; PMID:7683405

A;Accession: A47447

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-2223 <HOR>

A;Cross-references: UNIPROT:P56699

A;Note: sequence extracted from NCBI backbone (NCBI:P130671)

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.9%; Score 1656; DB 2; Length 2223;

Best Local Similarity 24.2%; Pred. No. 7.3e-93;

Matches 595; Conservative 385; Mismatches 811; Indels 668; Gaps 89;

QY 35 GSAEKDPGSADSEAGLPYAL---APV-----VFFYLSQDSRPSRWCLRTVCNPW 82

Db 44 GAAQGSAGFKOTRAQRAFTMALYNPIVVRHNLCTANRSLFEGEDNIVKRSARRVIEWPP 103

QY 83 FERISMLVILLNCVTLMFR--PCEDIAQSORCIRILOAFDDFFAFAFVEMVVMKVALG 140

Db 104 FEYMLATIIANCVVLALEQHPNGD---KTPMAKSLEQTEPYFIFCFEAGIKIVALG 160

QY 141 -IFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVSPSFAVTRVRLPLRAINRVPSMRI 199

Db 161 FVFHKGSYLRNGWVMDFIVVLSGLL--ATAATHFNRLTLRAVRVLRPLKLVSGIPSLQI 218

QY 200 LVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLFLENFSLPLSVDLERY 259

Db 219 VLKSIKAMVPLLIQIGLLFFAILMFAIGLEFYFGKLRHTCTYDDAAAEELDLQF--- 274

QY 260 QTENEDESPFICSPRENGMRSCRSVPTLRDGGGPPCGGLDYEAYNSSNTTCVNNQY 319

Db 275 -----PCGTQEPTRLCPNGTVCVSYW--- 294

QY 320 YTNCAGEHNPFKGAINFDNIGYAWIAIFQVITLEGVVDIMYFVMDA-HSFYNFIYFILL 378

Db 295 -----IGPNDGITQFDNILLFALLTVFQCITMEGWTIILYNTDDALGAMWNWLYFIPL 346

QY 379 IIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRFLSNASTLASFSEPGSC 432

Db 347 IIGSFFVLNLVGLVSGEFAKERERVENRRSFLKLRQQOIE----- 389

QY 433 YEELLKVLVYLKAAARLAAQVRAAGVRVGLSSPAPLGGQETQPSSSCSRSHRRLSVH 492

Db 390 -RELNGYRAWIDKAEVMLLEENKNAGEKSAL----- 420

QY 493 HLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSAPPGAES 552

Db 421 -----HVLRRATIKKGR----- 432

QY 553 VHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPTVHTSPPPETLKEKALVEVAA 612

Db 433 -----MEMIQTES-----SEDQYTEISS 450

QY 613 SSGPPTLTSLNIPPGPYSSMHKLETSQACQSSCKISSPCLKADSGACGPDSCPYCAR 672

Db 451 VGSPLARASI-----KSTKLEGGSS----- 470

QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRSGLPDAEPSSVLAFWRLL 732

Db 471 -----YFRKKE-----RML 479

QY 733 CDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMILL 792

Db 480 RISIRHMVKSHAFYIWLGLVALNTVCVAVVHYDQPLWLSNPLYAEFTFLGLFSSEMFL 539

QY 793 KLLVYGPFGYIKNPYNIFDGVIVVISVWEIV-----GQQGGSLSVLRTFRLMRVLKLVRF 847

Db 540 KMYGCGPRLYFHSFNCFCGVIIGSIFDVVWVTIIRPETSFGISVLRALRLRIFKITY 599

QY 848 LPALORQLVLMKTMNVATFCMLLMLFIFISILGMHLFGCKFASERDGDTPDRKNFD 907

Db 600 WASLRNLVSLMSSMKSIISLLFLFVIVFALLGMQLFGGQFNFE--GTPP--TNFD 655

QY 908 SLLWAIYTVFQILTQEDWNKVLNGMAS-----TSSWAALYFIALMTFGNYVLFNLLVAI 962

Db 656 TFPAAIITVFIQILTGEDWNEVMYNGIKSQGVNSGMWSSVYFIVLTFGNVTLNVLAI 715

QY 963 LVEGF-QABEISK-----REDASQQLSCIQ-----LPVDSQGGDANKSE----- 1000

Db 716 AVDNLANAQELTKEEQEEEEINQKHALQKAKEVSPMSAPGFPSTEREFRRHKHMSIWEA 775

QY 1001 -----SEPDDFFSPSLDG-DGDRKK-----CLALVSLGEHPBLRKSLLPPL 1039

Db 776 RTSQLRRRMQMSREALFTDALQLEGSRYYRRHRSRIFEAESLRLAEQQAASHQLGEV 835

QY 1040 IHTAATPMSLPKSTSTGLGEALGPASRRTS-----SSGSAEPGAHAHEMKSPPSA 1089

Db 836 GRREAFKRSRLNS-----WQPADGDKRSSIKVNGEQGRALGRSVEAGASFERMAEPIRA 890

QY 1090 RSSPHSPW-----SAASWTSSRRSNRSLGR-APSLKRRSPSG---ERRSLLSGEGQ 1137

Db 891 RRRYRSLYKEAKMGLSESAETSLSRPGKNKEGRLLQQLCEEQESGQLTQTPEVMDAQGO 950

QY 1138 ES-----QDEESSEERASPAGSDHHRGSLERE-----AKSSFOLDP----- 1176  
Db 951 MKAFSWQGEPHSSMTRTPDVDTD-PSGNGLEKESGRTPENGKEESANTSEQVNEQSNWL 1009  
QY 1177 TLQV-----PGLHRTASGRGSASEHQ-----DCNGKSASRLARALRPDDPPLD-- 1220  
Db 1010 NLQLNQATPGDRELTTGTTRDTKQDKTQEOTEIDVDCN-----TETPMDSL 1056  
QY 1221 ---GDDADDEGNLSKGERVRAWIRARLPACYLERSDSWAYIFPPQSRFRLLCHRIITHKM 1277  
Db 1057 VTPGNAYSSSSVKEDEKS---KAIIPYT-----SMFLFRKTNPIRRVCHFIIVNLRY 1106  
QY 1278 FDHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIPTAVFLAEMTVKVVALGWCFG 1337  
Db 1107 FEMCILLVIAASSVALAEDP-IHKDSARNQVLRFYDFTGVFTFEMVIKMDIDGLVFH 1165  
QY 1338 EQAYLRSSWNVLGGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRLPLRVISRAQ 1396  
Db 1166 EGSYFRDVWNILDFIVVSGALVAFATNLIGSSGKDINTIKSLRVLRVLRPLKIRLP 1225  
QY 1397 GLKLVVETIMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDDCA 1456  
Db 1226 KLKAVFDCVVTSLKNVENILIVYKLFMFIFAVIAVQLFKGKFFYC--TDSSKMT-KQDC- 1281  
QY 1457 EASYRWVRHK-----YNFDNLQOALMSFLVLASKDGWVDIMYDGLDAVGVDQO 1504  
Db 1282 RGQFVLRQRTKLSIENGNTVTHYDNVNVWALLTLFTVSTGEGWPQVLQHSVDVTEADQG 1341  
QY 1505 PIMNHNPNMLLYFISFLLVAFVFLNMVGVVVENFHKRQHQHEEEARRREKRLRLE 1564  
Db 1342 PIPGNRMEMSIYIVYFVFPFFVNFVALIIITP-----QEQGDKMLEES---SLE 1391  
QY 1565 KRRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLDFITGVIGLNVVTMAMEHY 1615  
Db 1392 KNERACIDFAISAKPLTRYMPQNRQTFQYRVWQFVVSPEYITLTMIALTNTVVLMMKHH 1451  
QY 1616 QPQILDEALKICNIYIFTVIFVLESVEKLVAFGFRFFQDRWNQLDLAIVLLSIMGITLE 1675  
Db 1452 SPPPGFASVLKMNIAFTITFTLECILKIIAFGFLNYFRDSWNVDFVTVVGSISEIIVT 1511  
QY 1676 EIE---VNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLDVTMOALPQVGNLGLLF 1732  
Db 1512 ECNLKFVNL-----FLKLFRAARLIKLLRQGITIRILLWTFVQSFKALPYVCLLI 1562  
QY 1733 MLLFFIFAALGVELFGDLECDETHPECEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD 1792  
Db 1563 AMLFFIYAIQMLFGNIGLDHHTP---INRHNFTTFNALMLLFRSATGESWQEIMLA 1619  
QY 1793 TL--RDCE--QESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEESNKEAK---- 1844  
Db 1620 CLSGKECEGTREPSC-GTDVAYFYFVSFIFLCSFLMLNLVAVIMDNFEYLTRDSSILGP 1678  
QY 1845 ----EAELEAELE-----LEMKTL-SPQPHSPLGSPFLWPG-----VE 1878  
Db 1679 HHLDEFVRVWAEYDRAACGRIHYTDMYQMLTLMSP----PLGLGKKCPKVAYKRLVLMN 1734  
QY 1879 GPDSPD-----SPKPGALHPAAHARSA-----SHFSLEHPTMQBHPTELPGPDL 1922  
Db 1735 MPVTEDKTVHFTSTLMGLIRLTALQIKLARGGADKQQLDABLKEIMTIWPHLSQ-KTLDL 1793  
QY 1923 L-----TVRKSGVSRTHSL-----PNDSYMCRHGSTAEGPLGHR----- 1956  
Db 1794 LVPMTYSDLTVGKIYAAMMIMDYKQSKNKKYQKLQEEQSRTPMFQRMESASLPPQIIS 1853  
QY 1957 -GWGLPKAQGSVLSVHSQPADTSYLQLPKQDAPHLLQPHSAPTWG-TIPKLPPGRSPL 2014  
Db 1854 STKGLPYLQTGTPDVDSR-SEFTPLVPLP---PVMFQQGTSSQGEEIHKQRPKELKKI 1909  
QY 2015 AQR-----PLRRQA-AIRTDSDLVQGLGSRDLLAEVSGSPPLARAYSFWGQSSTQ 2065  
Db 1910 KLEYPHYGHYLPENQGRAVSMRLEIE---SAED-----TSPLKRSL-----STF 1952  
QY 2066 AQQHSRSHSKISKHMTTPPAPCPGPE---PNWGKGP--PETRSSLELDTLSWISGDLPP 2120

Db 1953 AANHNS-TWLNEYSLERA---GPEDLYKRWRRPLRPPSRSS-----N 1992  
QY 2121 GGQEEPPSPRDLKKCYSEVAQSQRRPTSWLDEQRRHSIAVCLDSGSPHLGTDPSNLG 2180  
Db 1993 AGSRERGRSRERKHLSPERSVCS-----TGQCAH-----PSQHRGLD-ORLS 2034  
QY 2181 GQPLGGGSGSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKD-PLASGPP 2238  
Db 2035 RSPSPGYSHRPREQVN-SSVSESPVPSSSGTSPPKQG---QRLPQTSPKRPPLVSYSP 2089  
RESULT 15  
A37490  
voltage-dependent calcium channel alpha 1E - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A37490  
R;Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.  
Science 260, 1133-1136, 1993  
A;Title: Structure and functional expression of a member of the low voltage-activated ca  
A;Reference number: A37490; MUID:93262464; PMID:8388125  
A;Accession: A37490  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-2222 <SOO>  
A;Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083  
A;Experimental source: brain  
A;Note: sequence extracted from NCBI backbone (NCBIP:132101)  
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
Query Match 13.9%; Score 1651.5; DB 2; Length 2222;  
Best Local Similarity 23.6%; Pred. No. 1.4e-92;  
Matches 591; Conservative 374; Mismatches 831; Indels 707; Gaps 77;  
QY 62 FYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGNFR--PCEDIACDSQRCRIQA 119  
Db 21 FIFGEDNIVRKYAKKLIDWPPEYFMILATIIANCIVLALEQHLPEDDKTPMSRR---LEK 77  
QY 120 FDDFIFAFFAVEMVVMVALG-IFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQN--VSF 176  
Db 78 TEPYFIGIFCFEAGIKIVALGFIHFKGSYLNRGNWNVDFIVVLSGILATAGTHFNTHVDL 137  
QY 177 SAVRTVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGL 236  
Db 138 RTLRAVRVLRPLKLVSGIPSLQIVLSIKMAVPLLQIGLLFFAILMFAIIGLEFYSGK 197  
QY 237 LRNRCFLPENFSLPLSVDLERYYTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGP 296  
Db 198 LHRACFMNNSGIL-----EGFDP----PHPCGVQGC----- 224  
QY 297 PCGLDYEAYNSSNTTCVNMNQYVYTNCSAGEHNPFGAINPFDNIGYAWIAIFQVITLEGW 356  
Db 225 PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGW 262  
QY 357 VDIMYFYMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQVR 415  
Db 263 TTVLYNTNDALGATWNWLYFIPLIIGSFVFLNLVGLVLSGEFAKERERV-----ENRRA 317  
QY 416 FLSNASTLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRRAAGVRVGLLSSPAPLGGQE 475  
Db 318 FMK-----LRRQQOI----- 327  
QY 476 TQPSSSCSRRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLP 535  
Db 328 -----EREELNGYRAWI-- 338  
QY 536 PPSTPALSGAPPGAESVHSFYHADCHLEPVRCAQPPRPSFSEASGRTVSGSKVYPTVHT 595  
Db 339 ----- 338  
QY 596 SPPPETLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACQSSCKLSSPCL 655



339	----	DKAEEVMLAEENKNSGTSALEVLRRATIKRSTRTEAMTRDSSDEHCVDISSVGTPLA	394
656	KADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRS	715	
395	RASIKSTKVDGASY-----	413	
716	LGPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL	775	
414	-----	459	
776	EISNIVTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISWEIVGQ-----	830	
460	YAAEFLLGLFLLMSLKMGMGPRLYFHSSFCDFGVTVGSIFEVVWAI FRPGTSGFI	519	
831	SVLRTFRMLRVLKLVRFLPALORQLVVLMTMDNVATFCMLLMFLIFIFISILGMHLFGCK	890	
520	SVLRALLRIFKITKYWASLRNLVLSLSSMKSIISLLFLLFLFVVFALLGMQLFGGR	579	
891	FASERDGTLPDRKNFDSLLWAI VTFQILTQEDWNKVLNGM-----	945	
580	F-NFNDG--TPSANFDTFPAAIMTVFQILTGEDWNEVMYNGIRSGGVSSGMWSAIYFI	635	
946	ALMTFGYVLENLLVAILVEGF-QAEEISK-----	1000	
636	VLTLFGNYTLNVFLAIAVDNLANAQELTKDEQEEEFNQXHALQKAKEV-----	689	
1001	SEPdffPSLDGDGRKKCLAL-----	1030	
690	SAPNM--PSIERDRRRHHMSMWEPSSHLRERRRRHHMSVWEQRTSQLRRHMQSSQEA	747	
1031	LRKSLLPPLIHTAATPMS-----	1076	
748	LNKEEAPPNNPLNPLNPLNPLNAHPSLYRRPRPIEGLALGLLEKCEERISRGGSL	807	
1077	PGAAHEMKSPPSARSPHS-----	1104	
808	KDIGGLTSVLDNQSPSLSLGKREPPWLP RSCHGNCDPQTQETGGGTVVT FEDRARHRQ	867	
1105	SRSSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEEESSEERASPA GSDHRRHRSGL	1164	
868	SQRRSRHRRVRTEGKESASASRSR---SASQERSLDEGVSIDGEKEHEPQSSHR SKEPT	923	
1165	EREAKSSFDL--PDTLOVP--GL-----	1204	
924	IHEERTQDLRRTNSLMVPRGSLVGLALDEAETPLVQPQPELEV GKDAALTEQEAEGSSE	983	
1205	SGRLA-----	1219	
984	QALLADVQLDVGRGISQSEPDLSCTMTNMDKATTESTSVTVAI PDVDPLVDSTVWNISNK	1043	
1220	DGDDA-----	1267	
1044	TDGEASPLKEAETKEEEVEKKQKKEKRETGKAWPHS-----	1096	
1268	LCHRIITHKMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTL SNYIFTAVFLAEMTV	1327	
1097	ACHIVNLRIFYEMCILLVIAAASSIALAAEDPVL TNSERNKV-LRYFDYVFTGVFTFEMVI	1155	
1328	KVVALGWC FGEQAYLRSSWNVL DGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLRTL	1386	
1156	KMIDQGLILODGSYFRDLWNILD FVVVVGALVAFALANALG TNKGRDIKTIKSLRVLRL	1215	
1387	RPLRVISRAQGLKLVETLMSLKPIGNIVVICCAFFILFGILGVLFGKFFVC--QGE	1444	
1216	RPLKTIKRLPKLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAQLFGKFFYCTDSSK	1275	
1445	DTRN-----	1497	
1276	DTEKECIGNYVDHEKNKMEVKGREWKREHFFHYDNI I WALTTLFTVSTGEGWPVQLHSVD	1335	
1498	AVGVDOQPI MNHNPMLLYFTSFLLI VAFVFLNMFGVVVENFHKCRHQHEEEEARREE	1557	
1336	VTEEDGPPSRNRMEMSI FVVVYFVVPFFFFVNFIVFALLITF-----	1388	

Search completed: April 13, 2005, 16:40:40  
Job time : 87 secs



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: April 13, 2005, 16:01:41 ; Search time 276 Seconds  
(without alignments)  
4204.244 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAESGQPRSFM.....PKKDVLSLGLSSDPADLDP 2266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11815.5	99.3	2377	1 CCAG_HUMAN	O43497 homo sapien
2	11133.5	93.5	2295	2 Q9WUT2	Q9wut2 mus musculu
3	11111	93.3	2288	2 Q9WUB8	Q9wub8 rattus norv
4	10945	91.9	2254	1 CCAG_RAT	O54898 rattus norv
5	10913	91.7	2248	2 Q6PFV8	Q6pfv8 mus musculu
6	6573	55.2	1389	2 Q62PX4	Q6zpx4 mus musculu
7	6217.5	52.2	2359	1 CCAH_RAT	Q9eq60 rattus norv
8	6210	52.2	2353	1 CCAH_HUMAN	O95180 homo sapien
9	6176.5	51.9	2365	1 CCAH_MOUSE	O88427 mus musculu
10	5496.5	46.2	2223	1 CCAI_HUMAN	Q9p0x4 homo sapien
11	5383	45.2	1835	1 CCAI_RAT	Q9z0y8 rattus norv
12	4836	40.6	1994	2 Q7Z6S8	Q7z6s8 homo sapien
13	4200.5	35.3	1762	2 Q7PQV4	Q7pqv4 anopheles g
14	4180	35.1	2893	2 Q9W433	Q9w433 drosophila
15	3855	32.4	1837	2 Q967R4	Q967r4 caenorhabdi
16	3845.5	32.3	1852	2 Q7Z002	Q7z002 caenorhabdi
17	3828.5	32.2	1844	2 Q7YZR6	Q7yzi6 caenorhabdi
18	3823	32.1	1885	2 Q7Z003	Q7z003 caenorhabdi
19	3683.5	30.9	1460	2 Q80TJ2	Q80tj2 mus musculu
20	2925.5	24.6	1418	2 Q7JPB4	Q7jpb4 caenorhabdi
21	2866	24.1	1942	2 Q869H0	Q869h0 lymnaea sta
22	2089	17.5	1211	2 Q8MQ95	Q8mq95 caenorhabdi
23	1746.5	14.7	2339	1 CCAB_HUMAN	Q00975 homo sapien
24	1740.5	14.6	2333	2 O89089	O89089 rattus norv
25	1732.5	14.6	2327	1 CCAB_MOUSE	O55017 mus musculu
26	1729.5	14.5	2331	2 Q9TTA4	Q9tta4 bos taurus
27	1722	14.5	2336	1 CCAB_RAT	Q02294 rattus norv
28	1712.5	14.4	541	2 Q6PE92	Q6pe92 mus musculu
29	1710	14.4	2339	1 CCAB_RABIT	Q05152 oryctolagus
30	1697.5	14.3	2357	2 Q9PUM6	Q9pum6 gallus gall
31	1697	14.3	2259	1 CCAE_RABIT	Q02343 oryctolagus

RESULT 1									
CCAG_HUMAN									
ID	CCAG_HUMAN	STANDARD;	PRT;	2377	AA.				
AC	O43497;	O43498;	O94770;	Q9NYU4;	Q9NYU5;	Q9NYU6;	Q9NYU7;	Q9NYU8;	
AC	Q9NYU9;	Q9NYV0;	Q9NYV1;	Q9UHN9;	Q9UHP0;	Q9ULU6;	Q9UNG7;	Q9YST2;	
AC	Q9YST3;								
DT	15-JUL-1999	(Rel. 38,	Created)						
DT	16-OCT-2001	(Rel. 40,	Last sequence update)						
DT	05-JUL-2004	(Rel. 44,	Last annotation update)						
DE	Voltage-dependent	T-type	calcium channel	alpha-1G	subunit (Voltage-				
DE	gated calcium	channel	alpha	subunit Cav3.1)	(Cav3.1c)	(NBR13)			
GN	Name=CACNA1G;	Synonyms=KIAA1123;							
OS	Homo sapiens	(Human)							
OC	Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;			
OC	Mammalia;	Eutheria;	Primates;	Catarrhini;	Hominidae;	Homo.			
OX	NCBI_TaxID=9606;								
RN	[1]	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).							
RP	TISSUE=Brain;								
RC	MEDLINE=20014446;	PubMed=10548410;	DOI=10.1016/S0304-3940(99)00716-8;						
RX	Mittman S.,	Guo J.,	Agnew W.S.;						
RA	"Structure and	alternative	splicing of the	gene	encoding	alpha1G, a			
RT	human brain	T calcium	channel	alpha1	subunit."				
RT	human brain	T calcium	channel	alpha1	subunit."				
RL	Neurosci. Lett.	274:	143-146	(1999).					
RN	[2]								
RP	SEQUENCE FROM N.A. (ISOFORM 1).								
RC	TISSUE=Brain;								
RX	MEDLINE=20115462;	PubMed=10648811;	DOI=10.1016/S0014-5793(99)01756-1;						
RA	Cribbs L.L.,	Gomora J.C.,	Daud A.N.,	Lee J.-H.,	Perez-Reyes E.;				
RT	"Molecular	cloning and	functional	expression of	ca(v)3.1c, a	T-type			
RT	calcium	channel	from	human	brain."				
RL	FEBS Lett.	466:	54-58	(2000).					
RN	[3]								
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).								
RC	TISSUE=Brain;								
RX	MEDLINE=20158909;	PubMed=10692398;	DOI=10.1074/jbc.275.9.6090;						
RA	Monteil A.,	Chemin J.,	Bourinet E.,	Mennessier G.,	Lory P.,				
RA	Nargeot J.;								
RT	"Molecular	and	functional	properties of the	human	alpha1G	subunit		
RT	forms	T-type	calcium	channels."					
RL	J. Biol. Chem.	275:	6090-6100	(2000).					
RN	[4]								
RP	SEQUENCE FROM N.A. (ISOFORM 14).								
RA	Kishi F.;								
RL	Submitted (MAR-1998)	to the	EMBL/GenBank/DBJ	databases.					
RN	[5]								
RP	SEQUENCE OF 550-2377	FROM	N.A. (ISOFORM 13).						
RC	TISSUE=Brain;								
RX	MEDLINE=22158633;	PubMed=12168954;							
RA	Nakajima D.,	Okazaki N.,	Yamakawa H.,	Kikuno R.,	Ohara O.,	Nagase T.			
RT	"Construction	of	expression-ready	cDNA	clones	for	KIAA	genes: manual	
RT	curatation	of	330	KIAA	cDNA	clones."			
RL	DNA Res.	9:	99-106	(2002).					
RN	[6]								

ALIGNMENTS

32	1689	14.2	1810	2	O44930	O44930 aiptasia pa
33	1688.5	14.2	2295	2	Q923K6	Q923k6 rattus norv
34	1685	14.2	2346	2	Q9PW47	Q9pw47 gallus gall
35	1683	14.1	2332	2	Q9PW45	Q9pw45 gallus gall
36	1681	14.1	2272	1	CCAE_MOUSE	Q61290 mus musculu
37	1666.5	14.0	2312	1	CCAE_HUMAN	Q15878 homo sapien
38	1664.5	14.0	1891	2	O97017	Q97017 stylophora
39	1664.5	14.0	2321	2	Q9PUM4	Q9pum4 gallus gall
40	1662	14.0	2182	2	Q9PUM5	Q9pum5 gallus gall
41	1657	13.9	1847	2	Q6RKB0	Q6rkb0 brachydanio
42	1656	13.9	2223	1	CCAE_DISOM	P56699 discopyge o
43	1654	13.9	2304	2	Q9BMQ4	Q9bmq4 blattella g
44	1651.5	13.9	2222	1	CCAE_RAT	Q07652 rattus norv
45	1649.5	13.9	2171	2	Q9PW46	Q9pw46 gallus gall



FT	TRANSMEM	151	170	S3 of repeat 1 (Potential).
FT	DOMAIN	171	175	Extracellular (Potential).
Query Match				
Best Local Similarity 99.3%; Score 11815.5; DB 1; Length 2377;				
Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;				
QY	1	MDEEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV	60	
Db	1	MDEEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV	60	
QY	61	FFYLSQDSRPSWCLRTVCNPFWRISMLVILLNCVTLGMPRPCEDIACDSQRCRILQAF	120	
Db	61	FFYLSQDSRPSWCLRTVCNPFWRISMLVILLNCVTLGMPRPCEDIACDSQRCRILQAF	120	
QY	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVFSAVR	180	
Db	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVFSAVR	180	
QY	181	TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240	
Db	181	TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240	
QY	241	CFLPENFSLPSVDLERYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCCGL	300	
Db	241	CFLPENFSLPSVDLERYQTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCCGL	300	
QY	301	DYEAYNSSNTTCVNWNQYYTNCAGAHNPFKGAINFNDIGYAWIAFQVITLEGWVDIM	360	
Db	301	DYEAYNSSNTTCVNWNQYYTNCAGAHNPFKGAINFNDIGYAWIAFQVITLEGWVDIM	360	
QY	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRVFLSNA	420	
Db	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRVFLSNA	420	
QY	421	STLASFSBEGSCYEELLYVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGQETQPSS	480	
Db	421	STLASFSBEGSCYEELLYVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGQETQPSS	480	
QY	481	SCSRSHRRLSVHHLVHHHHHHHHLGNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540	
Db	481	SCSRSHRRLSVHHLVHHHHHHHHLGNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540	
QY	541	ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKVPTVHTSPPE	600	
Db	541	ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKVPTVHTSPPE	600	
QY	601	TLKEKALVEVAASSGPPTLTSNIIPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG	660	
Db	601	TLKEKALVEVAASSGPPTLTSNIIPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG	660	
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRORS LGPDA	720	
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRORS LGPDA	720	
QY	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780	
Db	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780	
QY	781	VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMR	840	
Db	781	VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMR	840	
QY	841	VLKLVRFPLALQRLVLMKTMNDVATFCMLLMFLFIFESILGMHLFGCKFASERDGDTL	900	
Db	841	VLKLVRFPLALQRLVLMKTMNDVATFCMLLMFLFIFESILGMHLFGCKFASERDGDTL	900	
QY	901	PDRKNFDSLWAIIVTVFOILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVYVLFNLLV	960	
Db	901	PDRKNFDSLWAIIVTVFOILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVYVLFNLLV	960	
QY	961	AILVEGFQABEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPLDGDGRKKCL	1020	

Db	961	AILVEGFQABEISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPLDGDGRKKCL	1020	
QY	1021	ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGTGCEALGPASRRTSSSGSAEPGAA	1080	
Db	1021	ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTGTGCEALGPASRRTSSSGSAEPGAA	1080	
QY	1081	HEMKSPSARSSPHSPWSAASWTSSRSSNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140	
Db	1081	HEMKSPSARSSPHSPWSAASWTSSRSSNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140	
QY	1141	DEESSEERASPAGSDHHRHGSLEREAKSSFDPDLTQVPGHLRTASGRGSASEHQDCN	1200	
Db	1141	DEESSEERASPAGSDHHRHGSLEREAKSSFDPDLTQVPGHLRTASGRGSASEHQDCN	1200	
QY	1201	GKSASGLARALRPDDPPLDGDADDEGNLSKGERVRARLARLPACYLERDSHSAIYFP	1260	
Db	1201	GKSASGLARALRPDDPPLDGDADDEGNLSKGERVRARLARLPACCLERDSHSAIYFP	1260	
QY	1261	PQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320	
Db	1261	PQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320	
QY	1321	FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380	
Db	1321	FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380	
QY	1381	RLRLRLRPLRVISRAOGLKVVTETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV	1440	
Db	1381	RLRLRLRPLRVISRAOGLKVVTETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFV	1440	
QY	1441	CQGEDTRNITNKSDCAEASVRVRHKYNFDNLQALMSLFLVLASKDGVIMYDGLDAVG	1500	
Db	1441	CQGEDTRNITNKSDCAEASVRVRHKYNFDNLQALMSLFLVLASKDGVIMYDGLDAVG	1500	
QY	1501	VDQQPIMNHNPMWLLYFISFLILVAFVFLNMFVGVVVENFHKCRQHQEEEEARRREKRL	1560	
Db	1501	VDQQPIMNHNPMWLLYFISFLILVAFVFLNMFVGVVVENFHKCRQHQEEEEARRREKRL	1560	
QY	1561	RRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGV	1602	
Db	1561	RRLEKKRRMLDDVIAAGSSASAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGV	1620	
QY	1603	IGLVVVTMAHEHYQQPQILDEALKICNYIFTVI FVLESVFKLVAFGFRFFQDRWNQDL	1662	
Db	1621	IGLVVVTMAHEHYQQPQILDEALKICNYIFTVI FVLESVFKLVAFGFRFFQDRWNQDL	1680	
QY	1663	AVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQAL	1722	
Db	1681	AVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQAL	1740	
QY	1723	PQVGNLGLL FMLLFFIFAALGVVELFGDLECEDETHPCBGLGRHATFRNFGMAFLTFRVST	1782	
Db	1741	PQVGNLGLL FMLLFFIFAALGVVELFGDLECEDETHPCBGLGRHATFRNFGMAFLTFRVST	1800	
QY	1783	GDWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE	1842	
Db	1801	GDWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKE	1860	
QY	1843	AKEEALEAELEEMKTLSPQPHSPGLGSPFLWPVGVEGSDSPSKPGALHPAAHARSASH	1902	
Db	1861	AKEEALEAELEEMKTLSPQPHSPGLGSPFLWPVGVEGSDSPSKPGALHPAAHARSASH	1920	
QY	1903	FSLEHPT-----	1909	
Db	1921	FSLEHPTDRQLFDTISLLIQGLEWELKLMDELAGPGQPSAFPSAPSLGSGSDPQIPLAE	1980	
QY	1910	-----MQPHPTELPGPDLLTVRKSG	1929	
Db	1981	MEALSLTSEIVSEPSCSLALTDDSLDDMTLLLSALESNMQPHPTELPGPDLLTVRKSG	2040	
QY	1930	VSRTSHLPNDSYMCRRHGSTAEGLGHRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAP	1989	
Db	2041	VSRTSHLPNDSYMCRRHGSTAEGLGHRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAP	2100	

QY	1990	HLLQPHSAPTWTG	TI PKLP	PPGRSPLAQR	PLRRQAIR	TD	SLDVQGLSREDLLAEV	SGPS	2049
Db	2101	HLLQPHSAPTWTG	TI PKLP	PPGRSPLAQR	PLRRQAIR	TD	SLDVQGLSREDLLAEV	SGPS	2160
QY	2050	PPLARAYFWGQS	STQAQ	QHSRSHSKISK	HMTPPAP	CGPEPNWKGPPET	RSSLE	DTE	2109
Db	2161	PPLARAYFWGQS	STQAQ	QHSRSHSKISK	HMTPPAP	CGPEPNWKGPPET	RSSLE	DTE	2220
QY	2110	LSWISGDLPPGQ	EEPPSPRDL	KKCYV	EAQSCORRPT	SWLDEQR	RHSIAV	SLDSGSQ	2169
Db	2221	LSWISGDLPPGQ	EEPPSPRDL	KKCYV	EAQSCORRPT	SWLDEQR	RHSIAV	SLDSGSQ	2280
QY	2170	PHLGTDPN	LGQPLGGP	SRPKKLSPP	SITIDPPES	QGPRTPPS	PGICLRRR	APSSDS	2229
Db	2281	PHLGTDPN	LGQPLGGP	SRPKKLSPP	SITIDPPES	QGPRTPPS	PGICLRRR	APSSDS	2340
QY	2230	KDPLASGPPD	SMAASPS	PKKDVLS	SLGSLSSDPADLDP				2266
Db	2341	KDPLASGPPD	SMAASPS	PKKDVLS	SLGSLSSDPADLDP				2377
RESULT 2									
Q9WUT2									
ID	Q9WUT2	PRELIMINARY;		PRT;		2295 AA.			
AC	Q9WUT2;								
DT	01-NOV-1999	(TrEMBLrel. 12, Created)							
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)							
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)							
DE	Voltage-gated calcium channel, alpha-1-G subunit.								
GN	Name=Cacnalg;								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Brain;								
RX	MEDLINE=99189326; PubMed=10087148;								
RA	Klugbauer N., Marais E., Lacinova L., Hofmann F.;								
RT	"A T-type calcium channel from mouse brain.";								
RL	Pflugers Arch. 437:710-715(1999).								
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).								
CC	-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.								
DR	EMBL; AJ012569; CAB40793.1; --								
DR	MGD; MGI:1201678; Cacnalg.								
DR	GO; GO:0016021; C:integral to membrane; TAS.								
DR	GO; GO:0005886; C:plasma membrane; IDA.								
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.								
DR	InterPro; IPR001682; Ca/Na_pore.								
DR	InterPro; IPR002111; Cat_channel_TrpL.								
DR	InterPro; IPR002077; Ca_channel_alpha.								
DR	InterPro; IPR005821; Ion_trans.								
DR	InterPro; IPR005820; M+channel_nlg.								
DR	InterPro; IPR005445; TVDCCalpha1.								
DR	Pfam; PF00520; Ion_trans; 4.								
DR	PRINTS; PR00167; CACHANNEL.								
DR	PRINTS; PR01629; TVDCCALPHA1.								
KW	Calcium; Calcium channel; Calcium transport; Calcium-binding;								
KW	Ion transport; Ionic channel; Transmembrane; Transport;								
KW	Voltage-gated channel.								
SQ	SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;								
Query Match 93.5%; Score 11133.5; DB 2; Length 2295;									
Best Local Similarity 93.3%; Pred. No. 0;									
Matches 2142; Conservative 32; Mismatches 91; Indels 31; Gaps 5									
QY	1	MDEEDGAGAEES	GGQPS	FWRLNDLSG	AGGRC	PGSAEKDP	GSADSEAEGL	PYPALAPV	60
Db	1	MDEEDGAGAEES	GGQPS	FWRLNDLSG	AGGRC	PGSAEKDP	GSADSEAEGL	PYPALAPV	60
QY	61	FFYLSQDSR	PRSWCL	RTVCN	PWFERIS	MLVILLNC	VTLMFR	PCDIA	QSCRILQAF 120

Db	61	FFYLSQDSR	PRSWCLRTVCN	PWFERVSM	VILLNCVTLM	FRPCEDIA	QSCRILQAF	120																																																			
QY	121	DDFIFAF	AVEMVKM	VALGIFGKK	CYLGDTWNRL	DDFFIVIA	IAGMLEYSLDLQNVSFS	SAVR 180																																																			
Db	121	DDFIFAF	AVEMVKM	VALGIFGKK	CYLGDTWNRL	DDFFIVIA	IAGMLEYSLDLQNVSFS	SAVR 180																																																			
QY	181	TVRVLRL	PLRAINRVPS	MRILVTLL	DTLPLMGNVLL	LCFFVFFIF	IGIVGVQLWAGLLRNR	240																																																			
Db	181	TVRVLRL	PLRAINRVPS	MRILVTLL	DTLPLMGNVLL	LCFFVFFIF	IGIVGVQLWAGLLRNR	240																																																			
QY	241	CFLPEN	FSPLSVDL	ERYQTENE	DESPFIC	SQPRENG	MWSCRSVPTLRGDGGGPPCGL	300																																																			
Db	241	CFLPEN	FSPLSVDL	ERYQTENE	DESPFIC	SQPRENG	MWSCRSVPTLRGDGGGPPCGL	300																																																			
QY	301	DYEAYN	SSNTTCVN	WNQYYTNC	SAGEHNPF	KGAINFDN	IGYAWIAIFQVITLEGWVDIM	360																																																			
Db	301	DYEAYN	SSNTTCVN	WNQYYTNC	SAGEHNPF	KGAINFDN	IGYAWIAIFQVITLEGWVDIM	360																																																			
QY	361	YFYMDA	HSFYFIY	FILLIIVG	SFFMINCL	VVIATQ	SETKQRESQLMREQVRFLSNA	420																																																			
Db	361	YFYMDA	HSFYFIY	FILLIIVG	SFFMINCL	VVIATQ	SETKQRESQLMREQVRFLSNA	420																																																			
QY	421	STLASF	SEPGSCYE	ELLKYL	VYILRKA	ARRLAQV	SRAAGVRVGLLSPAPLGQETQPSS	480																																																			
Db	421	STLASF	SEPGSCYE	ELLKYL	VYILRKA	ARRLAQV	SRAAGVRVGLLSPVARGQEQPQPSG	480																																																			
QY	481	SCSRSHRRL	SVHHLVHH	HHHHHH	HYHLGNG	TLRAPRAS	PEIQDRDANGSRRLMLPPPSTP	540																																																			
Db	481	SCSRSHRRL	SVHHLVHH	HHHHHH	HYHLGNG	TLRVPRAS	PEIQDRDANGSRRLMLPPPSTP	540																																																			
QY	541	ALSGAPP	GGAESVH	SFYHAD	CHLEP	VRCAOP	PPRSPSEASGRVTGSGKYPTVHTSPPE	600																																																			
Db	541	TPSGGP	PRGAESVH	SFYHAD	CHLEP	VRCAOP	PPRSPSEASGRVTGSGKYPTVHTSPPE	600																																																			
QY	601	TLKEKAL	VEVAAS	SGPPTLS	LNIPPG	PYSMMHKL	LETQSTGACQSSCKISSPCLKADSG	660																																																			
Db	601	MLKDKAL	VEVAPS	PGPPTLT	TFNIPPG	PFSSMHKL	LETQSTGACHSSCKISSPCSADSG	660																																																			
QY	661	ACGPD	SPYCAR	AGAGE	VELAD	REMPDSD	SEAVYFTQDAQHS	DLRDPHSRRQRS	LPDA 720																																																		
Db	661	ACGPD	SPYCART	GAGEPE	SADHE	MPDSD	SEAVYFTQDAQHS	DLRDPHRRRPS	LPDA 720																																																		
QY	721	EPSSVL	AFWR	LICDT	FRKI	VDSKYF	GRGIMIALVNTLS	MGIEYHEQPEELTNALEISNI	780																																																		
Db	721	EPSSVL	AFWR	LICDT	FRKI	VDSKYF	GRGIMIALVNTLS	MGIEYHEQPEELTNALEISNI	780																																																		
QY	781	VFTSL	FALE	MLKLL	VYGP	FGYIK	NPYNIFD	GVIVISW	EIVGQGGLS	VLRTFRLMR 840																																																	
Db	781	VFTSL	FALE	MLKLL	VYGP	FGYIK	NPYNIFD	GVIVISW	EIVGQGGLS	VLRTFRLMR 840																																																	
QY	841	VKLVR	FLPAL	QRLV	VL	MKTMD	NVATFC	MLLM	LFI	FIFSI	LGMHLFG	CKFASBRD	GD	DTL 900																																													
Db	841	VKLVR	FLPAL	QRLV	VL	MKTMD	NVATFC	MLLM	LFI	FIFSI	LGMHLFG	CKFASBRD	GD	DTL 900																																													
QY	901	PDRKN	FDSLL	WAI	VT	VFOILT	QEDWN	KVLYNG	MASTSS	WAALYFI	ALMTF	GNVY	FNLLV 960																																														
Db	901	PDRKN	FDSLL	WAI	VT	VFOILT	QEDWN	KVLYNG	MASTSS	WAALYFI	ALMTF	GNVY	FNLLV 960																																														
QY	961	A	I	L	V	E	G	F	Q	A	E	I	S	K	R	E	D	A	S	G	Q	L	S	I	Q	L	P	V	D	S	G	G	D	A	N	K	S	E	P	D	F	F	S	P	S	L	D	G	D	R	K	K	C	L 1020					
Db	961	A	I	L	V	E	G	F	Q	A	E	I	S	K	R	E	D	A	S	G	Q	L	S	I	Q	L	P	V	D	S	G	G	D	A	N	K	S	E	P	D	F	F	S	P	S	V	D	G	D	R	K	K	R	L 1020					
QY	1021	ALVSL	GEHPE	LKSL	LP	LI	IHTA	ATP	MSL	PKST	STGL	GEAL	GPAS	RR	TSS	SGS	AE	PGAA 1080																																									
Db	1021	ALVSL	GEHPE	LKSL	LP	LI	IHTA	ATP	MSL	PKST	STGL	GEAL	GPAS	RR	TSS	SGS	AE	PGTA 1080																																									
QY	1081	-	HEM	K	S	P	P	S	A	R	S	S	P	H	S	P	W	S	A	A	S	S	W	T	S	R	R	S	R	N	S	I	G	R	A	P	S	R	R	T	S	S	S	G	S	A	E	P	Q	E	S 1139								
Db	1081	H	H	E	M	K	S	P	P	S	A	R	S	S	P	H	S	P	W	S	A	A	S	S	W	T	S	R	R	S	R	N	S	I	G	R	A	P	S	R	R	T	S	S	G	S	A	E	P	Q	E	S 1140							
QY	1140	Q	D	E	E	S	S	E	E	R	A	S	P	A	G	S	D	H	R	H	R	G	S	L	E	R	E	A	K	S	S	F	D	L	P	D	T	L	Q	V	P	G	L	H	R	T	A	S	G	R	G	S	A	S	E	H	Q	D	C 1199



Db 1141 QDEEESSEDRASPAGSDHRRHGRSLEBEAKSSFDPDPTLQVPLHRTASGRSSASEHQDC 1200

Qy 1200 NGKSASGRALARPDPPDLGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWYIF 1259

Db 1201 NGKSASGRLARTRADDPPLDGGDDDEGNLSKGERLRAWVRARLPACCRERDSWYIF 1260

Qy 1260 PPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1319

Db 1261 PPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1320

Qy 1320 VFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRV 1379

Db 1321 VFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRV 1380

Qy 1380 LRLRLTRPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICAPFIIFGILGVQLFKGKFF 1439

Db 1381 LRLRLTRPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICAPFIIFGILGVQLFKGKFF 1440

Qy 1440 VCQGEDTRNITNKSDCAEASYSRWVRHKYNFDNLGQALMSLFVLASKDGVVDIMYDGLDAV 1499

Db 1441 VCQGEDTRNITNKSDCAEASYSRWVRHKYNFDNLGQALMSLFVLASKDGVVDIMYDGLDAV 1500

Qy 1500 GVDQQIPMHNPNWMLLYFISFLLIIVAFVFLNMFGVVVENFHKCRQHQQEHEEAREEKR 1559

Db 1501 GVDQQIPMHNPNWMLLYFISFLLIIVAFVFLNMFGVVVENFHKCRQHQQEHEEAREEKR 1560

Qy 1560 LRRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHY 1594

Db 1561 LRRLEKKRRSKEKQADMLDLDVVIASGSSASAAEQCKPYSDYSRFRLLVHHLCTSHY 1620

Qy 1595 LDLFITGVIGLVNVTMAMEHYQQQILDEALKICNYIFTVIFVLESVFVKLVAFGRFRFFQ 1654

Db 1621 LDLFITGVIGLVNVTMAMEHYQQQILDEALKICNYIFTVIFVLESVFVKLVAFGRFRFFQ 1680

Qy 1655 DRWNQDLAIVLISIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAL 1714

Db 1681 DRWNQDLAIVLISIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAL 1740

Qy 1715 LDTVMQALPOVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAF 1774

Db 1741 LDTVMQALPOVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAF 1800

Qy 1775 LTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMK 1834

Db 1801 LTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMK 1860

Qy 1835 HLEESNKEAKEBAEAELEAEMTKLSPQPHSPGLSPFLWFGVEGDPDSDSPKGAALHPA 1894

Db 1861 HLEESNKEAKEBAEAELEAEMTKLSPQPHSPGLSPFLWFGVEGVNSPDSPKPGAPHTT 1920

Qy 1895 AHARSASH-FSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAE 1950

Db 1921 AHIGAASSGFSLEHPTMVPHTEEGVPLGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAE 1980

Qy 1951 GPLGHRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSAPTWTGTPKLPPLPG 2010

Db 1981 RSLGHRGWGLPKAQSGSVLSVHSQPADTSCILQLPKDAHLLQPHGAPTWGAIPKLPPLPG 2040

Qy 2011 RSPLAQRPLRQAARTDSDLVQGLSREDLLAEVSGPSPFLARAYSFWGQSSTQAQOHS 2070

Db 2041 RSPLAQRPLRQAARTDSDLVQGLSREDLLSEVSGPSPFLTRSSSFWGSSIQVQORS 2100

Qy 2071 RSHKISKMTPTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLLPPGGQEEPPSPR 2130

Db 2101 GSQSKVSKHIRLPAPCPGLEPSWAKDPQETRSSLELDTLSWISGDLL-PSSQEEPLSPR 2159

Qy 2131 DLKKCYVSAQSCQRRPTSWLDEQRHRSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPGSR 2190

Db 2160 DLKKCYVSAQSCRRRPGSWLDEQRHRSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPGSR 2219

Qy 2191 PKKLSPPSITIDPPESQGRPTPPSPGICLRRRAPSSDSKDXPLASGPPDMSAASPSPKD 2250

Db 2220 PKKLSPPSISIDPPESQGRPTPPSPGICLRRRAPSSDSKDXPLASGPPDMSAASPSPKD 2279

Qy 2251 VLSLSGLSSDDPADLDP 2266

Db 2280 ALSLSGLSSDDPTDLDP 2295

RESULT 3

Q9WUB8

ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.

AC Q9WUB8;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE T-type calcium channel isoform.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RX MEDLINE=20081696; PubMed=10615950;

RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,

RA Wu S., Berggren P.O., Li M.;

RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting

RT cells.";

RL Diabetes 49:59-64(2000).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits

CC family.

DR EMBL; AF125161; AAD26858.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR001682; Ca/Na\_pore.

DR InterPro; IPR002111; Cat\_channel\_TrpL.

DR InterPro; IPR002077; Ca\_channel\_alpha.

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR005820; M+channel\_nlg.

DR Pfam; PF00520; Ion\_trans; 4.

DR PRINTS; PR00167; CCHANNEL.

DR PRINTS; PR01629; TVDCCALPHA1.

KW Calcium; Calcium channel; Calcium transport; Calcium-binding;

KW Ion transport; Ionic channel; Transmembrane; Transport;

KW Voltage-gated channel.

SQ SEQUENCE 2288 AA; 253476 MW; B89DBB5A1D81757F CRC64;

Query Match 93.3%; Score 11111; DB 2; Length 2288;

Best Local Similarity 93.3%; Pred. No. 0;

Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

Qy 1 MDEEDGAGAEESGQPRSFMRNLNLSGAGRPGPGSAEKDPGSGADSEAEGLYPALAPVW 60

Db 1 MDEEDGAGAEESGQPRSFMTQLNLSGAGRQPGSGTEKDPGSGADSEAEGLYPALAPVW 60

Qy 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIACDSQRILQAF 120

Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIACDSQRILQAF 120

Qy 121 DDFIFAFFAVEMVVKMVALGIFGKCYLGDTWNRLDFFVIAGMLEYSLDLQNVSFAVR 180

Db 121 DDFIFAFFAVEMVVKMVALGIFGKCYLGDTWNRLDFFVIAGMLEYSLDLQNVSFAVR 180

Qy 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Db 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Qy 241 CFLPENFSLPLSVDLERYQTENEDESPFICSQPRENGMRSCRSVPTLRGGGGPPCGGL 300



Db 241 CFLPENFSLPLSVLEPYQTENEDESPFICQPRENGMRSCRSVPTLRGEGGGPPCSL 300

QY 301 DYEAYNSSNTTCVNWQYNTNCSAGEHNPFKGAINFDNIGYAWIAFOVITLEGWVDIM 360

Db 301 DYETYNSSNTTCVNWQYNTNCSAGEHNPFKGAINFDNIGYAWIAFOVITLEGWVDIM 360

QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLYLVILRKAARRLAQVSRAGVVRGLLSSPAPLGGQETQPS 480

Db 421 STLASFSEPGSCYEELLYLVILRKAARRLAQVSRAGVVRGLLSSPVARSGQEPQPSG 480

QY 481 SCSRSRRLSVHLLVHHHHHHHHLGNGTLRAPASPEIQDRDANGSRRLMLPPPSTP 540

Db 481 SCSRSRRLSVHLLVHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP 540

QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRTVGSKVYPTVHTSP 600

Db 541 TPGSGPPRGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRTVGSKVYPTVHTSP 600

QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLELTQSTGACQSSCKISSPCLKADSG 660

Db 601 ILKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLELTQSTGACHSSCKISSPCKADSG 660

QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS - RRQ 719

Db 661 ACPDSCPCYARTGAGEPESADHVPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 720

QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779

Db 721 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780

QY 780 IVFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVSVWEIVGQGGGLSVLRTFR 839

Db 781 IVFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVSVWEIVGQGGGLSVLRTFR 840

QY 840 RVLKLVFLPALQRLVLVMTMDNVATFCMLLMFLIFIFSLGMHLFGCKFASERDGD 899

Db 841 RVLKLVFLPALQRLVLVMTMDNVATFCMLLMFLIFIFSLGMHLFGCKFASERDGD 900

QY 900 LPDRKNFDSLWAIWTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNVLF 959

Db 901 LPDRKNFDSLWAIWTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNVLF 960

QY 960 VAILVEGFQAEIISKREDASGQSLCIQLPVD SQGDANKSESEPFFSPSLDGDGRK 1019

Db 961 VAILVEGFQAEIISKREDASGQSLCIQLPVNSQGDATKSESEPFFSPSV DGDGRK 1020

QY 1020 LALVSLGEHPPELRLKSLPLIHTAATPMSLPKSTSTGLGHALGPASRRRTSSSGSAEPGA 1079

Db 1021 LALVALGEHAELRLKSLPLIHTAATPMSLPKSSSTGVGBALGSGRRRTSSSGSAEPGA 1080

QY 1080 A -HEMKSPPSARSPPSWSAASSWTSSRNSLGRAPSLKRRSPSGERRSLLSGEQE 1138

Db 1081 AHHEMKSPPSARSPPSWSAASSWTSSRNSLGRAPSLKRRSPSGERRSLLSGEQE 1140

QY 1139 SQDEEESSEERASPGSDHRRHRSGLERBAKSSFDLPDTLQVPLHRTASGRGSAEHQD 1198

Db 1141 SQDEEESSEEDRASPGSDHRRHRSGLERBAKSSFDLPDTLQVPLHRTASGRSSASEHQD 1200

QY 1199 CNGKSASGRLARALRPDDPPLDGDADDGNLSKGERVRAWTRARLPACYLERSWSAYI 1258

Db 1201 CNGKSASGRLARLTFRDDPQLDGDADDGNLSKGERIQAWVRSLPACCRERDSWSAYI 1260

QY 1259 FPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318

Db 1261 FPPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1320

QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLR 1378

Db 1321 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLR 1380

QY 1379 VLRLRLTLRLRVISRAOGLKLVVETLMSSLKPIGNIWVICCAFFIIFGILGVQLFKGKF 1438

Db 1381 VLRLRLTLRLRVISRAOGLKLVVETLMSSLKPIGNIWVICCAFFIIFGILGVQLFKGKF 1440

QY 1439 FVCOGEDTRNITNKSDCAEASYSRWRHKNFDNLGQALMSLVFVASKDGMVDIMYDGLDA 1498

Db 1441 FVCOGEDTRNITNKSDCAEASYSRWRHKNFDNLGQALMSLVFVASKDGMVDIMYDGLDA 1500

QY 1499 VGVDQQPIMNHNPMWMLLYFISFLIVAFVFLNMFVGVVVENFHKCRHQHEEEARRREK 1558

Db 1501 VGVDQQPIMNHNPMWMLLYFISFLIVAFVFLNMFVGVVVENFHKCRHQHEEEARRREK 1560

QY 1559 RLRLLEKRR-----KAQCKPYYSRFRLLVHHLCTSHYLDLFI 1600

Db 1561 RLRLLEKRRNMLDDVIASSSSAASEAQCKPYYSRFRLLVHHLCTSHYLDLFI 1620

QY 1601 GVIGLNVVTMAHEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQL 1660

Db 1621 GVIGLNVVTMAHEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQL 1680

QY 1661 DLAIVLLSIMGITLEIEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQ 1720

Db 1681 DLAIVLLSIMGITLEIEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQ 1740

QY 1721 ALPOVGNLGLLFMLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRV 1780

Db 1741 ALPOVGNLGLLFMLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRV 1800

QY 1781 STGDNWNGIMKDTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEESN 1840

Db 1801 STGDNWNGIMKDTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEESN 1860

QY 1841 KEAKEAELEAELEEMKTLSPQSPHPLGSPFLWPVGEGPDSDPSPKPGALHPAAHARSA 1900

Db 1861 KEAKEAELEAELEEMKTLSPQSPHPLGSPFLWPVGEGVNSDPSPKPGAPHTTAHIGAA 1920

QY 1901 SHFSLEHPTMQHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957

Db 1921 SGFSLEHPTMVPHEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHG 1980

QY 1958 WGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLOPHSAPTWTIPKLPPPGRSPLAQ 2017

Db 1981 WGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPPGRSPLAQ 2040

QY 2018 PLRQAARTDLDVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKIS 2077

Db 2041 PLRQAARTDLDVQGLGSRREDLLSEVSGSPCLTRSSFWGSSIQVQQRSGIQSKVS 2100

QY 2078 KHMTTPAPCPGPEPNWKGPPETRSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYS 2137

Db 2101 KHTRLPA PCGLEPSWAKDPPETRSLELDTLSWISGDL - PSSQEEPLSPRDLKKCYS 2159

QY 2138 VEAQSCORRPTSWLDEQRHSIAVSCLDGSGOPHLGTDPSNLGGQPLGGPSRPPKKLSP 2197

Db 2160 VETQSCRRRPGSWLDEQRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSRPPKKLSP 2219

QY 2198 PSITIDPPESQPRTPPGICLRRRAPSSDKDPLASGPPDSMAASPSPKDVLSLSGL 2257

Db 2220 PSISIDPPESQSRPPCPGVCLRRRAPASDKDPVSSPLDSTAASPSPKDVLSLSGL 2279

QY 2258 SSDPADLDP 2266

Db 2280 SSDPTMDP 2288

RESULT 4

CCAG RAT

ID -CCAG RAT

AC O54898;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1).

DE Name=Cacnalg;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=98154730; PubMed=9495342; DOI=10.1038/36110;

RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J., Williamson M.P., Fox M., Rees M., Lee J.-H.;

RA "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel.";

RT Nature 391:896-900(1998).

RL

CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1G gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression in heart; low expression in placenta, kidney and lung.

CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.

CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by Cam-kinase II.

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

CC -----

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CC -----

DR EMBL; AF027984; AAC67372.1; -.

DR PIR; T09053; T09053.

DR RGD; 68942; Cacnalg.

DR InterPro; IPR001682; Ca/Na\_pore.

DR InterPro; IPR002111; Cat\_channel\_TrpL.

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR005820; M\_channel\_nlg.

DR InterPro; IPR005445; TVDCCAlphal.

DR Pfam; PF00520; Ion\_trans; 4.

DR PRINTS; PR01629; TVDCCALPHAL.

KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;

KW Ionic channel; Multigene family; Phosphorylation; Repeat;

KW Transmembrane; Voltage-gated channel.

FT REPEAT 68 398 I.

FT REPEAT 730 968 II.

FT REPEAT 1242 1519 III.

FT REPEAT 1564 1822 IV.

FT DOMAIN 1 80 Cytoplasmic (Potential).

FT TRANSMEM 81 101 S1 of repeat I.

FT DOMAIN 102 119 Extracellular (Potential).

FT TRANSMEM 120 141 S2 of repeat I (Potential).

FT	DOMAIN	142	150	Cytoplasmic (Potential).
FT	TRANSMEM	151	170	S3 of repeat I.
FT	DOMAIN	171	175	Extracellular (Potential).
FT	TRANSMEM	176	193	S4 of repeat I.
FT	DOMAIN	194	213	Cytoplasmic (Potential).
FT	TRANSMEM	214	234	S5 of repeat I (Potential).
FT	DOMAIN	235	370	Extracellular (Potential).
FT	TRANSMEM	371	395	S6 of repeat I.
FT	DOMAIN	396	744	Cytoplasmic (Potential).
FT	TRANSMEM	745	765	S1 of repeat II (Potential).
FT	DOMAIN	766	778	Extracellular (Potential).
FT	TRANSMEM	779	800	S2 of repeat II (Potential).
FT	DOMAIN	801	806	Cytoplasmic (Potential).
FT	TRANSMEM	807	825	S3 of repeat II (Potential).
FT	DOMAIN	826	833	Extracellular (Potential).
FT	TRANSMEM	834	857	S4 of repeat II (Potential).
FT	DOMAIN	858	868	Cytoplasmic (Potential).
FT	TRANSMEM	869	889	S5 of repeat II (Potential).
FT	DOMAIN	890	940	Extracellular (Potential).
FT	TRANSMEM	941	965	S6 of repeat II (Potential).
FT	DOMAIN	966	1251	Cytoplasmic (Potential).
FT	TRANSMEM	1252	1274	S1 of repeat III (Potential).
FT	DOMAIN	1275	1292	Extracellular (Potential).
FT	TRANSMEM	1293	1313	S2 of repeat III (Potential).
FT	DOMAIN	1314	1323	Cytoplasmic (Potential).
FT	TRANSMEM	1324	1343	S3 of repeat III (Potential).
FT	DOMAIN	1344	1357	Extracellular (Potential).
FT	TRANSMEM	1358	1379	S4 of repeat III (Potential).
FT	DOMAIN	1380	1389	Cytoplasmic (Potential).
FT	TRANSMEM	1390	1413	S5 of repeat III (Potential).
FT	DOMAIN	1414	1490	Extracellular (Potential).
FT	TRANSMEM	1491	1516	S6 of repeat III (Potential).
FT	DOMAIN	1517	1578	Cytoplasmic (Potential).
FT	TRANSMEM	1579	1599	S1 of repeat IV (Potential).
FT	DOMAIN	1600	1613	Extracellular (Potential).
FT	TRANSMEM	1614	1635	S2 of repeat IV (Potential).
FT	DOMAIN	1636	1642	Cytoplasmic (Potential).
FT	TRANSMEM	1643	1661	S3 of repeat IV (Potential).
FT	DOMAIN	1662	1675	Extracellular (Potential).
FT	TRANSMEM	1676	1699	S4 of repeat IV (Potential).
FT	DOMAIN	1700	1713	Cytoplasmic (Potential).
FT	TRANSMEM	1714	1734	S5 of repeat IV (Potential).
FT	DOMAIN	1735	1794	Extracellular (Potential).
FT	TRANSMEM	1795	1822	S6 of repeat IV (Potential).
FT	DOMAIN	1823	2254	Cytoplasmic (Potential).
FT	TRANSMEM	290	295	Poly-Gly.
FT	DOMAIN	496	506	Poly-His.
FT	TRANSMEM	1527	1530	Poly-Glu.
FT	SITE	354	354	Calcium ion selectivity and permeability (By similarity).
FT	SITE	924	924	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1465	1465	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1770	1770	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	246	246	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	322	322	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1427	1427	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1430	1430	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1666	1666	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	2254 AA;	250405 MW;	697BBE06360CF0F6 CRC64;

Query Match 91.9%; Score 10945; DB 1; Length 2254;  
Best Local Similarity 92.5%; Pred. No. 0;  
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;

Oy	1	MDEEDGAGAEESGQPRSFMRNLNLSGAGGRPGSGAEKDPGSADSEAGLPALAPV	60
Db	1	MDEEDGAGAEESGQPRSFMRNLNLSGAGGRPGSGAEKDPGSADSEAGLPALAPV	60







QY 1260 PPSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1319  
Db 1221 PPSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTA 1280  
QY 1320 VFLAEMTVKVALGWCFCGQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLRV 1379  
Db 1281 VFLAEMTVKVALGWCFCGQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLRV 1340  
QY 1380 LRLRLTLRPLRVISRAQGLKLVVETLMSLSKPIGNIWVICCAFFIIPGILGVQLFKGKFF 1439  
Db 1341 LRLRLTLRPLRVISRAQGLKLVVETLMSLSKPIGNIWVICCAFFIIPGILGVQLFKGKFF 1400  
QY 1440 VCOGEDTRNITKSDCAEASRYRVRHKYNFNDNLGQALMSFLVLSKDGWVDIMYDGLDAV 1499  
Db 1401 VCOGEDTRNITKSDCAEASRYRVRHKYNFNDNLGQALMSFLVLSKDGWVDIMYDGLDAV 1460  
QY 1500 GVDQOPIMNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHOOEERREKR 1559  
Db 1461 GVDQOPIMNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHOOEERREKR 1520  
QY 1560 LRRLEKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTG 1601  
Db 1521 LRRLEKRRNMLDDVIASSSSASAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTG 1580  
QY 1602 VIGLNVVTNAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGRFRFFQDRWNQLD 1661  
Db 1581 VIGLNVVTNAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGRFRFFQDRWNQLD 1640  
QY 1662 LAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGNRALLDTVMQA 1721  
Db 1641 LAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGNRALLDTVMQA 1700  
QY 1722 LPQVGNLGLLFWMLFFIFAALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTFRVS 1781  
Db 1701 LPQVGNLGLLFWMLFFIFAALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTFRVS 1760  
QY 1782 TGDNWNNGIMKDTLRDCDQESTCNTVTISPPIYFVSFVLTAQFVLNVNVIIVLMKHEESNK 1841  
Db 1761 TGDNWNNGIMKDTLRDCDQESTCNTVTISPPIYFVSFVLTAQFVLNVNVIIVLMKHEESNK 1820  
QY 1842 EAKKEAELEAELEEMKTLSPQHSPLGSPFLWPVGEPDSDSPKPGALHPAAHARSAS 1901  
Db 1821 EAKKEAELEAELEEMKTLSPQHSPLGSPFLWPVGEGVNSPDSPKPGAPHTTAHIGAAS 1880  
QY 1902 H-FSLEHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHSGSTAEGPLGHRG 1957  
Db 1881 SGFSLEHPTMVPHTEGVPPLGPDLLTVRKSGVSRTHSLPNDSYMCRNNGSTAERSLGHG 1940  
QY 1958 WGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQ 2017  
Db 1941 WGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQ 2000  
QY 2018 PLRQAARTDSDLVQGLGSRDLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKIS 2077  
Db 2001 PLRQAARTDSDLVQGLGSRDLAEVSGSPCLTRSSSFVWGSSIQVQQRSGSQSVS 2060  
QY 2078 KHMTPPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYS 2137  
Db 2061 KHIRLPAPCPGLEPSWAKDPQETRSLSLELDTLSWISGDL-PPSQEEPLSPRDLKKCYS 2119  
QY 2138 VEAQSCORRPTSWLDEORRHSIAVSCLDGSGSQPHLGTDPNLSGQPLGGGSRPKKLSLSP 2197  
Db 2120 VEAQSCORRPTSWLDEORRHSIAVSCLDGSGSQPHLGTDPNLSGQPLGGGSRPKKLSLSP 2179  
QY 2198 PSITIDPPESQGRTPPSPGICLRRRAPSSDSKDPASGPPDSMAASPSPKDVLISLGL 2257  
Db 2180 PSISIDPPESQGRPPPCSPGVCLRRRAPASDSKDPASPLDSTAASPSPKDALISLGL 2239  
QY 2258 SSDPADLDP 2266  
Db 2240 SSDPTDLDP 2248

RESULT 6  
Q6ZPX4 PRELIMINARY; PRT; 1389 AA.  
ID Q6ZPX4  
AC Q6ZPX4;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE MKIAA1123 protein (Fragment).  
GN Name=MKIAA1123;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX PubMed=14621295;  
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
RA Saga Y., Nagase T., Ohara O., Koga H.;  
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:  
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous  
RT cDNAs identified by screening of terminal sequences of cDNA clones  
RT randomly sampled from size-fractionated libraries.";  
RL DNA Res. 10:167-180(2003).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
DR EMBL; AK129294; BAC98104.1; -.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; IDA.  
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.  
DR InterPro; IPR001682; Ca/Na pore.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR002077; Ca\_channel\_alpha.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR Pfam; PF00520; Ion\_trans; 3.  
DR PRINTS; PR00167; CACHANNEL.  
DR Calcium; Calcium channel; Calcium transport; Calcium-binding;  
KW Ion transport; Ionic channel; Transmembrane; Transport;  
KW Voltage-gated channel.  
FT NON TER 1  
SQ SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match 55.2%; Score 6573; DB 2; Length 1389;  
Best Local Similarity 92.0%; Pred. No. 7.8e-291;  
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;

QY 900 LPDRKNFDSLLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVFNLL 959  
Db 1 LPDRKNFDSLLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVFNLL 60  
QY 960 VAILVEGFOAEEISKREDASGOLSCIQLPVDSSQGDANKSESEPDFFPSLDGDRKKC 1019  
Db 61 VAILVEGFOAEEIGKREDTSGOLSCIQLPVNSQGGDATKSESEPDFFPSVDGDRKKR 120  
QY 1020 LALVSLGEHPELRKSLPPLIIHTAATPMSLIPKSTSTGLGEALGPASRRRTSSGSAEPGA 1079  
Db 121 LALVALGEHSELKSLPPLIIHTAATPMSLIPKSSSTGVGEALGSGSRRTSSGSAEPGT 180  
QY 1080 A-HEMKSPPSARSSPHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138  
Db 181 AHHEMKSPPSARSSPHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 240  
QY 1139 SQDEEESSEERASPCGSHRHGRGSLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQD 1198  
Db 241 SQDEEESSEEDRASPCGSHRHGRGSLEREAKSSFDLPDTLQVPLHRTASGRSSASEHQD 300  
QY 1199 CNGKSASGRALARLPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258  
Db 301 CNGKSASGRLARTRADDPPLDGDGDDDEGNLSKGERLARVRAWIRARLPACCRERDSWSAYI 360



QY 1259 FPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318  
Db 361 FPPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 420  
QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLR 1378  
Db 421 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLR 480  
QY 1379 VLRLRLRLPLRVISRAGQLKLVVETLMSSLPKIGNIVVICCAFFIIFGILGVQLFKGKF 1438  
Db 481 VLRLRLRLPLRVISRAGQLKLVVETLMSSLPKIGNIVVICCAFFIIFGILGVQLFKGKF 540  
QY 1439 FVQCQGEDTRNITNKSDCAEASVYRVRHKYNFDNLGQALMSLFLVLASKDGVWDIMYDGLDA 1498  
Db 541 FVQCQGEDTRNITNKSDCAEASVYRVRHKYNFDNLGQALMSLFLVLASKDGVWDIMYDGLDA 600  
QY 1499 VGVDQQPMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREEK 1558  
Db 601 VGVDQQPMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREEK 660  
QY 1559 RLRRLEKKRR-----KAQCKPYYSYDSYRFRLLLVHHLCTSHYLDLFT 1600  
Db 661 RLKRLEKKRRNMLDDVIASGSSASAASEAQCKPYYSYDSYRFRLLLVHHLCTSHYLDLFT 720  
QY 1601 GVIGLVNVTMAMEHYQQQILDEALKICNYIFTVIFVLESVEKLVAFGRFFQDRWNQL 1660  
Db 721 GVIGLVNVTMAMEHYQQQILDEALKICNYIFTVIFVLESVEKLVAFGRFFQDRWNQL 780  
QY 1661 DLAILLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGRALLDVTMQ 1720  
Db 781 DLAILLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGRALLDVTMQ 840  
QY 1721 ALPQVGNLGLLMLFFIFAAAGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRV 1780  
Db 841 ALPQVGNLGLLMLFFIFAAAGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRV 900  
QY 1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLKMHLEESN 1840  
Db 901 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLKMHLEESN 960  
QY 1841 KEAKEBAEAELEEMKTLSPQPHSPGLSPFLWPGEVGPDSPSDKPGALHPAAHARSA 1900  
Db 961 KEAKEBAEAELEEMKTLSPQPHSPGLSPFLWPGEVGNVSPSPKPGAPHTAHIGAA 1020  
QY 1901 SH-FSLEHTMQPHTPELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHSGTAEGPLGHR 1956  
Db 1021 SSGFSLHEHTMQPHTPELP---GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGR 1080  
QY 1957 GWGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLOPHSAPTWTGTIPKLPGRSPLAQ 2016  
Db 1081 GWGLPKAQSGSVLSVHSQPADTSYILQPKDAPHLLOPHSAPTWTGTIPKLPGRSPLAQ 1140  
QY 2017 RPLRQAARTDSDLVQGLSREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKI 2076  
Db 1141 RPLRQAARTDSDLVQGLSREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKI 1200  
QY 2077 SKHMTPPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPPGGQEEPPSPRDLKKCY 2136  
Db 1201 SKHMTPPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPPGGQEEPPSPRDLKKCY 1259  
QY 2137 SVEAQSCORRPTSWLDEQRRHSIAVSCLDSDSGSQPHLGTDPNLSGQPLGGPSRPKKLS 2196  
Db 1260 SVEAQSCORRPTSWLDEQRRHSIAVSCLDSDSGSQPHLGTDPNLSGQPLGGPSRPKKLS 1319  
QY 2197 PPSITIDPPESQGRPTPPSPGICLRRRAPSSDSKDLASGPPDMSAASPSPKDVLSSLG 2256  
Db 1320 PPSITIDPPESQGRPTPPSPGICLRRRAPSSDSKDLASGPPDMSAASPSPKDVLSSLG 1379  
QY 2257 LSSDPTDLDP 2266  
Db 1380 LSSDPTDLDP 1389

RESULT 7  
CCAH RAT  
ID CCAH RAT STANDARD; PRT; 2359 AA.  
AC Q9EQ60;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).  
DE gated calcium channel alpha subunit Cav3.2).  
GN Name=Cacnalh;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;  
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,  
RA Baillie D.L., Stea A., Snutch T.P.;  
RT "Molecular and functional characterization of a family of rat brain T-type calcium channels.";  
RL J. Biol. Chem. 276:3999-4011(2001).  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in brain.  
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.  
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DR EMBL; AF290213; AAC35187.1; -  
DR RGD; 68943; Cacnalh.  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCAlphal.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR01629; TVDCCALPHA1.  
KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;  
KW Multigene family; Phosphorylation; Repeat; Transmembrane;  
KW Voltage-gated channel.  
FT REPEAT 87 422 I.  
FT REPEAT 776 1015 II.  
FT REPEAT 1292 1569 III.



Db 1100 SRRSSGSDPQLG-DOKSLASLRSSPCTPWGPNAGSRRSSWNSLGRAPSLKRRNQC 1158  
QY 1127 ERRSLLSGEQESQDEEESSEERAS-----PAGSDHRHRRGSLEREAQSSFDL-- 1174  
Db 1159 ERESLLSGEGKSTDE--AEDSRPSTGTHPGASPGPRATPLRAESLDH--RSTLDLCP 1214  
QY 1175 --PDTLQVPGHLRTASGRGSAHEQDCNGKSASGRALARALRPDDPPLDGDADDEGNLSK 1232  
Db 1215 PRPAALLFTKFH-----DCNGQMVALPSEFFLRIDSHKEDAAEFDDIEDSC 1261  
QY 1233 GERVRAWTRARLPACYLERSDSAYIFPPQSRFRLLCHRIITHKMFHVVLVIFLNCIT 1292  
Db 1262 CFRLHKVLEPYAPQWCRSRESWALYLFPPQNLRVSCQKVIHAKMFDHVVLVIFLNCIT 1321  
QY 1293 IAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGL 1352  
Db 1322 IALERPDIDPGSTERAFLSVSNYIPTAIFVVMVMKVVALGLLWGEHAYLQSSWNVDGL 1381  
QY 1353 LVLSISVIDILVSMVSDSGTKILGMLRVLRLLRTLRLRVLVISRAQGLKLVVEILMSSLKPI 1412  
Db 1382 LVLVSLVDIIVAMASAGGAKILGVLRVVLRLLRTLRLRVLVISRAPGLKLVVETLISSLRPI 1441  
QY 1413 GNIVVICAPFIIFGILGVQLFKGFVFCQGEDTRNITNKSDCAEASRYWRHKNYFNDL 1472  
Db 1442 GNIVLICAFIIFGILGVQLFKGFYCEGTDTRNITTKAECHAAHYRVRKYNFDNL 1501  
QY 1473 GOALMSLFVLASKOGWVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIYAFFVLNMF 1532  
Db 1502 GOALMSLFVLSSKOGWVIMYDGLDAVGIDQPVQNHNPMWMLLYFISFLLIYFFVLNMF 1561  
QY 1533 VGVVVENFHKRQHQEEEEARRREKRLRLEKRRKAQCKPYSDYSRFRLLVHHLCTS 1592  
Db 1562 VGVVVENFHKRQHQAEEARRREKRLRLERRRRKAQRRPYADYSHTRRSIHSLCTS 1621  
QY 1593 HYLDLFTIGVIGLVNVTMAMEHYQOQILDEALKICNYIFTVIFVLESVKLVAFGRFR 1652  
Db 1622 HYLDLFTIICLVNITMSMEHYNQPKSLDEALKYCNVFTIVFVFEAALKLVAFGRFR 1681  
QY 1653 FQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMR 1712  
Db 1682 FKDRWNQDLAIVLLSIMGIALBEEIEMNAALPINPTIIRIMRVLRIRARVLKLLKMATGMR 1741  
QY 1713 ALLDTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCCEGLRHATFRNFGM 1772  
Db 1742 ALLDTVVQALPQVGNLGLLFMLFFIYAALGVLEFGRLCEDSEDNPCCEGLSRHATFTNFGM 1801  
QY 1773 AFLTLFRVSTGDNWNGIMKDTLRDC--DQESTCYNVTISPIYFVSFVLTAQFVLNVVVI 1829  
Db 1802 AFLTLFRVSTGDNWNGIMKDTLRCTREDKHCLSYLPALSPVYFVTFMLVAQFVLNVVV 1861  
QY 1830 AVLKMHLEESNKEAEAELEAELEEMKTLSPQPHSPILGSPFLWPVGVEGPDSPDKPG 1889  
Db 1862 AVLKMHLEESNKEAREDAEMDAEIELEM----- 1889  
QY 1890 ALHPAAHARSASHFSLEHPTMQPHPT--ELPG-----PDLLTVRKSGVSRTHSLPNDSYM 1942  
Db 1890 -----AQGSTAQPPPTAQESQGTQPTDPTNLLVVRKVSVSRMLSLPNDSYM 1934  
QY 1943 CRHGSTAGPLGHRGWGLP-----KAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHS 1996  
Db 1935 FRPVAPAAAPHSH-----PLQEVEMETYTGPVTSASHSPLEPRASFQVPSAA-----S 1982  
QY 1997 APTWGTIP--KLPPPG--RSPLAQRLRRQAAIRTDSLD--VQGLGSREDLLAEVSGPSP 2050  
Db 1983 SPARVSDPLCALSPRGTPRSLSLRILCRQEAHMSLESGKVDDVGG--DSIPDYTEPAE 2040  
QY 2051 PLARAYSFWG-----QSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWKGPPET 2100  
Db 2041 NMSTSQAOSTGAPRSPCSPRPASVTRKHTFGORCISSR--PPT-----LGGDEA 2088  
QY 2101 RSSLELDTLSWISGDLPL-----PGQEEPP-----SPRDLKKCYSVEAQSCQR 2145

Db 2089 EAADPADEEVSHITSSAHPWPATEPHSPASPTASPVKGTMGSDRDRRRCFSVDAQSF 2148  
QY 2146 RPTSWLDEQRRHSIAVSCLDGSGSQPHLGTDPNSNLGGQPLG-----GPGSRPKKLSPP 2198  
Db 2149 KP-GRPDAQRWSSVE--LDNG-ESHLES-----GEVGRASELEPALGSRKKKQVSP 2197  
QY 2199 SITIDPP-ESQGPRTPPSP---GICLRRRAPSSDSK-----DPLASGPP 2238  
Db 2198 CISIEPTKDEGSSRPAAEGGNTTLRRRTPSCEAALHRDCPEPTGPGTGGDPVAKGER 2257  
QY 2239 DSMAASPSPKDVLVLSGLSSDPADL 2264  
Db 2258 WQA---SCRAEHLTVPNFAFEPLDM 2280  
RESULT 8  
CCAH HUMAN  
ID CCAH HUMAN STANDARD; PRT; 2353 AA.  
AC O95180; O95802; Q8WWI6; Q96QI6; Q96R29; Q9NYI4; Q9NYI5;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2) (low-voltage-activated calcium channel alpha1 3.2 subunit).  
DE Name=CACNA1H;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Heart;  
RX MEDLINE=98333998; PubMed=9670923;  
RA Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N., Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.; "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family."; Circ. Res. 83:103-109(1998).  
RN [2]  
RP REVISIONS.  
RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Thyroid carcinoma;  
RX MEDLINE=99127945; PubMed=9930755;  
RA Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F., Prodanovich P., Harpold M.M., Stauderman K.A.; "Structure and functional characterization of a novel human low-voltage activated calcium channel."; J. Neurochem. 72:791-799(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339; Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.; "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Testis;  
RX MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200; Jagannathan S., Punt E.L., Gu Y., Arnoult C., Sakkas D., Barratt C.L., Publicover S.J.; "Identification and localization of T-type voltage-operated calcium channel subunits in human male germ cells. Expression of multiple isoforms."; J. Biol. Chem. 277:8449-8456(2002).  
RN [6]  
RP SEQUENCE OF 86-817 FROM N.A.

RA Cobley V.E.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).  
RA Mittman S., Agnew W.S.;  
RL "Organization and alternative splicing of CACNA1H";  
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the  
CC entry of calcium ions into excitable cells and are also involved  
CC in a variety of calcium-dependent processes, including muscle  
CC contraction, hormone or neurotransmitter release, gene expression,  
CC cell motility, cell division and cell death. The isoform alpha-1H  
CC gives rise to T-type calcium currents. T-type calcium channels  
CC belong to the "low-voltage activated (LVA)" group and are strongly  
CC blocked by nickel and mibefradil. A particularity of this type of  
CC channels is an opening at quite negative potentials, and a  
CC voltage-dependent inactivation. T-type channels serve pacemaking  
CC functions in both central neurons and cardiac nodal cells and  
CC support calcium signaling in secretory cells and vascular smooth  
CC muscle. They may also be involved in the modulation of firing  
CC patterns of neurons which is important for information processing  
CC as well as in cell growth processes.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=AlH-a;  
CC IsoId=O95180-1; Sequence=Displayed;  
CC Name=2; Synonyms=AlH-b;  
CC IsoId=O95180-2; Sequence=VSP\_000949;  
CC -!- TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.  
CC Isoform 2 seems to be testis-specific.  
CC -!- DOMAIN: Each of the four internal repeats contains five  
CC positively charged transmembrane segments (S1, S2, S3, S5, S6) and one  
CC probably represents the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II.  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
CC -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown  
CC in this entry. The additional 20 amino acids found in the Ref.4  
CC and Ref.6 sequences are due to a misunderstanding of the real type  
CC of splicing mechanism involved.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF051946; AAC67239.3; -;  
DR EMBL; AF073931; AAD17668.1; -;  
DR EMBL; AE006466; AAK61268.1; ALT\_SEQ.  
DR EMBL; AJ420779; CAD12646.1; -;  
DR EMBL; AL031703; CAC42094.1; ALT\_SEQ.  
DR EMBL; AF223562; AAF60162.1; -;  
DR EMBL; AF223563; AAF60163.1; -;  
DR Genew; HGNC:1395; CACNA1H.  
DR MIM; 607904; -;  
DR GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.  
DR GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.  
DR GO; GO:0006936; P:muscle contraction; TAS.  
DR GO; GO:0007520; P:myoblast fusion; TAS.  
DR GO; GO:0008016; P:regulation of heart rate; TAS.  
DR GO; GO:0006810; P:transport; TAS.  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCAlphal.

DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR01629; TVDCCALPHA1.  
KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;  
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;  
KW Repeat; Transmembrane; Voltage-gated channel.  
FT REPEAT 87 422 I.  
FT REPEAT 779 1018 II.  
FT REPEAT 1281 1558 III.  
FT REPEAT 1602 1863 IV.  
FT DOMAIN 1 100 Cytoplasmic (Potential).  
FT TRANSMEM 101 119 S1 of repeat I (Potential).  
FT DOMAIN 120 139 Extracellular (Potential).  
FT TRANSMEM 140 160 S2 of repeat I (Potential).  
FT DOMAIN 161 169 Cytoplasmic (Potential).  
FT TRANSMEM 170 184 S3 of repeat I (Potential).  
FT DOMAIN 185 193 Extracellular (Potential).  
FT TRANSMEM 194 212 S4 of repeat I (Potential).  
FT DOMAIN 213 232 Cytoplasmic (Potential).  
FT TRANSMEM 233 253 S5 of repeat I (Potential).  
FT DOMAIN 254 394 Extracellular (Potential).  
FT TRANSMEM 395 419 S6 of repeat I (Potential).  
FT DOMAIN 420 793 Cytoplasmic (Potential).  
FT TRANSMEM 794 814 S1 of repeat II (Potential).  
FT DOMAIN 815 827 Extracellular (Potential).  
FT TRANSMEM 828 849 S2 of repeat II (Potential).  
FT DOMAIN 850 855 Cytoplasmic (Potential).  
FT TRANSMEM 856 874 S3 of repeat II (Potential).  
FT DOMAIN 875 882 Extracellular (Potential).  
FT TRANSMEM 883 906 S4 of repeat II (Potential).  
FT DOMAIN 907 917 Cytoplasmic (Potential).  
FT TRANSMEM 918 938 S5 of repeat II (Potential).  
FT DOMAIN 939 990 Extracellular (Potential).  
FT TRANSMEM 991 1015 S6 of repeat II (Potential).  
FT DOMAIN 1016 1290 Cytoplasmic (Potential).  
FT TRANSMEM 1291 1313 S1 of repeat III (Potential).  
FT DOMAIN 1314 1331 Extracellular (Potential).  
FT TRANSMEM 1332 1352 S2 of repeat III (Potential).  
FT DOMAIN 1353 1362 Cytoplasmic (Potential).  
FT TRANSMEM 1363 1382 S3 of repeat III (Potential).  
FT DOMAIN 1383 1396 Extracellular (Potential).  
FT TRANSMEM 1397 1418 S4 of repeat III (Potential).  
FT DOMAIN 1419 1428 Cytoplasmic (Potential).  
FT TRANSMEM 1429 1452 S5 of repeat III (Potential).  
FT DOMAIN 1453 1529 Extracellular (Potential).  
FT TRANSMEM 1530 1555 S6 of repeat III (Potential).  
FT DOMAIN 1556 1616 Cytoplasmic (Potential).  
FT TRANSMEM 1617 1637 S1 of repeat IV (Potential).  
FT DOMAIN 1638 1651 Extracellular (Potential).  
FT TRANSMEM 1652 1673 S2 of repeat IV (Potential).  
FT DOMAIN 1674 1680 Cytoplasmic (Potential).  
FT TRANSMEM 1681 1699 S3 of repeat IV (Potential).  
FT DOMAIN 1700 1713 Extracellular (Potential).  
FT TRANSMEM 1714 1737 S4 of repeat IV (Potential).  
FT DOMAIN 1738 1751 Cytoplasmic (Potential).  
FT TRANSMEM 1752 1772 S5 of repeat IV (Potential).  
FT DOMAIN 1773 1835 Extracellular (Potential).  
FT TRANSMEM 1836 1863 S6 of repeat IV (Potential).  
FT DOMAIN 1864 2353 Cytoplasmic (Potential).  
FT DOMAIN 520 530 Poly-His.  
FT DOMAIN 1107 1110 Poly-Ser.  
FT DOMAIN 1583 1586 Poly-Arg.  
FT SITE 378 Calcium ion selectivity and permeability  
FT SITE 974 (By similarity).  
FT SITE 1504 Calcium ion selectivity and permeability  
FT SITE 1808 Calcium ion selectivity and permeability  
FT CARBOHYD 192 Calcium ion selectivity and permeability  
FT CARBOHYD 271 (By similarity).  
FT CARBOHYD 192 N-linked (GlcNAc..)(Potential).  
FT CARBOHYD 271 N-linked (GlcNAc..)(Potential).  
Query Match 52.2%; Score 6210; DB 1; Length 2353;



		Best Local Similarity 56.6%; Pred. No. 4.6e-274;		Matches 1364; Conservative 216; Mismatches 526; Indels 302; Gaps 59;	
QY	7	GAGAEESQOP-RSFMRLNDLSGAGRPPGPGSAEKDPGSADSEAEGLPYPALAPVFFYLS	65		
Db	27	GASPESGAFGREAERGSEL-GVSPSESP-AAERGAELGADEEQRPYPALAAATVFFCLG	84		
QY	66	QDSRPRSWCLRTVCNPFERISMLVILNCVTLMFRPCEDIAQDSQRCRILQAFDDFIF	125		
Db	85	QTRPRSWCLRLVCNPFHEVHSMVLVIMLNCVTLMFRPCDEVEGSERCNILEAFDAFIF	144		
QY	126	AFFAVEMVVMVALGIFGKKCYLGDWTNRLLDFFIVIAAGLMEYSLDLQNVFSAVRTVRVL	185		
Db	145	AFFAVEMVIMVALGLFGQKCYLGDWTNRLLDFFIVVAGWMEYSLDGHNVSLSAIRTVRVL	204		
QY	186	RPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLPE	245		
Db	205	RPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLDS	264		
QY	246	NFSLPLSVD-LERYYQOTENEDESPTICSQPRENGMRSRCSVP---TLRGDGGGPPCGLD	301		
Db	265	AFVRNNLTFLRPYYQTEEGEENPFICSSRRDGMQCKSHIPGRREL------MECTLG	318		
QY	302	YEAYN-----SSNTTCVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIQVITLE	354		
Db	319	WEAYTQOAEVGAARNACINWNQYINVCRSGDSNPHNGAINFDNIGYAWIAIQVITLE	378		
QY	355	GWVDIMYFMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRV	414		
Db	379	GWVDIMYFMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRA	438		
QY	415	RFLSNASTLASFSEPGSCYEELLKVLVYLKKAARLAQVSRAGVRVGLLSSPAPLGGQ	474		
Db	439	RHLSNDSTLASFSEPGSCYEELLKVVGHI FRKVKRRSLRLYARWQSRWRKVPDSAVQGQ	498		
QY	475	ETQPSSSCSRSHRR-LSVHHLV-HHHHHHHHHLNGTILRAPRASPEIQDRDANGSRRL	532		
Db	499	--GPGRQRAGRHTASVHLVTHHHHHHHHHYHFSHGSPRRPGPEPGACD-----TRLV	551		
QY	533	MLPPPSTPALS GAPPGAESVHSFYHADCHLE--PVRQAPPPRSPSEASGR-TVGSGKV	589		
Db	552	RAGAPSPSPGRGPPDAESVHSIYHADCHIEGQPERARVAHAAATAAASRLATGLGTM	611		
QY	590	-YPTV-----HTSP-----PPETLKEKALVEVAASSGPPTLTSLNIPPGPY	629		
Db	612	NYPTILPSGVSGKGSTSPGPKGWAGGPPGT-----GGHGPLSLNS-----PDYP	657		
QY	630	SSMHKLLLETQSTGACQS-----SKTISSPCLKADSGACGPDSCPYCARA-GAGEVELA	681		
Db	658	EKIPHVVEHGLGQAPGHLGSLVPCPLPSP--PAGTLTCELKSCPYCTRALEDPGELS	715		
QY	682	DREMPDSDSEAVYEFTQDAQHSDLRDP-----HRRQRSIGPDAPSSV	725		
Db	716	GSESGDSGRGVYEFTQDVRHGDRWDTPRPTRATDTPGPGSPQORRAQQAAPGEPGWM	775		
QY	726	LAFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIEVHEQPEELTNALEISNIVFTSL	785		
Db	776	GRLWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGVEYHEQPEELTNALEISNIVFTSM	835		
QY	786	FALEMLKLLVYGPFGYIKNPYINFDGVIWISVWEIVGQGGGLSVLRTFRLMRVLKLV	845		
Db	836	FALEMLKLLACGPLGYIRNPYNIPDGIWISVWEIVGQADGGLSVLRTFRLRLVLKLV	895		
QY	846	RFLPALQRLVVLKMTMDNVATFCMLLMFLIFIFSILGMHLFGCKFASERD-GDTLPDRK	904		
Db	896	RFLPALRRLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLFGCKFSLKTDGTGTVPDRK	955		
QY	905	NFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALFYALMTFGNYVLFNLLVAILV	964		
Db	956	NFDSLLWAIIVTFQILTQEDWNVVLNGMASTSSWAALFYVALMTFGNYVLFNLLVAILV	1015		
QY	965	EGFQAEIISKREDASQOLSCIQLPVDSQGGDANKSESEDFPSPSLDGD-----GD	1015		

Db	1016	EGFAE-----GDANRSDTDEDKTSVHFEEDFHKLRELQTTTE	1052		
QY	1016	RKKCLALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSA	1075		
Db	1053	LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRRGSSSGD	1112		
QY	1076	EPGAAHEMKSPPSARSSPHSPSAASSWTSSRRSNLSGRAPSLKRRSPSGERRSLISGE	1135		
Db	1113	PP--LGDQKPPASLRSSPCAPWPSGAWSSRRSSWSLGRAPSLKRRGQCGERESLLSGE	1170		
QY	1136	GOESQDEEESSEERASPA--GSDHRHRGSLEREAKSSFDLPDTL-----QVPLGH---	1184		
Db	1171	GKGSTDD-ABDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDGOVVVALPSDF	1228		
QY	1185	--RTASGRGSASEHQDCNGKSASGRLARALRPDDPLDGDADDEGNLSKGERVRAWIRA	1242		
Db	1229	FLRIDSHREDAEALDDSDSCCLRLHKVLEYPK-----QWCRS	1268		
QY	1243	RLPACYLERDSWAYIFPPQSRFLLCRRIITHKMFHVVLVIFLNCITIAMERPKIDP	1302		
Db	1269	-----REAWALYLFSPONFRVSCQKVITHKMFHVVLVIFLNCVTIALERPDIDP	1320		
QY	1303	HSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDIL	1362		
Db	1321	GSTERVFLSVSNYIFTAIFVAEMVMKVVALGLLSGEHAYLQSSWNLLDGLLVLSLVDIV	1380		
QY	1363	VSMVSDSGTKILGMLRLVRLRLTLRPLRVRISRAQGLKLVVETLMSSSLKPIGNIVVICAP	1422		
Db	1381	VAMASAGGAKILGVLRVLRLLTLRPLRVRISRAPGLKLVVETLISSLRPIGNIVLICAP	1440		
QY	1423	FIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASVRVWRHKYNFNDLGOALMSLFVL	1482		
Db	1441	FIIFGILGVQLFKGKFFYCEGPDTRNISTKAQCRAAHYRVRWRKYNFNDLGOALMSLFVL	1500		
QY	1483	ASKDGWVDIMYDGLDVGVDQOQIMNHNPMWLLYFISFLIVAFVFLNMFVVVVENFHK	1542		
Db	1501	SSKDGWVIMYDGLDVGVDQOQVQNHNPWMLLYFISFLIVSFFVLNMFVVVVENFHK	1560		
QY	1543	CRHQEERREARRRERKRLRLEKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLD	1596		
Db	1561	CRHQEAEERREARRRERKRLRLERRRRSTFPSPEAQRPPYADYSPTRRSIHSLCTSHYLD	1620		
QY	1597	LFITGIVGLNVVTMAMEHYQQOILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDR	1656		
Db	1621	LFITFICNVITMSMEHYNQPKSLDEALKYCNVFTIVFVFEAALKLVAFGFRFFQDR	1680		
QY	1657	WNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGNRALLD	1716		
Db	1681	WNQLDLAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGNRALLD	1740		
QY	1717	TVMQALPQVGNLGLLFLMLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLT	1776		
Db	1741	TVVQALPQVGNLGLLFLMLFFIYAALGVLELFGRLCESDNPCEGLSRHATFSNFGMAFLT	1800		
QY	1777	LFRVSTGDNWNGIMKOTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLM	1833		
Db	1801	LFRVSTGDNWNGIMKOTLRCSREDKHCLSYLPALSPYFVFTFVLVAQFVLNVVIAVLM	1860		
QY	1834	KHLEESNKEAEAEAELEAELEEMKTLSPQPHSPGSPFLWPVGVEGPDSP---DSPKPGA	1890		
Db	1861	KHLEESNKEAREDAELDAEIELEM-----AQPGSARRVDADR-1899	1899		
QY	1891	LHPAAHARSASHFSLEHPTMQPHPTELPG----PDLLTVRKSGVSRTHSLPNDSYMCRHG	1946		
Db	1900	-----PLPQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV	1937		
QY	1947	STAEGP-----LGHRGWGLPKAQSGSVLSVHSPADTSYILQLPKDAPHLLQPHSA	1997		
Db	1938	VPASAPHRPLQEVEMETYGAGTP---LGSVASVHSPAESCASLQIP-----LAVSSPA	1989		
QY	1998	PTWGTIPKLPPPG--RSPLAQRLRRQAAIRTDSLDVOQLGSRDILL--AEVSGPSP--P	2051		
Db	1990	RSGEPLHALSPRGTARSPSLSRLLCRQEAHVHTDSLEK-IDSPRDTLDPAECEKTPVRP	2048		





FT	TRANSMEM	1847	1874	S6 of repeat IV (Potential).
FT	DOMAIN	1875	2365	Cytoplasmic (Potential).
FT	DOMAIN	521	531	Poly-His.
FT	DOMAIN	1594	1597	Poly-Arg.
FT	SITE	378	378	Calcium ion selectivity and permeability (By similarity).
FT	SITE	971	971	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1515	1515	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1819	1819	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1477	1477	N-linked (GlcNAc. .) (Potential).
FT	CONFLICT	1823	1825	GIM -> ARG (in Ref. 2).
FT	CONFLICT	1914	1914	D -> E (in Ref. 2).
FT	CONFLICT	1945	1947	APA -> LQ (in Ref. 2).
FT	CONFLICT	1952	1952	S -> A (in Ref. 2).
FT	CONFLICT	1953	2351	Missing (in Ref. 2).
SQ	SEQUENCE	2365	AA; 261944	MW; 9A8A17570C210596 CRC64;
Query Match				
Best Local Similarity 51.9%; Score 6176.5; DB 1; Length 2365;				
Matches 1365; Conservative 235; Mismatches 528; Indels 285; Gaps 61;				
QY	2	DEEDGAGAEESGQPSRFMLNDLS-GAGGRP----	GPSS----AEKDPGS----AD----	SEA 48
Db	9	DEVVRPLGASPSA-PAAPVRASPASPGVPGREEQ	RGSSSVLAPESP	GTECGADLGADEE 67
QY	49	EGLPYPALAPVVFYLSQDSRRPRSWCLRTVCNP	WFERISMLVILLNCVT	LGMFRPCEDIA 108
Db	68	QVPYPALAAATVFFCLGQTTTRPRSWCLRLVCNP	WFEHISMLVIMLNCVT	LGMFRPCEDVE 127
QY	109	CDSQRCRILOAFDDFIFAFFAVEMVVMVALGIF	GKKCYLGD	TWNRLDFFIVIAGMLEYS 168
Db	128	CRSERCISLEAFDDFIFAFFAVEMVVMVALGIF	GKKCYLGD	TWNRLDFFIVMAGMWEYS 187
QY	169	LDLQNVFSAVRTRVRLPLRAINRVPSMRILVTL	LDLPLMLGNVLLLCFFV	FFIFIGIV 228
Db	188	LDGHNVSLSAIRTRVRLPLRAINRVPSMRILVTL	LDLPLMLGNVLLLCFFV	FFIFIGIV 247
QY	229	GVQLWAGLLRNRCFLPENFSLPLSDV-LERYQ	TENEDESPFICSQPRE	NGMRSRCSVPT 287
Db	248	GVQLWAGLLRNRCFLDSAFVRNNLTFLRPPYQ	TEEGEENPFICSSRR	RDNGMQCSHIP 307
QY	288	---LRGCGGGPPCGLDYEAY-----NSSNT	TCVNNQYITNC	SAGEHNPFGKAINF 337
Db	308	RREL-----VQCTLGWEAYGQQAEDGGAG	RNACINWNQYINVC	RSGEFNPHNGAINF 361
QY	338	DNIGYAWIAIFQVITLEGWVDIMYFVMDAHS	FYNFIYFILLIIVGS	FFMINCLVVIATQ 397
Db	362	DNIGYAWIAIFQVITLEGWVDIMYVMDAHS	FYNFIYFILLIIVGS	FFMINCLVVIATQ 421
QY	398	FSETKQRESQLMREQVRFLSNASTLASFSEPG	SCYEELLKYLVI	ILRKAARLQVSR 457
Db	422	FSETKQRENQLMREQARLYLSDSTLASFSEPG	SCYEELLKYVGHI	FRKVKRRSLRYAR 481
QY	458	AGVRVGLLSSP-APLGGOETQPSSSCSRSRHR	-LSVHILV-HHHHHHH	HYHLNGTLRA 514
Db	482	WQSRWRKKVDPSSTLHGQ--GPRRRPRR	AGRRTASVHLVY	HHHHHHHHHHYHFSHGPPRR 539
QY	515	PRASPEIQDRDANGSRRLM--LPPPTPAL	SAGAPP	GGGAEVSHSFYHADCHLEPVRCQAPP 572
Db	540	P--SPE----PGAGDTRLVRACVP	PPSPPGHGPP-DSESVHS	IYHADCHVEGPQERARV 592
QY	573	PRSPSEASGRVTGSG---KVYPTV-----	HTSPPETLKEKAL	VEVAASSGPPTL 619
Db	593	AHTIATAASLKASGLGTMTNYPTILPSG	AVNSKGSTSSRPKGLR-----	SAGTPGA 643
QY	620	TS---LNI-PPGPYSSMHKLLETQSTGACQS	-----SCKISSPCL	KADSGACPDSCP 668
Db	644	TAHSPLSLGSPSPYEKIQHVVGEGQLGR	ASSHLSGLSVPCPLPSP--	QAGTLTCELKSCP 701

QY	669	YCARA-GAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDP-----HSSRRQR	714
Db		: :	



CC belong to the "low-voltage activated (LVA)" group and are strongly  
CC blocked by nickel and mibefradil. A particularity of this type of  
CC channels is an opening at quite negative potentials, and a  
CC voltage-dependent inactivation. T-type channels serve pacemaking  
CC functions in both central neurons and cardiac nodal cells and  
CC support calcium signaling in secretory cells and vascular smooth  
CC muscle. They may also be involved in the modulation of firing  
CC patterns of neurons which is important for information processing  
CC as well as in cell growth processes. Gates in voltage ranges  
CC similar to, but higher than alpha 1G or alpha 1H (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=Delta36b;  
CC IsoId=Q9POX4-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9POX4-2; Sequence=VSP\_000951;  
CC Name=3; Synonyms=Alpha1I-a;  
CC IsoId=Q9POX4-3; Sequence=VSP\_000950, VSP\_000951;  
CC Name=4;  
CC IsoId=Q9POX4-4; Sequence=VSP\_000950;  
CC -!- TISSUE SPECIFICITY: Brain specific.  
CC -!- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one  
CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II (By similarity).

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
CC -!- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to  
CC erroneous gene model prediction.

CC -----  
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CC -----  
CC EMBL; AF129133; AAD45251.1; -.  
CC EMBL; AF142567; AAF25722.1; -.  
CC EMBL; AF211189; AAF44626.1; -.  
CC EMBL; AF393329; AAM67414.1; -.  
CC EMBL; AL008716; CAA15494.1; -.  
CC EMBL; AL022312; CAB62988.1; -.  
CC EMBL; AL022319; CAB62996.1; ALT\_SEQ.  
CC EMBL; AL022319; CAD92536.1; -.  
CC EMBL; AB032946; BAA86434.1; -.  
CC Genew; HGNC:1396; CACNA1I.  
CC MIM; 608230; -.  
CC GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.  
CC GO; GO:0008332; F:low voltage-gated calcium channel activity; NAS.  
CC GO; GO:0006816; P:calcium ion transport; NAS.  
CC InterPro; IPR001682; Ca/Na\_pore.  
CC InterPro; IPR002111; Cat\_channel\_TrpL.  
CC InterPro; IPR002077; Ca\_channel\_alpha.  
CC InterPro; IPR005821; Ion\_trans.  
CC InterPro; IPR005820; M+channel\_nlg.  
CC InterPro; IPR005445; TVDCCAlphal.  
CC Pfam; PF00520; Ion\_trans; 4.  
CC PRINTS; PR00167; CACHANNEL.  
CC PRINTS; PR01629; TVDCCALPHAL.  
CC KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;  
CC KW Ion transport; Ionic channel; Multigene family; Phosphorylation;  
CC KW Polymorphism; Repeat; Transmembrane; Voltage-gated channel.  
FT REPEAT 66 401 I.  
FT REPEAT 626 865 II.  
FT REPEAT 1157 1434 III.  
FT REPEAT 1472 1733 IV.  
FT DOMAIN 1 78 Cytoplasmic (Potential).

FT	TRANSMEM	79	99	S1 of repeat I (Potential).
FT	DOMAIN	100	120	Extracellular (Potential).
FT	TRANSMEM	121	141	S2 of repeat I (Potential).
FT	DOMAIN	142	148	Cytoplasmic (Potential).
FT	TRANSMEM	149	168	S3 of repeat I (Potential).
FT	DOMAIN	169	173	Extracellular (Potential).
FT	TRANSMEM	174	191	S4 of repeat I (Potential).
FT	DOMAIN	192	211	Cytoplasmic (Potential).
FT	TRANSMEM	212	232	S5 of repeat I (Potential).
FT	DOMAIN	233	377	Extracellular (Potential).
FT	TRANSMEM	378	398	S6 of repeat I (Potential).
FT	DOMAIN	399	640	Cytoplasmic (Potential).
FT	TRANSMEM	641	661	S1 of repeat II (Potential).
FT	DOMAIN	662	676	Extracellular (Potential).
FT	TRANSMEM	677	697	S2 of repeat II (Potential).
FT	DOMAIN	698	702	Cytoplasmic (Potential).
FT	TRANSMEM	703	721	S3 of repeat II (Potential).
FT	DOMAIN	722	729	Extracellular (Potential).
FT	TRANSMEM	730	753	S4 of repeat II (Potential).
FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).

Query Match

46.2%; Score 5496.5; DB 1; Length 2223;

Best Local Similarity 51.3%; Pred. No. 1.2e-241;

Matches 1241; Conservative 217; Mismatches 527; Indels 435; Gaps 60;

QY	31	RPGSGSAEKDPGSADSEAE	---	LPYPALAPVVFYLSQDSRPSRWCLRTVCNPFERI	86	
Db	25	QPGSRSPSPSGLEEPLDGADPHVPHDLAPIAFFCLRQTTSRPNWCIMKVCNPFECV	84			
QY	87	SMVLVLLNCVTLMFRPCEDIACDSQRCRILQAFDDIFAFEAFAVEMVMVMVALGIFGKKC	146			
Db	85	SMVLVLLNCVTLMGYQPCDDMDCLSDRCKILQVDFDIFIFFAMEMVLKMVALGIFGKKC	144			
QY	147	YLGDTWNRLLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLLD	206			
Db	145	YLGDTWNRLLDFFIVMAGMVEYSLDLQNLNSAIRTVRLRPLKAINRVPSMRILVNLLLD	204			
QY	207	TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYQTENEDE	266			
Db	205	TLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVALPPYQPEEDDE	264			
QY	267	SPFICSQPRENGMRSCRSVPTLRDGGGGPPCGL	----	DYEAYNSSNTT	318	
Db	265	MPFICSLSGDNGIMGCHEIPLKEQ	----	GRECCLSKDDVDFGAGRODLNASGLCVNWR	321	
QY	319	YYTNCAGEHNPFKGAINFNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILL	378			
Db	322	YYNVCRGTGSANPHKGAINFNIGYAWIVIFQVITLEGWVEIMYVYVMDAHSFYNFYIFILL	381			
QY	379	IIVGSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLK	438			
Db	382	IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQYLS	----	SSTVASYAEPGDCYEEIFQ	440	
QY	439	YLVYILRKAARRLAQVSRAGVRVGLLSPPALPGQETQPSSSCSRSHRRLSVHHLVHHH	498			
Db	441	YVCHILRKAKR	-----	RALGLYQALQSRRLQALGPEAPAKP	-----	GPH 480
QY	499	HHHHHHYH	----	LGNGTLRAPRASPEIQDRDAN	----	GSRRILM-LPPPSTPALSGAPPGAESV 553
Db	481	AKEPRHYHGKTKGQ	-----	DEGRHLGSRHCQTLHGPA	----	SP---GNDHSGRE-- 523
QY	554	HSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAAS	613			
Db	524	-----LC	----	PQHSPLDATPHTL	-----	VQIPATL----- 546



QY 614 SGPPTLTSLNIPPGPYSSMHKLLLETOSTGACQSSCKISSPCLKADSGACGPDSCPYCAR- 672  
Db 547 -----ASDPASCPCQOHE 559  
QY 673 -----AGAGEVELADREMPDSDSEAVYEFTOAQHSDLDRPHSRQRSLGPDAAEPSVL- 726  
Db 560 DGRPSGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSSEDGASSELGKEEEEEQAD 616  
QY 727 -----AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISN 779  
Db 617 GAVWLCGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHQPEELTNILEICN 676  
QY 780 IVFTSLFALEMLLKLVLVGPFGYIKPNYPNIFDGVIVVVISVWEIVGQGGSLVLRTRFLM 839  
Db 677 VVFTSMFALEMILKLAAGFLFDYLRPNYPNIFDSIIVISIWEIVGQADGGLSVLRTFRL 736  
QY 840 RVLKLVRFLPALOROLVVLMTMDNVATFCMLLMFLFIFISILGMHLFGCKFASERD-GD 898  
Db 737 RVLKLVRFPALRRQLVVLMTMDNVATFCMLLMFLFIFISILGMHLFGCKFSLRTDTGD 796  
QY 899 TLPDRKNFDSLWAIIVTFQILTOEDWNKVLVNGMASTSSWAALYFIATLMTFGNYVLFNL 958  
Db 797 TVPDRKNFDSLWAIIVTFQILTOEDWNVVLVNGMASTSPWASLYFVALMTFGNYVLFNL 856  
QY 959 LVAILVEGQAEIEISKREDASQGLSCIQLPVDSQGDANKSESEPDDFFSPS----- 1009  
Db 857 LVAILVEGQAE-----GDANRSYDEDEDQSSNIEEFDKLQE 893  
QY 1010 -LDGDRKCKLALVSLGEHPELRKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRR 1068  
Db 894 GLDSSGDPKLCPIPMTPNGH-----LDP-----SLPLGHLGPAGAAGPAPRL 936  
QY 1069 T-----SSSGSAEPGAHEMKSPPSARSPPHSPWASAASSWTSSRNSLGR 1115  
Db 937 SLQDPMLVALGSRKSSVMSLGRMSYDQRLSSRSSSYGPGWGRSAAWASRRSSWN---- 992  
QY 1116 APSLKRSPSGRRSLLSGE-GQESQDEEESSEE--ERASPGASDH----- 1158  
Db 993 --SLKHKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHIIHGPHLAHRH 1050  
QY 1159 -RHGSLEREAKSSFDPDLTQVPLGHLRTASGR--GSASEHQDCNGKSASGRALARLRPD 1215  
Db 1051 RHHRRTLSDNRSDVDLAELVPAVGHAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMG 1110  
QY 1216 DPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITH 1275  
Db 1111 DRGDRGED-EEEDIDYTLCFVRKMDIVYKPDWCEVREDWSVYLFSPENRFRVLCQTIH 1169  
QY 1276 KMFEDHVVLVIIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVVALGWC 1335  
Db 1170 KLFDYVVLAFIIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSGLY 1229  
QY 1336 FGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLTLRPLRVISRA 1395  
Db 1230 FGEQAYLRSSWNVDGLVVFVSIIDIVVSLASAGGAKILGVLRVLRLLRPLRVISRA 1289  
QY 1396 QGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDC 1455  
Db 1290 PGLKLVVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGKFFYHCLGVDTRNITNRSDC 1349  
QY 1456 AEASYRWVRHKYNFNDLGOALMSLVFLASKDGVVDIMYDGLDAVGVDQOQIMNHNPMWLL 1515  
Db 1350 MAANYRWVHKYNFNDLGOALMSLVFLASKDGVVNIMYNGLDVAVDQOQVTNHNPMWLL 1409  
QY 1516 YFISPLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRRLRLEKRRKKAQCKPY 1575  
Db 1410 YFISPLLIIVSVFVLNMFVGVVVENFHKCRHQHEAEARRREKRRLRLEKRRKKAQRLPY 1469  
QY 1576 YSDYSRFRLLVHLCCTSHYLDLFTITGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVI 1635  
Db 1470 YATYCHTRLLIHSMTCTSHYLDLFTITFIICLVNVTMSLEHYNQPTSLETALKYCNYMFTTV 1529  
QY 1636 FVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRV 1695

Db 1530 FVLEAVLKLVAFLGRFFQDRWNQDLAIVLLSVMGITLEEIEINAALPINPTIIRMRV 1589  
QY 1696 LRIARVLKLLKMAVGMRAALLDTVMQALPOVGNLGLLMLLFFIFAALGVFELGDLCEDET 1755  
Db 1590 LRIARVLKLLKMATGMRAALLDTVMQALPOVGNLGLLMLLFFIYAALGVFELGKLVNCDE 1649  
QY 1756 HPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIY 1812  
Db 1650 NPCEGMSRHAFTENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSLQFVSPLY 1709  
QY 1813 FVSFVLTAQFVLNVNVIIVLMKHLEESNKEAKEEALEAELELEM-KTLSQPSPHPLGSP 1871  
Db 1710 FVSFVLTAQFVLINVVAVLMKHLDDSNKEAQEDAEMDAELEMAHGLGPGPRLPTGSP 1769  
QY 1872 FLWPGVEGPD-----SP-----DSPKPG 1889  
Db 1770 GA-PG-RGPGAGGGDTEGGLCRRCYSPAQENWLDVSLI IKDSLEGELTIIDNLGS 1827  
QY 1890 ALH-----PAA-----HARSAS-----HFSLEHPTMQP-----H 1913  
Db 1828 IFHYYSSPAGCKKCHDKQEVOLAEATEAFSLNSDRSSILLGDDLSLEDTACPPGRKDS 1887  
QY 1914 PTELPGPDLTVRKSG-----VSRTHSLPN-DSYMRHGSTAEGPLHGRGWGLPKAQSGS 1967  
Db 1888 KGELDPPEPMPRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFPV--RSW--LKHDSSQ 1943  
QY 1968 VLSVHSQPADTSYILQLPKDAPH-----LLQPHSAPTWTGTPKLPPLPG-----RSPLAQ 2016  
Db 1944 APPSPFSPDASSPLLPMPAEFFHPAVSASQKGPEKGTGTLPKIALQGSWASLRSPRVN 2003  
QY 2017 RPLRQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYFWGQSSTQAAQHRSRSHSKI 2076  
Db 2004 CTLLRQATGSDTSLD-----ASPSSAGSLQTTLEDSTLSDSPRA----- 2045  
QY 2077 SKHMTPPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCY 2136  
Db 2046 ---LGPPAPAPGPRAGLS---PAARRLSL-----RGRGLFSLR 2078  
QY 2137 SVEAQSCORRPTSWLDDEQRRHSIAVSCUDSGSQPHLGTDPN--LGGQPLGGPGSRPKK 2193  
Db 2079 GLRA-----HORSHSGGS-TSPGCTHHDSDMPDSEGRGGAGGGAGSEHSE 2125  
QY 2194 KLSPPSIT---IDPPESQGPRTPPSPGICLRRRAPSSDS----KDPLASGPPDMSMAASPS 2246  
Db 2126 TLSLSLTSLFCPPP-----PPPAPGLTPARKFSSTSSLAAPCRPHAAALAHGLARSPS 2179  
QY 2247 PKKDVLSLSGLSSDPADLDP 2266  
Db 2180 WAAD-----RSKDPGGRAP 2193

RESULT 11  
CCAI RAT

ID CCAI RAT STANDARD; PRT; 1835 AA.  
AC Q9Z0Y8; Q9EQ59;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Voltage-dependent T-type calcium channel alpha-11 subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (CaVt.3).  
GN Name=Cacnali;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=99165796; PubMed=10066244;  
RA Lee J.-H., Daud A.N., Cribbs L.L., Lacerda A.E., Pereverzev A.,  
RA Kloeckner U., Schneider T., Perez-Reyes E.;  
RT "Cloning and expression of a novel member of the low voltage-activated



RT T-type calcium channel family.";  
RL J. Neurosci. 19:1912-1921(1999).  
RN [2]  
RP REVISIONS TO 345; 1656 AND 1737.  
RA Perez-Reyes E.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;  
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,  
RA Baillie D.L., Stea A., Snutch T.P.;  
RT "Molecular and functional characterization of a family of rat brain T-  
RT type calcium channels.";  
RL J. Biol. Chem. 276:3999-4011(2001).  
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the  
CC entry of calcium ions into excitable cells and are also involved  
CC in a variety of calcium-dependent processes, including muscle  
CC contraction, hormone or neurotransmitter release, gene expression,  
CC cell motility, cell division and cell death. Isoform alpha-11  
CC gives rise to T-type calcium currents. T-type calcium channels  
CC belong to the "low-voltage activated (LVA)" group and are strongly  
CC blocked by nickel and mibefradil. A particularity of this type of  
CC channels is an opening at quite negative potentials, and a  
CC voltage-dependent inactivation. T-type channels serve pacemaking  
CC functions in both central neurons and cardiac nodal cells and  
CC support calcium signaling in secretory cells and vascular smooth  
CC muscle. They may also be involved in the modulation of firing  
CC patterns of neurons which is important for information processing  
CC as well as in cell growth processes. Gates in voltage ranges  
CC similar to, but higher than alpha 1G or alpha 1H.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Brain.  
CC -!- DOMAIN: Each of the four internal repeats contains five  
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one  
CC positively charged transmembrane segment (S4). S4 segments  
CC probably represent the voltage-sensor and are characterized by a  
CC series of positively charged amino acids at every third position.  
CC -!- PTM: In response to raising of intracellular calcium, the T-type  
CC channels are activated by CaM-kinase II (By similarity).  
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
CC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF086827; AAD17796.2; --  
DR EMBL; AF290214; AAG35188.1; --  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002111; Cat\_channel\_TrpL.  
DR InterPro; IPR002077; Ca\_channel\_alpha.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR005445; TVDCCALpha1.  
DR Pfam; PF00520; Ion\_trans; 4.  
DR PRINTS; PR00167; CCHANNEL.  
DR PRINTS; PR01629; TVDCCALPHA1.  
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;  
KW Ionic channel; Multigene family; Phosphorylation; Repeat;  
KW Transmembrane; Voltage-gated channel.  
FT REPEAT 64 399 I.  
FT REPEAT 584 823 II.  
FT REPEAT 1116 1393 III.  
FT REPEAT 1431 1692 IV.  
FT DOMAIN 1 76 Cytoplasmic (Potential).  
FT TRANSMEM 77 97 S1 of repeat I (Potential).  
FT DOMAIN 98 115 Extracellular (Potential).  
FT TRANSMEM 116 137 S2 of repeat I (Potential).

FT DOMAIN 138 146 Cytoplasmic (Potential).  
FT TRANSMEM 147 166 S3 of repeat I (Potential).  
FT DOMAIN 167 171 Extracellular (Potential).  
FT TRANSMEM 172 189 S4 of repeat I (Potential).  
FT DOMAIN 190 209 Cytoplasmic (Potential).  
FT TRANSMEM 210 230 S5 of repeat I (Potential).  
FT DOMAIN 231 371 Extracellular (Potential).  
FT TRANSMEM 372 396 S6 of repeat I (Potential).  
FT DOMAIN 397 598 Cytoplasmic (Potential).  
FT TRANSMEM 599 619 S1 of repeat II (Potential).  
FT DOMAIN 620 632 Extracellular (Potential).  
FT TRANSMEM 633 654 S2 of repeat II (Potential).  
FT DOMAIN 655 660 Cytoplasmic (Potential).  
FT TRANSMEM 661 679 S3 of repeat II (Potential).  
FT DOMAIN 680 687 Extracellular (Potential).  
FT TRANSMEM 688 711 S4 of repeat II (Potential).  
FT DOMAIN 712 722 Cytoplasmic (Potential).  
FT TRANSMEM 723 743 S5 of repeat II (Potential).  
FT DOMAIN 744 795 Extracellular (Potential).  
FT TRANSMEM 796 820 S6 of repeat II (Potential).  
FT DOMAIN 821 1125 Cytoplasmic (Potential).  
FT TRANSMEM 1126 1148 S1 of repeat III (Potential).  
FT DOMAIN 1149 1166 Extracellular (Potential).  
FT TRANSMEM 1167 1187 S2 of repeat III (Potential).  
FT DOMAIN 1188 1197 Cytoplasmic (Potential).  
FT TRANSMEM 1198 1217 S3 of repeat III (Potential).  
FT DOMAIN 1218 1231 Extracellular (Potential).  
FT TRANSMEM 1232 1253 S4 of repeat III (Potential).  
FT DOMAIN 1254 1263 Cytoplasmic (Potential).  
FT TRANSMEM 1264 1287 S5 of repeat III (Potential).  
FT DOMAIN 1288 1364 Extracellular (Potential).  
FT TRANSMEM 1365 1390 S6 of repeat III (Potential).  
FT DOMAIN 1391 1445 Cytoplasmic (Potential).  
FT TRANSMEM 1446 1466 S1 of repeat IV (Potential).  
FT DOMAIN 1467 1480 Extracellular (Potential).  
FT TRANSMEM 1481 1502 S2 of repeat IV (Potential).  
FT DOMAIN 1503 1509 Cytoplasmic (Potential).  
FT TRANSMEM 1510 1528 S3 of repeat IV (Potential).  
FT DOMAIN 1529 1542 Extracellular (Potential).  
FT TRANSMEM 1543 1566 S4 of repeat IV (Potential).  
FT DOMAIN 1567 1580 Cytoplasmic (Potential).  
FT TRANSMEM 1581 1601 S5 of repeat IV (Potential).  
FT DOMAIN 1602 1664 Extracellular (Potential).  
FT TRANSMEM 1665 1692 S6 of repeat IV (Potential).  
FT DOMAIN 1693 1835 Cytoplasmic (Potential).  
FT SITE 355 Calcium ion selectivity and permeability  
FT SITE 779 (By similarity).  
FT SITE 1339 Calcium ion selectivity and permeability  
FT SITE 1637 (By similarity).  
FT CARBOHYD 171 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 242 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 309 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1301 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1304 N-linked (GlcNAc... ) (Potential).  
FT CONFLICT 193 M -> L (in Ref. 3).  
FT CONFLICT 291 C -> V (in Ref. 3).  
FT CONFLICT 394 V -> L (in Ref. 3).  
FT CONFLICT 406 E -> N (in Ref. 3).  
FT CONFLICT 485 C -> S (in Ref. 3).  
FT CONFLICT 512 D -> Y (in Ref. 3).  
FT CONFLICT 558 S -> R (in Ref. 3).  
FT CONFLICT 683 G -> S (in Ref. 3).  
FT CONFLICT 691 F -> S (in Ref. 3).  
FT CONFLICT 739 MH -> ID (in Ref. 3).  
FT CONFLICT 833 C -> Y (in Ref. 3).  
FT CONFLICT 846 F -> L (in Ref. 3).  
FT CONFLICT 856 S -> R (in Ref. 3).  
FT CONFLICT 905 L -> R (in Ref. 3).  
FT CONFLICT 913 M -> YW (in Ref. 3).

FT	CONFLICT	936	936	W -> G (in Ref. 3).
FT	CONFLICT	996	996	A -> R (in Ref. 3).
FT	CONFLICT	1060	1060	I -> M (in Ref. 3).
FT	CONFLICT	1094	1094	D -> CC (in Ref. 3).
FT	CONFLICT	1197	1198	SS -> TD (in Ref. 3).
FT	CONFLICT	1229	1231	Missing (in Ref. 3).
FT	CONFLICT	1422	1422	K -> Y (in Ref. 3).
FT	CONFLICT	1623	1625	FGM -> SAR (in Ref. 3).
FT	CONFLICT	1656	1656	S -> T (in Ref. 3).
FT	CONFLICT	1737	1737	P -> A (in Ref. 3).
SQ	SEQUENCE	1835	AA; 205348 MW; E6025E0F1BE80CCA	CRC64;
Query Match				
Best Local Similarity 45.2%; Score 5383; DB 1; Length 1835;				
Matches 1139; Conservative 184; Mismatches 344; Indels 336; Gaps 38;				
QY	27	GAGRPGPSAEKDPGSADEAEG----	LPYPALAPVFFYLSQDSRPSWCLRTVCNPW	82
Db	19	GITEQGPSPPPPPGLEPLEGTNPDPVPHDLPAPVAFFCLRQTTSPRNWCIMKVCNPW	78	
QY	83	FERTSMLVILLNCVTGLMFRPCEDIA	QSORCRLQAFDDFIFAFFAVEMVVMVALGIF	142
Db	79	FECVSMVILLNCVTGLMYQPCDDMECLSDRCKILQVDDDFIFIFFAMEMVLKVALGIF	138	
QY	143	GKKCYLGDTWNRDLFFIVIAAGLMEYS	LDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVT	202
Db	139	GKKCYLGDTWNRDLFFIVWAGVVEYS	LDLQNLNSAIRTVRLRPLKAINRVPSMRILVN	198
QY	203	LLLDTLPLMGNVLLLCFFVFFIFIGIV	QVQWAGLLNRCLFPENFSLPLSVDLERYQTE	262
Db	199	LLLDTLPLMGNVLLLCFFVFFIFIGIV	QVQWAGLLNRCLFLEENFTIQGDVALPPYQPE	258
QY	263	NEDESPICQPRENGMRSRCSVP	TLRGDGGGPPCGL-----DYEAYNSSNTT--CV	314
Db	259	EDDEMFCISLTGDNIGMCGCHEIP	PLKEQ---GRECLSDDVYDFGAGQDNLASGLCV	315
QY	315	NWNQYITNCAGEHNPFKGA	INFNDNIGYAWIAIFQVITLEGVVDIMYFMDAHSFYNFYI	374
Db	316	NWNRYNVRTGNANPHKGA	INFNDNIGYAWIVIFQVITLEGVVEIMYVMDAHSFYNFYI	375
QY	375	FILLIIVGSFFMINCLVVIATQ	SETKQRESQLMREQVRFLSNASTLASFSEPGSCYE	434
Db	376	FILLIIVGSFFMINCLVVIATQ	SETKQREHRLMLEQRQYLS-SSTVASYAEPGDCYE	434
QY	435	ELKYLVIYLRKAARRLAQV	SRAAGVRVGLLSSPAPLGQEQETQPSSSCSRSHRRLSVHHL	494
Db	435	EIFQYVCHILRKARRALGLY	QALQNR-----	461
QY	495	VHHHHHHHHYHLGNGTLRA	PRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVH	554
Db	462	-----	-----RQAMG-----PGTPA--PAKPGP----	477
QY	555	SFYHADCHLEPVR	COAPPPRSPSEASGRTVSGKVYPTVHTSPPETLKEKALVEVAASS	614
Db	478	---HAK---	EPHCKLCPRHSPLD-----TPHTLVQP-----	504
QY	615	GPPTLSLNI	PPGPYSSMHKULETQSTGACQSSCKLSSPCLKADSGACGPDSCPYCAR--	672
Db	505	-----	-----ISAILASD-----PSSCPHCQHEA	523
QY	673	---AGAGEVELADREMP	DSDEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVLA-	727
Db	524	GRRPSGLGSTD-SQ	EGSGGSAEAEANGDG-----LQSSSEDGVSSDLGKEEEDGAAR	578
QY	728	---FWRLICDTFRKI	VDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFT	783
Db	579	LCGDVWRETRK	KLGI VDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNI	638
QY	784	SLFALEMLLKL	LVYGPFGYIKPNYINIFDGVIVVISVWEIVGQGGLSVLRTFRLMRVLK	843
Db	639	SMFALEMILK	LAAGFLFDYLRPNYINIFDSIIIVISWEIVGADGGLSVLRTFRLLRVLK	698
QY	844	LVRFLPALQ	RQLVLMKTMNDNVATFCMLLMFLIFIFSILGMHLFGCKFASERD-GDTLPD	902

Db	699	LVRFPALRRQLVLMKTMNDNVATFCMLLMFLIFIFSILGMHIFGCKFSLRTDGTVPD	758			
QY	903	RKNFDSLLWAI	VTVFQILTOEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAI	962		
Db	759	RKNFDSLLWAI	VTVFQILTOEDWNVVLNGMASTTPWASLYFVALMTFGNYVLFNLLVAI	818		
QY	963	LVEGFQAE	EISKREDASGQLSCIQLPVD	SOGGDANKSESEPDFFSPS-----LDG	1012	
Db	819	LVEGFQAE	-----GDANRSCSDEQSSNLEEFDXLPEGLDN	855		
QY	1013	DGDRKKCLALVSLGEHPELRK	SLLPPLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS	1071		
Db	856	SRDLKLCPI	PMTPNGH-----LDP-----SLP-----LGAHLGPAGTMGTAP	892		
QY	1072	SGSAEPG	-----AAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSL	1113		
Db	893	RLSLQDP	PVLVALDSRKSSVMSLGRMSYDQ	RLSSSSSSSYYPGWRSGT	WASRRSSWN--	950
QY	1114	GRAPSLKRRSP	SGERRSLLSGEQESQDEE-ESSEEE---	RASPAGSDH-----	1158	
Db	951	---SLKHKPPSA	EHESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAAHHAHGHPLA	1006		
QY	1159	---RHRGSLER	EAKSFDLPDTLQVPLHRTAS--GRGSASEHQDCNGKSASGLARAL	1212		
Db	1007	HRRHRR	RTLSLDTFSDVLDGELVPVVG	AHRAAWRGAGQAPGHEDCNGRMPNIAKDVT	1066	
QY	1213	RPDDPPLD	GDDADDEGNLSKGERVRAWIRARLPACYLERSWSAYIP	PPQSRFLLCHRI	1272	
Db	1067	KMDRRDRGED	-EEIDYTLCFVRVKMIDVYKPDWCEVREDWSVYLFSPENKFRILCQTI	1125		
QY	1273	ITHKMF	DHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL	1332		
Db	1126	IAHKLF	DYVVLAFILNCITIALERPQIEAGSTERIFLTVSNYIFTAIVGEMTLKVVS	1185		
QY	1333	GWCFGEQ	AYLRSSWNVDGLLVLISVIDILVMSVSDSGTKILGMLRVLRLTLRPLRVI	1392		
Db	1186	GLYFGEQ	AYLRSSWNVDGFLVFSIIDIVSVASAGGAKILGVLRLTLRPLRVI	1245		
QY	1393	SRAQGLK	LVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNITNK	1452		
Db	1246	SRAPGLK	LVVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGFYHCLGVDTRNITNR	1305		
QY	1453	SDCAEAS	YRWRHKYNFNDNLGOALMSLFLVASKDGWVDIMYDGLD	AVGVDQOQPMHNHPW	1512	
Db	1306	SDCVA	ANYRWHHKYNFNDNLGOALMSLFLVASKDGWVIMYNGLD	AVAVDQOQPVTNHNHPW	1365	
QY	1513	MLLYFIS	FLLIIVAFFVLNMFVGVVVENFHKRQHQHEEEARRRREKRLRLEKRRKAQC	1572		
Db	1366	MLLYFIS	FLLIIVSFFVLNMFVGVVVENFHKRQHQHEEARRRREKRLRLEKRRKAQR	1425		
QY	1573	KPYSDY	SRFRLLVHLC	TSHYLDLFIITVIGLNVVTMAMEHYQQPQILDALKICNYIF	1632	
Db	1426	LPYYATY	CPTRLLIHS	MCTSHYLDIFITFICLNVVTMSLEHYNQPTSLTALKYCNYMF	1485	
QY	1633	TVIFVLES	VFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRI	1692		
Db	1486	TTVFVLE	AVLKLVAFLRRFFKDRWNQDLAIVLLSVMGITLEEIEINAALPINPTIIRI	1545		
QY	1693	MRVLIAR	VLKLLKMAVGMRALDVTVMQALPQVGNLGLLMLLFFI	FAALGVLEFGDLEC	1752	
Db	1546	MRVLIAR	VLKLLKMATGMRALDVTVMQALPQVGNLGLLMLLFFI	YAALGVLEFGKLVC	1605	
QY	1753	DETHPCE	GLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--IS	1809		
Db	1606	NDENPCE	GMSRHATFRNFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDSRCLSSQLQFVS	1665		
QY	1810	PIYFVS	SVLTAQFVLNVVIAVLMKHLEESKEAKEAELEAELELEM-KT	LSQPQHSPL	1868	
Db	1666	PLYFVS	SVLTAQFVLNVVIAVLMKHLDSDSKEAQEDAEMDAEIELEMAHGLGPCP----	1721		
QY	1869	CSPFLWP	GVEGPDSPDKPGALHPAAHARSASHFSLEHPTMQHPTELPGPDLLTV---	1925		

Db	1722	-----GPCPG-----PCPCPCPCPCGPRRLPTSSPG	1747
QY	1926	---RKSGVSRTHSLPNDSYMCRH	1945
Db	1748	APGRSGGAGAGG-DTSHLCRH	1769
RESULT 12			
QY	Q7Z6S8	PRELIMINARY;	PRT; 1994 AA.
AC	Q7Z6S8;		
DT	01-OCT-2003	(TReMBLrel. 25, Created)	
DT	01-OCT-2003	(TReMBLrel. 25, Last sequence update)	
DT	01-MAR-2004	(TReMBLrel. 26, Last annotation update)	
DE	DJ17B20.1	(Calcium channel, voltage-dependent, alpha 1I subunit)	
DE	(Fragment).		
GN	Name=CACNAL1;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Phillips S.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL022319; CAD92537.1; -.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005261; P:cation channel activity; IEA.		
DR	GO; GO:0006812; P:cation transport; IEA.		
DR	InterPro; IPR001682; Ca/Na_pore.		
DR	InterPro; IPR002111; Cat_channel_TrpL.		
DR	InterPro; IPR000345; CytC_heme_BS.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR005820; M+channel_nlg.		
DR	Pfam; PF00520; Ion_trans; 4.		
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.		
KW	Ion transport; Ionic channel; Transmembrane; Transport.		
FT	NON_TER 1 1		
SQ	SEQUENCE 1994 AA; 220004 MW; A5EFAE5FA32DCF76 CRC64;		
Query Match			
Best Local Similarity 40.6%; Score 4836; DB 2; Length 1994;			
Matches 1117; Conservative 188; Mismatches 484; Indels 456; Gaps 55;			
QY	197	MRILVTLLDTPMLGNVLLLCFFVFFPIGIVGVQLWAGLLNRCLFPENFSLPSVDLE	256
Db	1	MRILVLLDTPMLGNVLLLCFFVFFPIGIIQVQLWAGLLNRCLFLEENFTIQGDVALP	60
QY	257	RYQTEDESPFICSQPRENGRSCRSVPTLRGDGGGPPCGL-----DYEAYNSSN	310
Db	61	PYYQPEDEMPFICSLSGDNGIMGCHEIPLKEQ---GRECCLSKDDVYDFGAGRQDLN	117
QY	311	TT--CVNWNQYNTCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHS	368
Db	118	ASGLCVNWNRYNVCRGTSANPHKGAINFDNIGYAWIVFQVITLEGWVEIMYVMDAHS	177
QY	369	FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSE	428
Db	178	FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRLS-SSTVASYAE	236
QY	429	PGSCYEELLYILRKAARLAQVSRAAGVRVGLSSPAPLGQETQPSSSCSRSHRR	488
Db	237	PGDCYEETFYVCHILRKAKR-----RALGLYQALQSRRAQALG-----	274
QY	489	LSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSAPPG	548
Db	275	-----PEAPA--PAKPG	284
QY	549	GAESVHSFYHADCHLEPVRCAQPPRSPSEASGRITVSGKVPYTVHTSPPETLKEKALV	608
Db	285	P-----HAK---EPRHYQLCPQHSPLDATPHTL-----VQIPATL-----	317
QY	609	EVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCP	668

Db	318	-----ASDPASCP	325
QY	669	YCAR-----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRSLGPDAP	722
Db	326	CQHEGRRRPSGLSTD-SQEGSGSGSSAGGE--DEADGDGARSSESDGASSELGKEEB	382
QY	723	SSVL-----AFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNA	774
Db	383	EEQADGAVWLCGDVWRETRAKLRGIVDSKYFNRMMAILVNTVSMGIEHHEQPEELTNI	442
QY	775	LEISNIVFTSLFALEMLLKLIVYPPFYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLR	834
Db	443	LEICNVVFTSMFALEMILKLAAPGLFDYLRPNYNIFDSIIVIISIWEIVGQADGGLSVLR	502
QY	835	TFRLMRVLKVRFLPALQROLVVLMTMDNVATFCMLLMLFIFISILGMLHFGCKPASE	894
Db	503	TFRLRLVLKVRFPALRRQLVVLMTMDNVATFCMLLMLFIFISILGMLHFGCKPSLR	562
QY	895	RD-GDTLPDRKNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNY	953
Db	563	TDTGDTVDRKNFDSLLWAIIVTFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGNY	622
QY	954	VLFNLLVAILVEGFOAEISKREDASQLSCIQLPVDSSQGDANKSESEPDFSPS----	1009
Db	623	VLFNLLVAILVEGFOAE-----GDANRSYDEQSSSNIIEEF	659
QY	1010	-----LDGDGDRKKCLALVSLGEHPELRSLLPPLIHTAATPMSLPKSTSTGLGEALG	1063
Db	660	DKLQEGLDSSGDPKLCPIPMTPNGH-----LDP-----SLPLGGLHPAGAAG	702
QY	1064	PASRRT-----SSSGSAEPGAHEMKSPSARSSPHSPWSAASSWTSRRSSR	1110
Db	703	PAPRLSLQDPMLVALGSRKSSVMSLGRMSYDQRLSSRSSSYGPGWGRSAWASRRSSW	762
QY	1111	NSLGRAPSLKRSPSGRRSLLSGE-GQESQDEEESSEE--ERASPAGSDH-----	1158
Db	763	N-----SLKHKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHHIIHGPH	816
QY	1159	-----RHRGSLEREAKSSFDLPTLQVPLGHRHTASGR--GSASEHQDCNGKSASGRLAR	1210
Db	817	LAHRHRHRRRTSLDNRDSVDLAELVPAVGAPRAAWRAAGPAPGHEDCNGRMPSTAKDV	876
QY	1211	ALRPDDPPLDGDADDDEGNLSKGERVRAWIRALPACYLERSWSAYIFPPQSRFRLLCH	1270
Db	877	FTKMGDRGDRGED-EEIIDIYTLCFVRKMDIVYKPDWCVEVDWSVYLFSPENFRVLCQ	935
QY	1271	RIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKV	1330
Db	936	TIIAHKLFDYVVLAFIFLNCITIALERPOIEAGSTERIFLTVSNYIFTAIFVGMTLKV	995
QY	1331	ALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRPLR	1390
Db	996	SLGLYFGEQAYLRSSWNVLDGLVLFVSVIIVVSLASAGGAKILGLVLRVLRLLTLRPLR	1055
QY	1391	VISRAQGLKVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNIT	1450
Db	1056	VISRAPGLKVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGEDTRNIT	1115
QY	1451	NKSDCAEASRYRWRHKYNFNLGQALMSLFLVLSKDGWVDIMYDGLDVGVDQOQIMNHN	1510
Db	1116	NRSDCMAANYRWHKYNFNLGQALMSLFLVLSKDGWVIMYNGLDVAVDQOQVPTNHN	1175
QY	1511	PWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRHQHEEEAARRRREKRLRLEKRRKA	1570
Db	1176	PWMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRHQHEEEAARRRREKRLRLEKRRKA	1235
QY	1571	QCKPYSDYSRFRLLVHLCTSHYLDLFTITVIGLVNVTWAMEHYQQOQILDEALKICNY	1630
Db	1236	QRLPYATYCHTRLLIHSMTCTSHYLDLFTITVIGLVNVTWAMEHYQQOQILDEALKICNY	1295
QY	1631	IFTVIFVLESVFKLVAFGRFRFFQDRWNQLDLAIVLLSIMGITLEEIEVNASLPINPTII	1690

Db 1296 MFTTVFVLEAVLKLVAFLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTII 1355

QY 1691 RIMRVLIARVLKLLKMAVGRALLDTVMQALPQVGNLGLLMLLFFIFAALGVELFGDL 1750

Db 1356 RIMRVLIARVLKLLKMATGRALLDTVVQALPQVGNLGLLMLLFFIYAALGVELFGKL 1415

QY 1751 ECDETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDC-DQESTCYNTV-- 1807

Db 1416 VCNDENPCEGMSRHAFTFENFGMAFLTLFQVSTGDNWNGIMKOTLRDCTHDSRCLSSLOF 1475

QY 1808 ISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAELLEM-KTLPSPQHS 1866

Db 1476 VSPLYFVSFVLTAQFVLINVVAVLMKHLDDSNKEAQEDAEMDAELELEMAHGLGPGRL 1535

QY 1867 PLGSPFLWPGEVGPD-----SP-----D 1884

Db 1536 PTGSPGA-PG-RGPGGAGGGGTGGLCRRCYSPAQENLWDSVSLIIKDSLEGELTIID 1593

QY 1885 SPKPGALH-----PAA-----HARSAS-----HFSLEHPTMQP- 1912

Db 1594 NLGSIFFHYSSPAGCKKHDKQEVQLAETEAFSLNSDRSSILLGDDLSLEDPTACPP 1653

QY 1913 ---HPTELPGPDLLTVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLHGRWGGLPK 1962

Db 1654 GRKDSKGELDPPEPMRVGDLGECFFPLSSTAVSPDENFELCEMEEIPFNPV--RSW--LK 1709

QY 1963 AQSGSVLSVHSQPADTSYIOLPKDAPH-----LLQPHSAPTGWTIKLPPLPPG-----R 2011

Db 1710 HDSSQAPPSPPSPDASSPLLPMPAEFFHPAVSASQKPEKGTGTGLPKIALQGSWASLR 1769

QY 2012 SPLAQRPLRRQAAIIRTDLDVQGLGSRREDLLAEVSGSPPLARAYSFWGOSSTQAQHSR 2071

Db 1770 SPRVNCVTLRQATGSDTSLD-----ASPSSAGSLQTTLEDLSLTLSDSPRR 1815

QY 2072 SHSKISKHMTPPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDLPLPGQGEPPSPRD 2131

Db 1816 A-----LGPPAPAPGPRAGLS---PAARRLSL-----RGRG 1844

QY 2132 LKKCVSVEAQSCORRPTSWLDEQRRHSIAVCLDSGSQPHLGTDPNS---LGQPLGGPG 2188

Db 1845 LFLSLGLRA-----HQRSHSSGGS-TSPGCTHDSMDPSDEGRGGAGGGGAG 1891

QY 2189 SRPKKLSPPSIT---IDPESQGPRTPPSPGICLRRRAPSSDS---KDPLASGPPDSM 2241

Db 1892 SEHSETLSLSLTSLFCPPP-----PPAPGLTPARKFSSSTSLAAPGRPHAAALAHGL 1945

QY 2242 AASPSPKDVLSSLGSLSDPADLDP 2266

Db 1946 ARSPSWAAD-----RSKDPGGRAP 1964

RESULT 13

Q7PQV4

ID Q7PQV4 PRELIMINARY; PRT; 1762 AA.

AC Q7PQV4;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE ENSANGP0000003024 (Fragment).

GN Name=ENSANGG0000002480;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

OX NCBI\_TaxID=180454;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PEST;

RA Anopheles Genome Sequencing Consortium;

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AAB0100859; EAA08229.2; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR001682; Ca/Na\_pore.

DR InterPro; IPR002111; Cat\_channel\_TrpL.

DR InterPro; IPR005821; Ion\_trans.

DR InterPro; IPR005820; M+channel\_nlg.

DR InterPro; IPR005445; TVDCCAlphal.

DR Pfam; PF00520; Ion\_trans\_4.

DR PRINTS; PRO1629; TVDCCAlphal.

KW Ion transport; Ionic channel; Transmembrane; Transport.

FT NON\_TER 1

FT NON\_TER 1762 1762

SQ SEQUENCE 1762 AA; 199928 MW; AF70F5349068EDE2 CRC64;

Query Match 35.3%; Score 4200.5; DB 2; Length 1762;

Best Local Similarity 48.6%; Pred. No. 8.8e-183;

Matches 923; Conservative 268; Mismatches 446; Indels 261; Gaps 48;

QY 82 WFERISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIAFFAVEMVVKMVALGI 141

Db 2 WFERISMLVILLNCVTILGMYPQCVDDACVTNCKILQIFDDIIFAFSLEMTIKIVAMGA 61

QY 142 FGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSPSAVRTVRVLRPLRAINRVPSMRILV 201

Db 62 WKGKGYLADSWNRDLDFIVLAGALEYCLQVENLNLTAIRTIRVLRPLRAINRIPSMRILV 121

QY 202 TLLDRTLPLMGNVLLCFFVFFIFGIVGVQLWAGLLNRCF--LPENFSLPLSVDLERY 259

Db 122 MLLDRTLPLMGNVLLCFFVFFIFGIVGVQLWEGILRQRCVILKLPDQNVSPPSYLVSFY 180

QY 260 QTENEDESPFICSPRENGMRSRCSVPTLRDGGGGP----PCGLDYEAYNSSNTTCVN 315

Db 181 EFSKEQD--YICSKPEDSGMHLCQNLPPYR----IGPLLNCDSALPY-SENEPTATACVN 233

QY 316 WNOYITNCISAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNIYF 375

Db 234 WNOYITNCTQLGNNPFQGTISFDNIGLAWAIFLVISLEGWTDIMYVQDAHSFWDWIYF 293

QY 376 ILLIIVGSFFMINCLVVIATQFSETKQRESQIMREQVRFLSNASTILASF---SEPGSC 432

Db 294 VLLIVIGSFFMINCLVVIATQFSETKKREMRMRQERARFTS-SSILASSTNNSEPTTC 352

QY 433 YEELLKYLVIILKAAARLAQVSRAAGVRV----GLLSSPAPLGGQETQPSSSCSRSHR 487

Db 353 YAEIVKYIGHLYRRFRRLIKRLLYKYHMQKKEGLI-----PCTPETI 397

QY 488 RLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSR----- 530

Db 398 TLSPNKIKAHHP-----KCPRMGALLQQQHASITNLQQQKNKHDLQSSLSIN 444

QY 531 ---RLMLPPPSTPALSG---APPGAESV-----HSFYHADCHLEPVRCQA---PPP 573

Db 445 RTGVTLNHPPEGTIVPSADNQVSSPEVSEIVSLENIKNNALNNSTTYLNEDRQKVLLKI 504

QY 574 RSPSEASGRITVSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTL---TSLNIPPGPYS 630

Db 505 NNEDQSQNGQVRGMGLWGMVW-----EGRSTFEQSSSLAPQDDHH 545

QY 631 SMHKLLETQSTGACQSSC-----KISSP-----CL-KADSGACGPDSD---C 667

Db 546 CMPSLLSPPSAGRRRRSSVMFNEYVVLHTPTTTEPPQDKNVYCLEKMTQAAANPATSRRA 605

QY 668 PYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVLA 727

Db 606 PASTRCRCPASTTSTWPSLPAATST-----TKTRAWRRRRSDRS-APSARGRSSWR 653

QY 728 FWRLICDTFR---KIVDSKYFGRGIMIALVNTLSMGIEYHEQPEELTNALEISNIVFT 783

Db 654 CFRRTCHLTRVLVKLVVDHKYFQOGILLAILINTLSMGIEYHDQPAELTAIVETSNI VFS 713









Db 1352 PPIITTAATPQDSPSTTLEPGMSFRQWGMEDPPSPSPSLRPPNIFTGGQSLDEGIP 1411  
QY 1055 -----STGLGEALG-----PASRRTSSGSA 1075  
Db 1412 SIDLPPSPVLSHKPLNILNASQLGVGMGGVPSTAGSSSMHSHVIIDISKSSSTAAA 1471  
QY 1076 EPGAHEMKSPPSARSSPHS-----PWSAAS-----SWTSRRSSRNSLGR 1115  
Db 1472 TPIYVPTISSTADAQSQSHSLNDVSVGSSPGGEIPATGMSRNVANTGASTGSSSERLPL 1531  
QY 1116 AP-----SLK---RRSPSGERS-----LLSGEGESQDEE----- 1144  
Db 1532 APPPOQGSFKQLRRGSSKKRRASALALATDDNPARRTLDNQARRTQDEEEEQQLNNGG 1591  
QY 1145 -----SSEERASPAGSDHRRHRSGL-----ERAKS---SFDL 1174  
Db 1592 DNSCLLRNSNAVVGSSSGTKETNRLSPONSIRRLSNTLSIGSGPVGSRASACIFNSQV 1651  
QY 1175 PDTLQVPLHRTASGRGSA-----EHQDCNGKSAS----- 1205  
Db 1652 YQNLNPPKLRPGSGQRRMSSIELAFSKTSHLNLHNEANRKSLSYTNKMDLDKWNKSY 1711  
QY 1206 GRLARALRPDDPLDGDADDEG-----NLK----- 1232  
Db 1712 GNLN---EPDNMLQOYMEARDKRNKNSISHYNLKKRLEBKELQQLHQQLQQRQDSF 1768  
QY 1233 -----GER---VRAWIRARLPACY-LERDSW 1254  
Db 1769 SSTTQQOQQQLQHLRSKDOQLAMQPHSMVPGGGERYSKLMLEQLTPKHFTTEREDY 1828  
QY 1255 SAYIFPQSRFRLLCHRIITHKMFHDHVLVIIFLNCITIAMERP KIDPHSAERIFLTLSN 1314  
Db 1829 SLYIFEDNRFRQICTWFFVNQKWFNDVLLFIALNCITIAMERNIPSPSTERLFLATAN 1888  
QY 1315 YIFTAVFLAEMTVKVALGWCGEQAYLRSSWNLVGLLVLSVIDILVMSVSDSGTKIL 1374  
Db 1889 YVFTVVTVMEMFIKVATGMFYGHDAYFTSGWNIMDGLSVTISIIDLMSLISESSPRIF 1948  
QY 1375 GMLRVLLRLTLRPLRVISRAQGLKLVVETLMSLXKPIGNIVWICCAFFIIFGILGVQLF 1434  
Db 1949 GILRVFRLRLSRPLRVINRAPGLKLVVQTLSSLRPIGNIVLICCTFFIIFGILGVQLF 2008  
QY 1435 KGKFFVCOGEDTRNITNKSDCABASYR-WVRHKYNFDNLQALMSLFLVASKDGWVDIMY 1493  
Db 2009 KGTFYCEGENIKGVRNADECRRIPGNVWTRNRYNFDLKGALMSLFLVSSRDGWVNIMY 2068  
QY 1494 DGLDAVGVDQOQPIMNHPNMLLYFISFLILVAFVFLNMFVGVVVENFHKRCRQHEEEAR 1553  
Db 2069 TGLDAVGVDQOQPIVNYNEWRLLYFIALLVGVFFVFLNMFVGVVVENFHRCREEQKEEKI 2128  
QY 1554 RREEKRLRLEKKRRKAQCKPYDYSRFRLLVHLCTSHYLDLFTITVIGLVNVTMAME 1613  
Db 2129 RRAAKRALQMEKKRRRMHEPPYTYNYSPTRMFVHNVVTSKYFDLAIAAVIGLVNVTMAME 2188  
QY 1614 HYQPOQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQOLDLAIVLLSIMGIT 1673  
Db 2189 YKMPSPGLKYALKIFNYFFTAFFILEANMKLVALGWKLYLKDRWNQLDVGIVLLSIVGIV 2248  
QY 1674 LEEIEVNAS--LPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTVMQALPOVGNLGLL 1731  
Db 2249 LEELETNTHQIIPINPTIIRVMRVLRIARVLKLLKMANGIRALLDVTVMQALPOVGNLGLL 2308  
QY 1732 FMLLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMK 1791  
Db 2309 FFLFFIFAALGVLEFGRLCESDIIPCQGLGEHAHFANFGMAFLTLFRVATGDNWNGIMK 2368  
QY 1792 DTLRD-CDQ-----ESTCYNTVTSPIYFVSFVLTAQFVLNVVIVAVLMKHLSESNKEAKE 1845  
Db 2369 DTLRNCDDAADCVRNCCVSSVIAPIFFVIFVLMAQFVLNVVIVAVLMKHLSESHKQMED 2428  
QY 1846 EAELEAELELEM-----KTLSPQPHSL-----GSPFL- 1873

Db 2429 ELDMEVELERELVREQEFAQEQKLCQQLAEAAQSKAAAPRPLAKVKSLPKNFYIYTPSLD 2488  
QY 1874 --WPGVEGPDSPD-----SPKPGALHPAAHAARSASHFSLEHPTMQPH 1913  
Db 2489 KKFPAVSGVNNPSLTSSAATNLNQVATAGSGGAAPGAV-PAGSGAGPRRTQVY-FQQPP 2546  
QY 1914 PTELPGPDL-----LT-----VRKSGV----- 1930  
Db 2547 QSMGLGSLAEMGGTLTPQALCARLGEFPGGGGNGKSGPRRQSYWQINPIRKRGVLSKER 2606  
QY 1931 -----SRT--HSLP--NDSYMCRHGSGTAB-----GPIGHRGWGLP 1961  
Db 2607 SLDEQAIRRRNLEAKRTSCDSLPGWGDALDCRRGTIFESLESDGGVGGGGGGGGLG 2666  
QY 1962 KAQSGSVLSV-----HSQ-----PADTSYI---LQLPKDAPHLLQPHSAP 1998  
Db 2667 GGVSYDLRSVRADVGHSEMDGDVLSVVSALVPSVTPLPPLSLP-----IVTPTSTP 2721  
QY 1999 TWGTIP-KLPPPGRSPLAQRLRRQAAIRTDLSLVQGLSREDLLAEVSGSPPLARAYS 2057  
Db 2722 T-----PLQLPMPMPMAHPHPPRRPFG-WSQSV-DQC-LRSNLLSVSRMPPRSRSGS 2774  
QY 2058 FWQGSSTQAQHSRSHSKISHMTTPPAPCPGPEPNWKGKPPPE---TRSSLELDTLSWI 2113  
Db 2775 TKQLFKQALDEADMDENS--LLLPTAAG-----GSGPGSVAVIASSSLDLPDQ-SGS 2826  
QY 2114 SGDLLP 2119  
Db 2827 SKQILP 2832  
  
RESULT 15  
Q967R4  
ID Q967R4 PRELIMINARY; PRT; 1837 AA.  
AC Q967R4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Voltage-dependent calcium channel alpha13 subunit (T-type calcium  
DE channel alpha1 subunit isoform A) (Calcium channel, alpha subunit  
DE protein 1, isoform a).  
GN Name=cca-1; ORFNames=C54D2.5;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mittman S.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Steger K.A., Thacker C., Snutch T.P., Avery L.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Minx M.;  
RT "The sequence of C. elegans cosmid C54D2.";  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
DR EMBL; AF368920; AAK53427.1; -.
DR EMBL; AY313898; AAP79881.1; -.
DR EMBL; U37548; AAM51534.1; -.
DR WormBase; WBGene0000367; cca-1.
DR WormPep; C54D2.5a; CE30919.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005891; C: voltage-gated calcium channel complex; IEA.
DR GO; GO:0005261; F: cation channel activity; IEA.
DR GO; GO:0005245; F: voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P: calcium ion transport; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR001682; Ca\_Na\_pore.
DR InterPro; IPR002111; Cat\_channel\_TrpL.
DR InterPro; IPR02077; Ca\_channel\_alpha.
DR InterPro; IPR005821; Ion\_trans.
DR InterPro; IPR005820; M\_channel\_nlg.
DR InterPro; IPR005445; TVDCCALpha1.
DR Pfam; PF00520; Ion\_trans\_4.
DR PRINTS; PR00167; CCHANNEL.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
SQ SEQUENCE 1837 AA; 210160 MW; 113367B5298A49B5 CRC64;

Query Match 32.4%; Score 3855; DB 2; Length 1837;
Best Local Similarity 43.0%; Pred. No. 4.8e-167;
Matches 897; Conservative 267; Mismatches 514; Indels 406; Gaps 58;

QY 15 QPSFMRNLDSGAGGRPG-----PGSAEKDPG-----SADSEA 48
DQ 39 QSQSTRHEDVEALGSIEGSKETQLSEHGRGLASSSEASPSRWEGRQIEWGNEEQIEES 98
QY 49 EGLYPALAPVFFYLSQSRPSRWCLRTVCNPNWFERISMLVILLNCVTGLGMRPCED-I 107
DQ 99 E-LPYGFAEPALRCFYQARPPRKWALQVMVMSPFDRITMAVIMINCVTLGMYRPCEDGP 157
QY 108 ACDSQRCRILQAFDDFIFAFPAFVEMVVKMVALGIFGKKCYLGDTWNRDLDFIVIAGMLEY 167
DQ 158 DCDTYRCQILDIIIDNCIFVYFAPFEMVIKIMALGFYGPAAAYMSDTWNRDLDFIVMAGIAEF 217
QY 168 SLDLQ--NVSFSAVRTVRPLRPLRAINRVPSMRILVTLTLLDTLPMGLGNVLLCCFFVFFI 224
DQ 218 VLHEVYLGNNINLTARTVRVLRPLRAVNRIPSMRILVNLLDTLPMGLGNVLLCCFFVFFI 277
QY 225 FGIVGVQLWAGLLRNRCF--LPENFS-----LPLSVDLERYQYOTENEDESPFICSQPREN 277
DQ 278 FGIVGVQLWAGLLRNRCVNLNPKTISENQSALEFNNVKLTRFYIPE-DTSLEYICSDPAN 336
QY 278 GMRSCRSVPTLRGDDGGGPPCGLDYEAYNSSNTVCNWNQYTNCSAGEHNPFKGAINF 337
DQ 337 GLHTCSNLPPTVD---GVKCNLTLDYDKVTNDSICINWNIYNECQVMQRNPFQGSVSF 393
QY 338 DNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINCLVVIATQ 397

DQ 394 DNIGFAWVAIFLVISLEGWTDIMYYVQDAHSFNNWIYFVLLIVIGAFFMINCLVVIATQ 453
QY 398 FSETKQRESQLMREQVRFLSNASTLASFSEPG-----SCYEELLYLVYILRKAA 448
DQ 454 FAETKRRETERMLQERKMLLRDSDISCTGSEIGGASSKEEGDTVYAAFVRFIGHTFERR-T 512
QY 449 RRLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLG 508
DQ 513 KRAAKKKTAYMEE----- 526
QY 509 NGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVR 568
DQ 527 ----RAERKSSERQOR----RKSCLDDMAT--LS----- 550
QY 569 QAPPRSPSEASGRVTGSKVYPTVHTSPPPETLKEKALVEVAASSGPPPTLTSLNIPPGP 628
DQ 551 -----RIEKAED-----EDETITREN----- 569
QY 629 YSSMHKLLLETQSTGACQSSCKI-SSPCLKADSGACGPDSCPYCARAGAGEVELADREMPD 687
DQ 570 ---GDDQIEQNGDGVRIKRVKIEEPKIKIGN---GNSNGPHYKHSSE----- 613
QY 688 SDSEAVYEFTQDAQHSDLRDPHSRRORSGLPDAEPSSVLAFWRLLICDTFRKIVDSKYFGR 747
DQ 614 -----EDEDGEEDQVYDGEAAKKS-----TPSKL--WW--FREKIQKFVICDHFT 657
QY 748 GIMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGFYIKNPY 807
DQ 658 GILVAILVNTLSMGVEYHQPEILTVILEYSNLFPTALFALEMLLKIISGLFGYLADGF 717
QY 808 NIFDGVIVVISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVVLMTMDNVAT 867
DQ 718 NLDGGIVALSVLELFEQEGKGLSVLRTFRLLRLKLVRFMPALRYQLVVMRLTMDNVT 777
QY 868 FCMLLMFLFIFISILGMHLFGCKFASERD---GDTLP--DRKNFDSLWAIIVTVFOILTQ 922
DQ 778 FFGLLVLFIFISILGMNLFGCKFCKVEEKLGLAKKCKERKNFDTLLWALITVFOILTQ 837
QY 923 EDWNVLYNGMASTSWAALYFIALMTFGNVYVFNLLVAILVEGFQABEISKREDASGQL 982
DQ 838 EDWNVLFNGMAQTPNWAALYFVALMTFGNVYVFNLLVAILVEGFQE---SKEE----- 889
QY 983 SCTQLPVDSQGDANKSESEPFFSPSLDGDGRKKCLALVSLGHEPBLRKSLLPLLIH 1042
DQ 890 -----KRQLEEDARKQAVEEEDERKRELEI----- 915
QY 1043 TAATPMSLPKSTSTGLGEALGPASRRSTSSGSAEPGAHAHEMKSPSARSSPHSPWSAASS 1102
DQ 916 -----IAKTSPAFNNGVAPA-----ECTQRPSSPEESPRLLSANYH----- 955
QY 1103 WTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLSGEQESQDEEESSEERASPA 1157
DQ 956 -----PSPERKHSANLDAIIDKRLV-----RNSAPFDR-SPV-SE 989
QY 1158 HRHRSGLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQDCN-----GK----- 1202
DQ 990 GRDDSRNLNRHA--SLVLPVANGVPYRRQRVHSWGLCHHFNPCPVHGRRALIETYAREK 1047
QY 1203 --SASGRALARALRPDDPPLDGDADDEGNLSKGE-RVRAWIRARL-PACYLERDSWSAYI 1258
DQ 1048 FLEASQELKQAL-----AEEE---KRNEAKQNTFVRKLLKKTCLHNRTEFSLFL 1093
QY 1259 FPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
DQ 1094 MGPKNPLRIKCLQTQKKWFDYTVLFFIGINCITLAMERPSIPDPSPERQFLHISGYIFT 1153
QY 1319 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLDTLLVLSVIDILVSMVSDSGT-KILGML 1377
DQ 1154 VIFTGEMMKVIANGCFIGQAAFYKDGWNILDGILVVISLINIAFELLATGDSPKIFGVI 1213
QY 1378 RVLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGK 1437
DQ 1214 RVLRLRLRPLRVINRAPGVKLVVMTLISLKPIGNIVLICCTFFIIFGILGVQLFKGM 1273



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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 00:03:00 ; Search time 20628 Seconds  
(without alignments)  
5322.839 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAEESGQPRSFM.....PKKDVLSLSSDPADLDP 2266

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-O=/cgn2 1/USPTO spool/US09611257/runat 13042005 170152 155/app\_query.fasta\_1.2439  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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Database :

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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	11877.5	99.8	6822	6 AR201014	AR201014 Sequence
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4	11877.5	99.8	7741	6 AR201015	AR201015 Sequence

5	11872	99.7	6855	9 AF227749	AF227749 Homo sapi
6	11843.5	99.5	6966	9 AF227745	AF227745 Homo sapi
7	11838	99.4	6999	9 AF227750	AF227750 Homo sapi
8	11815.5	99.3	7648	9 AF134986	AF134986 Homo sapi
9	11758.5	98.8	7253	9 AF126965	AF126965 Homo sapi
10	11741	98.6	7274	9 AF126966	AF126966 Homo sapi
11	11741	98.6	7349	9 AF190860	AF190860 Homo sapi
12	11735.5	98.6	6786	9 AF227747	AF227747 Homo sapi
13	11707	98.3	6897	9 AF227746	AF227746 Homo sapi
14	11703	98.3	6921	9 AF227748	AF227748 Homo sapi
15	11251.5	94.5	7030	9 AF134985	AF134985 Homo sapi
16	11246.5	94.5	7030	6 CQ724231	CQ724231 Sequence
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18	11111	93.3	7129	6 BD224078	BD224078 T-type ca
19	11111	93.3	7285	6 BD224079	BD224079 T-type ca
20	11111	93.3	7286	10 AF125161	AF125161 Rattus no
21	10945	91.9	6942	10 AF290212	AF290212 Rattus no
22	10945	91.9	7542	10 RNCAA1G	AF027984 Rattus no
23	10913	91.7	7527	10 BC057399	BC057399 Mus muscu
24	10890.5	91.5	7540	6 AX068898	AX068898 Sequence
25	8977	75.4	5475	9 AB032949	AB032949 Homo sapi
26	7705	64.7	4903	9 AB012043	AB012043 Homo sapi
27	6573	55.2	4944	10 AK129294	AK129294 Mus muscu
28	6315.5	53.1	3993	9 AF124351	AF124351 Homo sapi
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30	6223	52.3	8447	6 AX068900	AX068900 Sequence
31	6222.5	52.3	7868	10 AF290213	AF290213 Rattus no
32	6215.5	52.2	7898	6 BD087035	BD087035 Calcium c
33	6215.5	52.2	7898	9 AF073931	AF073931 Homo sapi
34	6214.5	52.2	7898	6 BD087032	BD087032 Calcium c
35	6211.5	52.2	7762	9 AF051946	AF051946 Homo sapi
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37	5637.5	47.4	6924	6 CQ730788	CQ730788 Sequence
38	5496.5	46.2	6990	9 AF142567	AF142567 Homo sapi
39	5493	46.1	6911	10 AF086827	AF086827 Rattus no
40	5492.5	46.1	6816	6 AR175747	AR175747 Sequence
41	5492.5	46.1	6816	6 AR352550	AR352550 Sequence
42	5484	46.1	6855	6 AR175748	AR175748 Sequence
43	5484	46.1	6855	6 AR352551	AR352551 Sequence
44	5484	46.1	9896	9 AF393329	AF393329 Homo sapi
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ALIGNMENTS

RESULT 1	AF227751	6801 bp	mRNA	linear	PRI 06-MAR-2000
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DEFINITION	AF227751	AF227751.1	GI:7159274		
ACCESSION	AF227751				
VERSION	AF227751.1				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 6801)			
AUTHORS	Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.				
TITLE	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels.				
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)				
MEDLINE	20158909				
PUBMED	10692398				
REFERENCE	2	(bases 1 to 6801)			
AUTHORS	Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)				
FEATURES	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France				
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AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.  
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QY 1221 GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
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QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
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QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
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QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
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QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033  
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RESULT 3  
AF227744 6822 bp mRNA linear PRI 06-MAR-2000  
LOCUS Homo sapiens voltage-dependent calcium channel alpha 1G subunit  
DEFINITION isoform ae (CACNA1G) mRNA, complete cds.  
ACCESSION AF227744  
VERSION AF227744.1 GI:7159260  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 6822)  
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.





QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Dbb 1021 GGCTATGCTGGATCGCCATCTTCCAGGTTCATCACGCTGGAGGGCTGGGTCCGACATCATG 1080  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380  
Dbb 1081 TACTTTGTGATGGATGCTCATCTTCTTCTACAAATTCATCTACTTTCATCTCCTCATCATC 1140  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
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ORGANISM Unknown.  
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AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.  
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Db	6463	CAGCCAGCAGATACCACTACATCCTGCAGCTTCCCAAGATGCACCTCATCTGCTCCAG	6522
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LOCUS AF227749 6855 bp mRNA linear PRI 06-MAR-2000  
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isoform bce (CACNA1G) mRNA, complete cds.  
ACCESSION AF227749  
VERSION AF227749.1 GI:7159270  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 6855)  
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.  
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels  
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)  
MEDLINE 20158909  
PUBMED 10692398  
REFERENCE 2 (bases 1 to 6855)  
AUTHORS Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.  
TITLE Direct Submission  
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)  
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France  
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ORIGIN

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Percent Similarity: 99.12% Mismatches: 1  
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REFERENCE 1 (bases 1 to 6966)  
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.  
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels  
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)  
MEDLINE 20158909  
PUBMED 10692398  
REFERENCE 2 (bases 1 to 6966)  
AUTHORS Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.  
TITLE Direct Submission  
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.) U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France  
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CDS

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ORIGIN

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Db	781	ACAGAAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACCGGAGAACGCGCATCGG	840	
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu	300	
Db	841	TCCTGCAAGCGTGTCCACGCTGCGGGGACGGGGGGCGGTGGCCCACTTGGGTCTG	900	
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr	320	
Db	901	GACTATGAGGCCCTACACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC	960	
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340	
Db	961	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTTGACAAACATT	1020	
QY	341	GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet	360	
Db	1021	GGCTATGCTGGATCGCCATCTTCCAGGTTCATCAGCTGGAGGGCTGGGTCCGACATCATG	1080	
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380	
Db	1081	TACTTTGTGATGGATGCTCATCTTCTTCTACAATTTCTACTTCTTCTCTCTCATCATC	1140	
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu	400	
Db	1141	GTGGGCTCCTTCTTTCATGATCAACCTGTGCCTGGTGGTGATGGCCAGCAGTCTCTCAGAG	1200	
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420	
Db	1201	ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCCTGTCCACAGCC	1260	
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440	



Db ||||| 1261 AGCACCTGGCTAGCTTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1320  
QY ||||| 441 ValTyrIleLeuArgLysAlaAlaAArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db ||||| 1321 GTGTACATCCTTCGTAAGGCAGCCCGCAGGTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380  
QY ||||| 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db ||||| 1381 CGGGTTGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC 1440  
QY ||||| 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
Db ||||| 1441 AGCTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACCTGGTGACACCACCCACCAC 1500  
QY ||||| 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db ||||| 1501 CATCACCACTACCACTGGCAATGGGTCCTCCGCGGCTCATGCTGTCACCACTCGACGCCT 1560  
QY ||||| 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Db ||||| 1561 ATCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGCTGTCACCACTCGACGCCT 1620  
QY ||||| 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db ||||| 1621 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1680  
QY ||||| 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
Db ||||| 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGGCCCCCTCCAGGTCCCATCTGAGGCATCC 1740  
QY ||||| 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
Db ||||| 1741 GGCAGGACTGTGGCAGCGGAAGGTGTATCCACCGTGCACACCCAGCCCTCCACCCGAG 1800  
QY ||||| 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
Db ||||| 1801 ACGCTGAAGGAGAGGCACTAGTAGAGTGGTGCCAGCTCTGGGCCCCCAACCTCACC 1860  
QY ||||| 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db ||||| 1861 AGCCTCAACATCCACCCCGGCCCTACAGTCCATGCACAAGCTGCTGGAGACACAGAT 1920  
QY ||||| 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db ||||| 1921 ACAGGTGCCTGCCAAAGCTCTTGCAAGATCCAGCCCTTCTGAAAGCAGACAGTGA 1980  
QY ||||| 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db ||||| 1981 GCCTGTGTTCCAGACAGCTGCCCTACTGTGCCGGCGCGGGCAGGGAGGTGGAGTTC 2040  
QY ||||| 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db ||||| 2041 GCCGACCGTGAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTTACACAGGATGCC 2100  
QY ||||| 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Db ||||| 2101 CAGCACAGCGACCTCCGGGACCCCCACAGCGCGGGCAACGGAGCCTGGGCCAGATGCA 2160  
QY ||||| 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740  
Db ||||| 2161 GAGCCCAGCTCTGTGTGGCCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220  
QY ||||| 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
Db ||||| 2221 GACAGCAAGTACTTTTGGCCGGGAATCATGATCGCCATCCTTGGTCAACACACACTCAGCATG 2280  
QY ||||| 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Db ||||| 2281 GGCATCGAATACCAACGAGCAGCCCGAGGAGTTACCAACGCCCTTAGAAATCAGCAACATC 2340  
QY ||||| 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800

Db ||||| 2341 GTCTTACCAGCCTCTTTGGCCCTGGAGATGCTGTGAAGCTGCTGTGTATGGTCCCTTT 2400  
QY ||||| 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820  
Db ||||| 2401 GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTCAATGTGGTTCATCAGCGTGTGG 2460  
QY ||||| 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
Db ||||| 2461 GAGATCGTGGGCCAGCAGGGGGCGGCTGTCTGGTGTCTCGGACCTTCCGCCGTGATGEGT 2520  
QY ||||| 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
Db ||||| 2521 GTGCTGAAGCTGGTGGCTTCTCTCGCGCGCTGCAGCGGCAGCTGGTGGTCTCATGAAG 2580  
QY ||||| 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
Db ||||| 2581 ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTTCATCTT 2640  
QY ||||| 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
Db ||||| 2641 ATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCTG 2700  
QY ||||| 901 ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu 920  
Db ||||| 2701 CCAGACCGGAAGAATTTGACTCTCTGCTTGGGCCATCGTCACTGTCTTTCAGATCCTG 2760  
QY ||||| 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
Db ||||| 2761 ACCCAGGAGGACTGGAAACAAAGTCTCTACAATGGTATGGCCTCCACGTCGTCCTGGGCG 2820  
QY ||||| 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
Db ||||| 2821 GCCCTTTATTTTCATTGCCCTCATGACCTTCGGCAACTACGTCCTTCAATTTGTGTC 2880  
QY ||||| 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
Db ||||| 2881 GCCATTCTGTGGAGGGCTTCCAGCGGAGGAAATCAGCAAACGGGAAGATGCGAGTGA 2940  
QY ||||| 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
Db ||||| 2941 CAGTTAAGCTGTATTTCAGCTGCCTGTCGACTCCAGGGGGAGATGCCAACAAAGTCCGAA 3000  
QY ||||| 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
Db ||||| 3001 TCAGAGCCCCGATTTCTTCTCACCCAGCCTGGATGGTGTATGGGACAGGAAGAAGTGTG 3060  
QY ||||| 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040  
Db ||||| 3061 GCCTTGGTGTCCCTGGGAGAGCACCCCGAGCTGCGGAAGAGCTGCTGCCGCCCTCTCATC 3120  
QY ||||| 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
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QY ||||| 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
Db ||||| 3181 GCGCTGGGCCCTGCGTCGCGCCGCACAGCAGCAGCGGGTCCGAGAGCCTGGGGCGGCC 3240  
QY ||||| 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
Db ||||| 3241 CACGAGATGAAGTCAACCGCCAGCGCCCGCAGCTCTCCGCACACGCCCTTGAGCGCTGCA 3300  
QY ||||| 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
Db ||||| 3301 AGCAGCTGGACACAGAGGGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3360  
QY ||||| 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln 1140  
Db ||||| 3361 CGGAGAAAGCCCAAGTGGAGAGCGCGGTCCCTGTTGTCCGGAGAAGGCCAGGAGGCCAG 3420  
QY ||||| 1141 AspGluGluSerSerGluGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln 1160  
Db ||||| 3421 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTTGGGGCAGTGACCATCGCCAC 3480

QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
DB	3481	AGGGGTCCTGGAGCGGAGGCCAAGAGTTTCCTTTGACCTGCCAGACACACTGCAGGTG	3540
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
DB	3541	CCAGGGCTGCATCGCATGCGCATGCGAGTGGCCGAGGGTCTGCTTCTGAGCACACAGGACTGCAAT	3600
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
DB	3601	GGCAAGTCGGCTTCAGGGCGCCTGGCCGGGCCCTGCGGCCTGATGACCCCCCACTGGAT	3660
QY	1221	GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
DB	3661	GGGGATGACGCCGATGACGAGGGCACTGAGCAAAGGGGAACGGGTCCGCGCGTGGATC	3720
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
DB	3721	CGAGCCCGACTCCCTGCCTGCTGCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCT	3780
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
DB	3781	CCTCAGTCCAGGTTCCGCTCCTGTGTACCGGATCATCACCCACAAGATGTTTCGACCAC	3840
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
DB	3841	GTGGTCTTGTTCATCATCTTCTTAACGTGCATCACCATCGCCATGAGCGGCCCAAAAT	3900
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
DB	3901	GACCCCCACAGCGCTGAACGATCTTCTCTGACCTCTCCAAATTACATCTTCACCGCAGTC	3960
QY	1321	PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla	1340
DB	3961	TTTCTGGCTGAAATGACAGTGAAGTGTGGTGGCTGGCTGGTGTCTCATCTCCGTTCATCGAC	4020
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
DB	4021	TACCTGCGGAGCAGTTGGAACGTGTGGACGGGTGTGGTGTCTCATCTCCGTTCATCGAC	4080
QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
DB	4081	ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTCTG	4140
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
DB	4141	CGGTGCTGCGGACCTGCGGCCGCTCAGGGTGTATCAGCGGGCGCAGGGGTGAAGCTG	4200
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
DB	4201	GTGGTGGAGACGCTGATGTCTCTCACTGAAACCCATCGCAACATTGTAGTCATCTGCTGT	4260
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
DB	4261	GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTG	4320
QY	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
DB	4321	TGCCAGGGCGAGGATACCAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC	4380
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
DB	4381	CGGTGGGTCCGGCACAAGTACAACCTTGACAACCTTGCCAGGCCCTGTATGTCCTGTTTC	4440
QY	1481	ValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
DB	4441	GTTTTGGCCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGCTGGATGCTGTGGGC	4500
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
DB	4501	GTGGACCAGACCCCATCATGAACCAACCCCTGGATGCTGTACTTTCATCTCTCTTC	4560

QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4561	CTGCTCATGTGGCCCTCTCTTCTCTGAACATGTTTGGGTGTGGTGGAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluGluLysArgLeu	1560
Db	4621	CACAAAGTGTGGCAGCACCCAGGAGGAAGAGGAGGCGCGCGGGAGGAGAGCGCCTA	4680
QY	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
Db	4681	CGAAGACTGGAGAAAAAGAGAGAGTAAGGAGAACGACATGGCTGAAGCCCCAGTGCAAA	4740
QY	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuValHisHisLeuCysThrSerHis	1593
Db	4741	CCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTCGTCCACCACTTGTGCACACGCCAC	4800
QY	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	4801	TACCTGGACCTCTTCATCACAGGTGTTCATCGGGCTGAACGTGGTCAACATGGCCATGGAG	4860
QY	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	4861	CACACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT	4920
QY	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	4921	GTTCATCTTTGTCTTGGAGTCAGTTTCAAACCTTGTGGCCTTTGGTTTCCGTCCGTTCTTC	4980
QY	1654	GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	4981	CAGGACAGGTGGAAACCAGCTGGACCTCGCTGCCATTTGTCTGTCTCCATCATGGGCATCAG	5040
QY	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	5041	CTGGAGGAAATCGAGGTCAACGCCTCGCTGCCATCAACCCCACTCATCCGCATCATG	5100
QY	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5101	AGGCTGCTCGCATTTGCCGAGTGTCTGAGTGTGAAGATGGCTGTGGGCATGCGGGCG	5160
QY	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5161	CTGCTGGACACGGTGATGTCAGGCCCTGCCCCAGGTGGGAAACCTGGACTTCTCTTCATG	5220
QY	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5221	TTGTGTTTTTTCATCTTTTCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGAC	5280
QY	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	5281	GAGACACACCCCTGTGAGGGCCTGGGCCCTCATGCCACCTTTCGGAACCTTTGGCATGGCC	5340
QY	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	5341	TTCTTAACCCCTCTTCCGAGTCTCCACAGGTGACAAATGGAAATGGCAATTATGAAGACACC	5400
QY	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5401	CTCCGGACTGTGACCGGCCCTGCGTGTAGTCAACACCGGTTCATCTCGCCCTATCTACTTT	5460
QY	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5461	GTGTCCCTTCGTGCTGACGGGCCCTGCGTGTAGTCAACGTGGTGTATCGCCGTGCTGATG	5520
QY	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluAlaGluLeu	1853
Db	5521	AAGCACCTTGAGGAGAGCAACAAGAGGGCCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTG	5580
QY	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
Db	5581	GAGCTGGAGATGAAGACCCCTCAGCCCCCAGCCCCCACTCGCCACTGGGCAGCCCCCTTCCTC	5640
QY	1874	TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro	1893

Db 5641 TGGCCTGGGTCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCA 5700  
QY 1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThr----- 1909  
Db 5701 GCGGCCCCACGGAGATCAGCCTCCCACTTTCCCTGGAGCACCCACGGACAGGCAGCTG 5760  
QY 1909 ----- 1909  
Db 5761 TTTGACACCATATCCCTGCTGTATCCAGGGCTCCCTGGAGTGGAGCTGAAGCTGATGGAC 5820  
QY 1909 ----- 1909  
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Db 5881 TCCGACCCACAGATGCAGCCCCACCCCGAGCTGCCAGGACGACTTACTGACTGTG 5940  
QY 1926 ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHis 1945  
Db 5941 CGGAAGTCTGGGGTCAGCCGAACGCACCTCTGTGCCAATGACAGCTACATGTGTCCGCAT 6000  
QY 1946 GlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSer 1965  
Db 6001 GGGAGCACTGCCAGGGGGCCCCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCA 6060  
QY 1966 GlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPro 1985  
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QY 1986 LysAspAlaProHisLeuGlnProHisSerAlaProThrTrpGlyThrIleProLys 2005  
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QY 2006 LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIle 2025  
Db 6181 CTGCCCCCACCAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGGCCAGGCAGCAATA 6240  
QY 2026 ArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGluVal 2045  
Db 6241 AGGACTGACTCCTTGGACGTTTCCGGGTCAGGGTCTGGGCAGCCGGGAAGACCTGTGGCAGAGTG 6300  
QY 2046 SerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGln 2065  
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QY 2066 AlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaPro 2085  
Db 6361 GCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCGCCCCCT 6420  
QY 2086 CysProGlyProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGlu 2105  
Db 6421 TGCCCGAGGCCAGAACCCCACTGGGGCAAGGGCCCTCCAGAGACCAGAACGACTTAGAG 6480  
QY 2106 LeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGlu 2125  
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QY 2126 ProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArg 2145  
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QY 2186 GlyProGlySerArgProLysLysLeuSerProProSerIleThrIleAspProPro 2205

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Db 6781 GAGAGCCCAAGTCTCGGACCCCGCCAGCCCTGGTATCTGCCTCCGAGGAGGCTCCG 6840  
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QY 2246 SerProLysLysAspValLeuSerLeuSerGlyLeuSerSerSerAspProAlaAspLeuAsp 2265  
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QY 2266 Pro 2266  
Db 6961 CCC 6963  
RESULT 7  
AF227750 6999 bp mRNA linear PRI 06-MAR-2000  
LOCUS Homo sapiens voltage-dependent calcium channel alpha 1G subunit  
DEFINITION isoform bcef (CACNA1G) mRNA, complete cds.  
ACCESSION AF227750  
VERSION AF227750.1 GI:7159272  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 6999)  
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.  
TITLE Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels  
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)  
MEDLINE 20158909  
PUBMED 10692398  
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AUTHORS Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.  
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FEATURES  
source Location/Qualifiers  
1..6999 /organism="Homo sapiens"  
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6999  
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US-09-611-257A-37 (1-2266) x AF227750 (1-6999)

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DB	241	CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGGCATG	300
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DB	301	TTCCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCGGATCCTGCAGGCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTTCATCTTTGGCTTGGAGATGGTGGTGAAGATGGTGGCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal	160
DB	421	ATCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180

DB	481	ATCGAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTGAGCTTCTCAGCTGTCTCAGG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	541	ACAGTCCGTGTGCTGCACCGCTCAGGGCCATTAAACCGGGTCCCGAGCATGCGCATCTT	600
QY	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	601	GTACAGTGTGCTGGATACGCTGCCCATGTGGGCAACGTCTCTGCTGCTGCTCTTCTTC	660
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QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
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QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
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Db 5461 TGCTACAACACGGTTCATCTCGCCTATCTACTTTGTGTCTTCTGCTGACGGCCAGTTC 5520  
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluUserAsnLysGlu 1842  
Db 5521 GTGCTAGTCAACGTGGTGTATCGCCGTGCTGTATGAAGACACCTGGAGGAGAGCAACAAGAG 5580  
QY 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862  
Db 5581 GCCAAGGAGGAGGCGGAGCTAGAGGCTGAGCTGGAGTGGAGATGAAGACCTCAGCCCC 5640  
QY 1863 GlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyProAspSer 1882  
Db 5641 CAGCCCCACTCGCCACTGGGCGAGCCCCCTTCTCTGGCTGGGCTCGAGGGCCCGACAGC 5700  
QY 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902  
Db 5701 CCCGACAGCCCCAAGCCTGGGCTCTGCACCCAGCGGCCACGCGAGATCAGCCTCCAC 5760  
QY 1903 PheSerLeuGluHisProThr 1909  
Db 5761 TTTTCCCTGGAGCACCCCAACGACAGGCAGCTGTTTGACACCATATCCCTGTGTATCCAG 5820  
QY 1909 ----- 1909  
Db 5821 GGCTCCCTGGAGTGGAGCTGAAGCTGTATGACGAGCTGGCAGGCCCGGGGCCAGCCCC 5880  
QY 1910 -----MetGlnProHisPro 1914  
Db 5881 TCTGCTTCCCTTCTGTCCCCCAGCCTGGAGGCTCCGACCCACAGATGACGCCCCACCCCC 5940  
QY 1915 ThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHis 1934  
Db 5941 ACGGAGCTGCCAGGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCTGCGCGAAGCAC 6000



PDSPKPGALHPAAHARSASHFSLEHPTDRQLFDTISLLIQGSLEWELKLMDELAPGG  
QPSAFPSPSLGSDPOIPLAEMEALSLTSEIVSEPSCSLALTDLSLPDDMHTLLLSA  
LESNMQPHPTLPGLTVPKSGVSRHSLPNDSDMCRHGSTAEPLGHRGWLPKA  
QSGSVLSVHSQPADTSYILQPKDAPHLLOPHSAPWTGIPKLPGRSPLAQRLRR  
QAAITDSDLVDQGLGSRDLAEVSGPSPPLARAYSFWGQSTQAQOHSRSHSKIKH  
MTFPAPCPGPEPNWKGPPETRRSSLELDTELWSIGDLLPPGGQEPFPPSRDLKKCYS  
VEACSQRRTPTSWLDEQRHSIAVSCLDGSPHLGTDPSNLGGQPLGGPGRPKKL  
SPPSITIDPPESQGRTPPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVL  
LSGLSSDPADLDP"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 7648  
Score: 11815.50 Matches: 2264  
Percent Similarity: 95.29% Conservative: 1  
Best Local Similarity: 95.25% Mismatches: 1  
Query Match: 99.26% Indels: 111  
DB: 9 Gaps: 2

US-09-611-257A-37 (1-2266) x AF134986 (1-7648)

QY	1	MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20
Db	1	ATGGACGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGACAGCCCCGGAGTTCATG	60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40
Db	61	CGGCTCAACGACCTGTGGGGGCCGGGGCGGGCGGGGGTCAGCAGAAAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	121	CCGGCAGCGGGACTCCGAGGCGGGGGCTGCCGTACCGGGCGTGGCCCCGGTGGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
Db	181	TTCTTCTACTTGAGCCAGGACAGCCGCCCGGGAGCTGGTGTCTCCGACCGTCTGTAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	241	CCCTGGTTTGCGGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGATCCTGACGSCCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
Db	361	GATGACTTTCATCTTGGCTTCTTTGGCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
Db	421	ATCTTTGGGAAAAGTGTACCTGGGAGACACTTGAACCGCTTGACTTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	481	ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTGAGCTTCTCAGCTGTGAGG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGTGCCAGCATGCGCATCCTT	600
QY	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCACGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCTGCTGCTCTGCTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	661	GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGGAGGGCTGCTTCGGACCGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	721	TGCTTCTCTACCTGAGAAATTTACAGCTCCCTGAGCGTGGACTGGAGCGCTATTACCA	780

QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACGGAGAACGGCATGCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyGlyProCysGlyLeu	300
Db	841	TCCTGCAGAAAGCGTGCCACGCTGCGGGGAGCGGGGGCGGTGGCCACCTTGCGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGGCCTACACAGCTCCAGCAACACCACCTGTGTCAACTGGAAACCACTACTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTGACAACATT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Db	1021	GGCTATGCCTGGATCGCCATCTTCCAGGTCAACGCTGGAGGGCTGGGTCCGACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle	380
Db	1081	TACTTTGTGATGGATGCTCATCTCTTCTTCAATTTCACTACTTCTCATCTCTCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu	400
Db	1141	GTGGCTCCTTCTTTCATGATCAACCTGTGCCCTGGTGGTGTATGCCACGAGTTCTCAGAG	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCCTGTCCAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
Db	1261	AGCACCTGGTAGCTTCTCTGAGCCCGGCGAGCTGCTATGAGGAGTGTCTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1321	GTGTACATCCTTCGTAAAGCAGCCCGCAGGCTGGTCTCAGGTCTCTCGGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1381	CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
Db	1441	AGTGTCTCTCGTCCCAACCGCGCCTATCCGTCCACCACTGGTGCACCAACCAACCCAC	1500
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1501	CATCACCACTACCTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGGCCAGCCCGGAG	1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
Db	1561	ATCCAGGACAGGGATGCCAATGGGTCCCGCAGGCTCATGTGCCACCACTCGACGCCT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1621	GCCCTTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer	580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCCATCTGAGGCATCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
Db	1741	GGCAGGACTGTGGCAGCGGGAAGGTGTATCCACCGTGCACACCAAGCCCTCCACCGGAG	1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1801	ACGCTGAAGGAGGAGGACACTAGTAGAGGTGGCTGCCAGCTCTGGGGCCCCCAACCTCAC	1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640



Db 1861 AGCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAGT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db 1981 GCCTGTGTTCCAGACAGCTGCCCTACTGTGCCGGCCGGGCGAGGGAGGTGGAGCTC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCCGACCGTGAAATGCTGACTCAGACAGCGAGGCAGTTTATGAGTTTCACACAGGATGCC 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Db 2101 CAGCACAGCGACCTCCGGGACCCCAACAGCGCGGCAACGGAGCCTGGGCCCAGATGCA 2160  
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740  
Db 2161 GAGCCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCGAAAGATTGTG 2220  
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
Db 2221 GACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAACACACTCAGCATG 2280  
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Db 2281 GGCATCGAATACCACGAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340  
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800  
Db 2341 GTCTTCACCAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTGTATGGTCCCTTT 2400  
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820  
Db 2401 GGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTCAATGTGGTCAICAGCGTGG 2460  
QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
Db 2461 GAGATCGTGGGCAGCAGGGGGCGGCTGTCGGTGTGTCGGACCTTCGCGCTGATGCGT 2520  
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
Db 2521 GTGCTGAAGCTGTGCGCTTCTCGCGCGCTGCAGCGGAGTGGTGGTGTCTCATGAAG 2580  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
Db 2581 ACCATGGACAACGTGGCCACCTTCTGCGTGTCTTATGCTTATGCTTTCATCTTCAGC 2640  
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
Db 2641 ATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCTG 2700  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
Db 2701 CCAGACCGGAAGAATTTTGACTCCTTGCTCTGGGCCATCGTCACTGTCTTTCAGATCTG 2760  
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
Db 2761 ACCCAGGAGACTGGAACAAAGTCTCTACAATGGTATGGCTCCACGCTCGTCTGGGCG 2820  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 960  
Db 2821 GCCCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGTGTC 2880  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
Db 2881 GCCATTTCTGTGGAGGGCTTCCAGCGGAGGAAATCAGCAACGGGAAGATGCCAGTGA 2940  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000

Db 2941 CAGTTAAGCTGTATTTCAGCTGCCTGTCTGACTCCCAGGGGGAGATGCCAACAGTCCGAA 3000  
QY 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
Db 3001 TCAGAGCCCGATTCTTCTCACCCAGCCTGGATGGTGTATGGGGACAGGAAGTCTTG 3060  
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040  
Db 3061 GCCTTGGTGTCCCTGGGAGAGCACCCGAGAGTCCGGAAGAGCCTGTCTGCCCTCTCATC 3120  
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
Db 3121 ATCCACACGGCCGCCACACCCATGTCTGCTGCCAAGAGACACAGACACGGGCTGGCGAG 3180  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
Db 3181 GCGCTGGGCCCTGCTCGCGCCGACACAGCAGCAGCGGGTCCGAGAGCCTGGGCGGCC 3240  
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
Db 3241 CACGAGATGAAGTCAACGCCCCAGCGCCGCGAGCTCTCCGCAACAGCCCTGGAGCGCTCA 3300  
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
Db 3301 AGCAGCTGGACACAGAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3360  
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln 1140  
Db 3361 CGGAGAAAGCCAAAGTGGAGAGCGCGGTCCCTGTTGTGGGAGAAGGCCAGGAGGCCAG 3420  
QY 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
Db 3421 GATGAAGAGAGAGACTCAGAAGAGAGCGGGCCAGCCCTCGCGGAGTGACCATCGCCAC 3480  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
Db 3481 AGGGGTCCCTGGAGCGGGAGGCCAAAGATTCTTTGACCTGCCAGACACACTGCAGGTG 3540  
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
Db 3541 CCAGGGTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACACGAGACTGCAAT 3600  
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProProLeuAsp 1220  
Db 3601 GGCAAGTCGGCTTCAGGGCGCTTGGCCCGGCCCTGCGGCTGTATGACCCCCACTGGAT 3660  
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
Db 3661 GGGATGACGCCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGGTCCGCGCGTGGATC 3720  
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
Db 3721 CGAGCCCGACTCCCTGCCTGCTGCTCGAGCGAGACTCTCTGGTTCAGCCTACATCTTCCT 3780  
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
Db 3781 CCTCAGTCCAGGTTCCGCTTCTGTGTCAACCGGATCATACCCCAAGATGTTTCGACCAC 3840  
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
Db 3841 GTGGTCTTGTTCATCATCTTCTTAACGTGATCACCATCGCCATGGAGCGCCCAAAAT 3900  
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
Db 3901 GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATATACATCTTCACCGCAGTC 3960  
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340  
Db 3961 TTTCTGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTGTCTCGGGGAGCAGGCG 4020  
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
Db 4021 TACCTGGGAGCAGTTGGAACTGTGGACGGGCTGTGGTGTCTCATCTCTCGTTCATCGAC 4080

QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
DB	4081	ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGTGCTG	4140
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
DB	4141	CGGCTGTCGGGACCGCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTG	4200
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys	1420
DB	4201	GTGGTGGAGACGCTGATGTCTCACTGAAACCCATCGGCACATCTGTAGTCATCTGCTGT	4260
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
DB	4261	GCCTTCTTCATCAITTTTCGGCATCTTGGGGGTGCGAGCTCTTCAAAGGGAAGTTTTCGTG	4320
QY	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
DB	4321	TGCCAGGGCGAGGATACCGAACAATCAACCAATAAATCGGACTGTGCGGAGGCCAGTTAC	4380
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
DB	4381	CGGTGGGTCCGGCACAAAGTACAACCTTTGACAACTTGGCCAGGCCCTGATGTCTCCTGTTTC	4440
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
DB	4441	GTTTTGGCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTGTGGGC	4500
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
DB	4501	GTGGACCAGCAGCCCCATCATGAACCAACCAACCCCTGGATGCTGTACTTCATCTCGTTTC	4560
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
DB	4561	CTGCTCATTTGTGGCCCTCTTTGTCTCTGAACATGTTTGTGGTGTGGTGGAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu	1560
DB	4621	CACAAAGTGTGGCAGCACCAAGGAGGAAGAGGAGGCCCGCGGGAGGAGAGCGCCTA	4680
QY	1561	ArgArgLeuGluLysLysArgArg-----	1568
DB	4681	CGAAGACTGGAGAAAAGAGAAGGAATCTAATGCTGGACGATGTAATTGCTTCGGCAGC	4740
QY	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1582
DB	4741	TCAGCCAGCGTGGTCCAGAAAGCCAGTGCAACCTTACTACTCCGACTACTCCCGCTTC	4800
QY	1583	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
DB	4801	CGGCTCCTCGTCCACCACTGTGCACCAGCCACTACCTGGACCTCTTTCATCACAGGTGTC	4860
QY	1603	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1622
DB	4861	ATCGGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACCCAGCAGCCCCAGATTCTGGAT	4920
QY	1623	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
DB	4921	GAGGCTCTGAAGATCTGCACTACATCTTCACTGTCTCTTGTCTTGGAGTCACTTTTC	4980
QY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1662
DB	4981	AAACTTGTGGCCCTTTGGTTTCCGTGCGTTCTTCCAGGACAGGTGGAAACCGCTGGACCTG	5040
QY	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682
DB	5041	GCCATTGTGCTGTCTGCCATCATGGGCATCACGCTGGAGAGAAATCGAGGTCAACGCTCG	5100
QY	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702
DB	5101	CTGCCCATCAACCCCACTCATCCGCATCATGAGGGTGTGCGCATTCGCCGAGTGCTG	5160

QY	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
DB	5161	AAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGACACGGTGATGCAGGCCCTG	5220
QY	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu	1742
DB	5221	CCCCAGGTGGGAACCTTGGACTTCTCTTCATGTTGTTGTTTTTCATCTTTGCAGCTCTG	5280
QY	1743	GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1762
DB	5281	GGCGTGGAGCTCTTTGGAGACCCTGGAGTGTGACGAGACACCCCTGTGAGGGCCTGGGC	5340
QY	1763	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1782
DB	5341	CGTCATGCCACCTTTGGAACTTTGGCATGGCCTTCTTAACCCCTCTTCCAGATCTCCACA	5400
QY	1783	GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr	1802
DB	5401	GGTGACAAATTGGAATGGCAATTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGTCCACC	5460
QY	1803	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1822
DB	5461	TGCTACAACACAGGTCACTCGCCTATCTACTTTGTGTCTTCGTGCTGACGGGCCAGTTTC	5520
QY	1823	ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1842
DB	5521	GTGCTAGTCAACGTGGTGATCGCCGTGCTGATGAAGCACCTGGAGGAGAGCAACAAGGAG	5580
QY	1843	AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro	1862
DB	5581	GCCAAGGAGGAGGCCGAGCTAGAGGTGAGCTGGAGCTGGAGATGAAGACCTCAGCCCC	5640
QY	1863	GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer	1882
DB	5641	CAGCCCCACTCGCCACTGGGCAGCCCCTTCTCTGGCCTGGGGTCGAGGGCCCCGACAGC	5700
QY	1883	ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis	1902
DB	5701	CCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCCCACGCGAGATCAGCCTCCCAC	5760
QY	1903	PheSerLeuGluHisProThr-----	1909
DB	5761	TTTTTCCCTGGAGCACCCACGGACAGGCAGCTGTTTGACACCATAATCCCTGCTGATCCAG	5820
QY	1909	-----	1909
DB	5821	GGCTCCCTGGAGTGGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCGAGGGGCCAGCCC	5880
QY	1909	-----	1909
DB	5881	TCTGCCTTCCCTTCTGCCCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAG	5940
QY	1909	-----	1909
DB	5941	ATGGAGGCTCTGTCTGTGACGTCAGAGATTGTGTCTGAACCGTCCTGCTCTTAGCTCTG	6000
QY	1909	-----	1909
DB	6001	ACGGATGACTCTTTGCCCTGATGACATGCACACACTCTTACTTAGTGCCTGGAGAGCAAT	6060
QY	1910	MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly	1929
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QY	1930	ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla	1949
DB	6121	GTCAGCCGAACGCACCTCTTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCC	6180
QY	1950	GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu	1969
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||||| 6241 TCCGTTCACTCCAGCCAGAGATACAGCTACATCCTGCAGTTCCTCCAAAGATGCACCT 6300

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Db 6601 GAACCCAACTGGGCAAGGGCCCTCCAGAGACCAGAGCAGCTAGAGTTGGACAGGAG 6660

QY 2110 LeuSerTTPleSerGlyAspLeuLeuProProGlyGlnGluGluProProSerPro 2129

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RESULT 9

AF126965

LOCUS AF126965 7253 bp mRNA linear PRI 29-FEB-2000

DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit b isoform (CACNA1G) mRNA, complete cds.

ACCESSION AF126965

VERSION AF126965.1 GI:4761538

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 7253)

AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and

Nargeot,J.

Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels

J. Biol. Chem. 275 (9), 6090-6100 (2000)

20158909

PUBMED 10692398

REFERENCE 2 (bases 1 to 7253)

AUTHORS Monteil,A., Menessier,G., Bourinet,E., Lory,P. and Nargeot,J.

DIRECT SUBMISSION

TITLE Human Genetics Institute (I.G.H.) U.P.R.

JOURNAL Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.

1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France

FEATURES

Location/Qualifiers

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ORIGIN

Alignment Scores:

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Score: 11758.50 Matches: 2242

Percent Similarity: 98.94% Conservative: 0

Best Local Similarity: 98.94% Mismatches: 1

Query Match: 98.78% Indels: 23

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RESULT 10

AF126966

LOCUS

DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit a isoform (CACNA1G) mRNA, complete cds.

ACCESSION AF126966

VERSION AF126966.1 GI:4761540

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 7274)

AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.

TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels

JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)

MEDLINE 20158909

PUBMED 10692398

REFERENCE 2 (bases 1 to 7274)

AUTHORS Monteil,A., Menessier,G., Bourinet,E., Lory,P. and Nargeot,J.

TITLE Direct Submission

JOURNAL Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R. 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France

FEATURES

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ORIGIN

Alignment Scores:

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Percent Similarity: 98.64% Conservative: 1

Best Local Similarity: 98.59% Mismatches: 1

Query Match: 98.63% Indels: 30

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DEFINITION splice variant CavT.1a (CACNA1G) mRNA, complete cds.  
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VERSION AF190860.1 GI:7021332  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 7349)  
AUTHORS Cribbs,L.L., Gomora,J.C., Daud,A.N., Lee,J.H. and Perez-Reyes,E.

TITLE Molecular cloning and functional expression of Ca(v)3.1c, a T-type calcium channel from human brain  
JOURNAL FEBS Lett. 466 (1), 54-58 (2000)  
MEDLINE 20115462  
PUBMED 10648811  
REFERENCE 2 (bases 1 to 7349)  
AUTHORS Cribbs,L.L., Gomora,J.C., Lee,J.-H., Daud,A.N. and Perez-Reyes,E.  
TITLE Direct Submission  
JOURNAL Submitted (29-SEP-1999) Physiology, Loyola University Medical Center, 2160 South First Avenue, Maywood, IL 60153, USA

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Db	1057	TCCTGCAAGACGTGCCCCACGTGCGCGGGACGGGGCGGTGGCCACCTTTCGGGTCTG	1116		
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr	320		
Db	1117	GACTATGAGGCCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCACTACTAC	1176		

QY	321	ThrAsn	CysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	1177	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTTGACAACATT	1236	
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360	
DB	1237	GGCTATGCCTGGATCGCATCTTCCAGGTCAACGCTGGAGGCTGGTTCGACATCATG	1296	
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380	
DB	1297	TACTTTGTGATGGATGCTCATCTCTTACAAATTTTCATCTACTTTCATCTCTCTCATCATC	1356	
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400	
DB	1357	GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTATGGCCACGCGAGTTCTCAGAG	1416	
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420	
DB	1417	ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTTCCTGTCCAACGCC	1476	
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440	
DB	1477	AGCACCCCTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTGCTCAAGTACCTG	1536	
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460	
DB	1537	GTGTACATCCTTCGTAAGGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG	1596	
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480	
DB	1597	CGGGTTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC	1656	
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500	
DB	1657	AGTGCTCTCGCTCCCAACCGCGCCTATCCGTCCACCACTGGTGCACCAACCACCCAC	1716	
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520	
DB	1717	CATCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG	1776	
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540	
DB	1777	ATCCAGGACAGGGATGCCAATGGGTCCCAGCGGCTCATGCTGCCACCAACCTCGACGCT	1836	
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560	
DB	1837	GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC	1896	
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580	
DB	1897	TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCCATCTGAGGCATCC	1956	
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600	
DB	1957	GGCAGGACTGTGGGCAGCGGAAGGTGTATCCCAACCGTGCACACCAAGCCCTCCACCGGAG	2016	
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620	
DB	2017	ACGCTGAAGGAGAAGGCACTAGTAGAGTGGTGGCTGCCAGTCTGGGCCCCCAACCCCTCACC	2076	
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640	
DB	2077	AGCCTCAACATCCCAACCCGGGCGCTACAGCTCCATGCAACAAGCTGTGGAGACACAGAT	2136	
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660	
DB	2137	ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCCCTGCTTGAAAGCAGACAGTGA	2196	
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680	
DB	2197	GCCTGTGGTCCAGACAGCTGCCCTACTGTGCCCGGGCCGGGCGAGGTGGAGTCC	2256	

QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
DB	2257	GCCGACCGTGAAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTCACACAGGATGCC	2316
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
DB	2317	CAGCACAGCGACCTCCGGGACCCCCACAGCGCGGCAACGGAGCCTGGGCCCAGATGCA	2376
QY	721	GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal	740
DB	2377	GAGCCCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG	2436
QY	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
DB	2437	GACAGCAAGTACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAACACACTCAGCATG	2496
QY	761	GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
DB	2497	GGCATCGAATACCCAGCAGCAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATC	2556
QY	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe	800
DB	2557	GTCTTACCAGCCTCTTGGCCTGGAGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTT	2616
QY	801	GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp	820
DB	2617	GGCTACATCAAGATCCCTACAACATCTTCGATGGTGTCTATTTGGTTCATCAGCGTGTGG	2676
QY	821	GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg	840
DB	2677	GAGATCGTGGGCCAGCAGGGGGGGCGCCTGTGGTGTCTGCGGACCTTCCGCCTGATGCGT	2736
QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
DB	2737	GTGCTGAAGCTGGTGGCCTTCTGCCGGCGCTGCAGCGGCAGCTGGTGGTGTCTCATGAAG	2796
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
DB	2797	ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTTCATCTTTCATCTT	2856
QY	881	IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu	900
DB	2857	ATCCTGGGCATGCATCTCTCGGCTGCAAGTTTGCTCTGAGCGGGATGGGACACCCCTG	2916
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
DB	2917	CCAGACCGGAAGATTGTACTCCTTGCTCTGGCCATCGTCACTGTCTCTTTCAGATCCTG	2976
QY	921	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	940
DB	2977	ACCCAGGAGGACTGGAAACAAAGTCCTCTACATGGTATGGCCTCCACGTCGTCCTGGGCG	3036
QY	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal	960
DB	3037	GCCCTTTATTTTCAATTGGCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTTGTGCTC	3096
QY	961	AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly	980
DB	3097	GCCATTCTGGTGGAGGCTTCAGGCGGAG-----GGAGATGCCAACAAAGTCCGAA	3126
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu	1000
DB	3127	-----GGAGATGCCAACAAAGTCCGAA	3147
QY	1001	SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu	1020
DB	3148	TCAGAGCCCGATTCTCTCACCCAGCCTGGATGGTATGGGACAGGAAGAAGTGTGTG	3207
QY	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle	1040
DB	3208	GCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCCTGTGTCGCCCTCTCATC	3267
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060



Db 3268 ATCCACACGGCCGCACACCCATGTCGCTGCCAAGAGCACACGACGGCCTGGCGGAG 3327  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
Db 3328 GCGCTGGCCCTCGCTGCGCGCCACACGACGAGCGGGTCGGCAGAGCCTGGGGCGGC 3387  
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
Db 3388 CACGAGATGAAGTCAACGCCCCAGCGCCCGAGCTCTCCGCACAGCCCTGGAGCGTGCA 3447  
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
Db 3448 AGCAGCTGGACCAAGCGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3507  
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluSerGln 1140  
Db 3508 CGGAGAAGCCCAAGTGGAGAGCGCGCTCCTGTTGTCGGGAGAGGCCAGGAGCCAG 3567  
QY 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
Db 3568 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCAGCCCTGCGGGCAGTGACCATCGCCAC 3627  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
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QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
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QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
Db 3748 GGCAAGTCGGCTTCAGGGCGCCTGGCCCGGCCCTGCGGCCCTGATGACCCCTACTGGAT 3807  
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
Db 3808 GGGGATGACCGCATGACGAGGGCAACCTGAGCAAAGGGGAACGGGTCCGCGGTGGATC 3867  
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
Db 3868 CGAGCCCGACTCCCTGCCTGCTGCCGAGGAGACTCCTGGTCAGCCTACATCTTCCT 3927  
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
Db 3928 CCTCAGTCCAGGTCCGCCCTCCTGTGTACCGGATCATCACCACAAGATGTTCCGACCAC 3987  
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
Db 3988 GTGGTCTTGTATCATCTCTCCTTAAGTGCATCACCATCGCCATGGAGCGCCCCAAAT 4047  
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
Db 4048 GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAAATTACATCTTCAACCGCAGTC 4107  
QY 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340  
Db 4108 TTTCTGGCTGAATGACAGTGAAGGTGGTGACACTGGGCTGGTCTTCCGGGAGCAGGCG 4167  
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerValIleAsp 1360  
Db 4168 TACCTGGGAGCAGTTGGAACGTGCTGACGGGCTGTGGTGTCTCATCTCCGTATCGAC 4227  
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValIle 1380  
Db 4228 ATTCTGGTGTCCATGTTCTGTACAGCGGCACCAAGATCTCTGGCATGCTGAGGGTCTG 4287  
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
Db 4288 CGGCTGCTGCGAACCTTCGCCCGCTCAGGGTGATCAGCCCGGCGCAGGGGCTGAAGCTG 4347  
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420

Db 4348 GTGGTGGAGACGCTGATGTCTCTCACTGAAACCCCATCGGCAACATTGTAGTCACTGCTGT 4407  
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
Db 4408 GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4467  
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
Db 4468 TGCCAGGGCGAGGATACCAGGAACATCAACATAATCGGACTGTGCCGAGGCCAGTTAC 4527  
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
Db 4528 CGGTGGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTT 4587  
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Db 4768 CACAAGTGTCCGACGACCAGGAGGAAGAGGAGGCCCGCGGGAGGAGAGCGCCTA 4827  
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Db 4828 CGAAGACTGGAGAAAAAGAGAGGAGTAAGGAGAGAGAGATGGCTGAAGCCCAGTGCAAA 4887  
QY 1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysThrSerHis 1593  
Db 4888 CCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTCGTCCACCACTTGTGCACCAGCCAC 4947  
QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613  
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Db 5008 CACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT 5067  
QY 1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe 1653  
Db 5068 GTCATCTTTGTCTTGGAGTCAAGTTTCAAACCTTGTGGCCTTGTGGTTCGTCGGTCTTC 5127  
QY 1654 GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673  
Db 5128 CAGGACAGGTGGAACACAGCTGGACCTGGCCATTGTGTGCTGTCCATCATTGGGCATCAG 5187  
QY 1674 LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693  
Db 5188 CTGGAGGAATCGAGGTCAACGCCCTCGCTGCCCATCAACCCCAACCATCATCCGCATCATG 5247  
QY 1694 ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla 1713  
Db 5248 AGGGTGTGCGCATTTGCCGAGTGTGAAGTGTGTGAAGATGGCTGTGGGCATGCGGGCG 5307  
QY 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733  
Db 5308 CTGCTGGACACGGTGATGCAGGCCCTGCCAGGTGGGGAACCTGGGACTTCTCTTCATG 5367  
QY 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753  
Db 5368 TTGTTGTTTTTTCATCTTTGCAGCTCTGGCGGTGGAGCTCTTTGGAGACCTTGGAGTGTGAC 5427  
QY 1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773  
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6786  
Score: 11735.50 Matches: 2241  
Percent Similarity: 98.16% Conservative: 1  
Best Local Similarity: 98.12% Mismatches: 1  
Query Match: 98.58% Indels: 41  
DB: 9 Gaps: 2

US-09-611-257A-37 (1-2266) x AF227747 (1-6786)

QY	1	MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
Db	1	ATGGACGAGGAGGATGGAGCGGGCGCGGAGGATCGGGACAGCCCCCGGAGCTTCATG	60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
Db	61	CGGCTCAACGACCTGTCGGGGCGCGGGGCGCGGGCGCGGGGTCAGCAGAAAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	121	CCGGGACGCGGACTCCGAGCGGAGGGGCTGCCGTACCCCGCGCTGGCCCCCGTGGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
Db	181	TTCTTCTACTTGAGCCAGGACAGCCCGCGGGAGCTGGTGTCTCCGACCGTCTGTAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	241	CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCCGGCCATCGCAGGACATCGCCTGTGACTCCAGCGCTCCCGATCCTGCAGGCCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140

Db	361	GATGACTTTCATCTTTGCCTTCTTTTGGCGTGAGATGGTGGTGAAGATGGTGGCCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal	160
Db	421	ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGAACCGGCTTGACTTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	481	ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCACTTCTCAGCTGTCAAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTT	600
QY	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCACGTTGCTGGATACGCTGCCCATGCTGGCAACGTCTCTGCTGCTCTGCTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	661	GTCTTCTTCTTCTTGGCATCGTGGCGTCCAGCTGTGGGACGGGCTGCTTCGGAACCGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	721	TGCTTCTTCTTCTTGGCATCGTGGCGTCCAGCTGTGGGACGGGCTGCTTCGGAACCGA	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAACGAGGATGAGAGCCCCCTTCTCTCCAGCCACGCGAGAACGGCATGCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu	300
Db	841	TCCTGCAGAGCGTGGCCACCGCTGCGGGGGACCGGGGGCGGTGGCCACCTTGGCGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGGCTTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCATCTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAACAT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Db	1021	GGCTATGCTGATCGCCATCTTCCAGGTCAATCAGCTGAGGAGGCTGGGTGACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
Db	1081	TACTTTGTGATGATGCTCATCTCTTCTTACAATTTTCACTACTTCTCTCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1141	GTGGGCTCCTTCTTTCATGATCAACCTGTGCCTGGTGGTGAATGCCACGAGTTCTCAGAG	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGGGTTCCTGTCCAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
Db	1261	AGCACCTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGTGTCTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1321	GTGTACATCTTCTGTAAGGAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1381	CGGGTTGGGCTGCTCAGCAGCCCGCAGCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500

Db 1441 AGCTGCTCGCTCCACCGCGCGCTATCCGTCCACCACTGGTGCACCAACCACCCAC 1500  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CATCACCACTACCACTGGCAATGGACGCTCAGGSCCCCCCGGCCAGCCGGAG 1560  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
Db 1561 ATCCAGGACAGGATGCCAATGGTCCCGCGGCTCATGTGCCACCACTCGACGCCT 1620  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
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QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
Db 1681 TGCCACTTAGACCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCCATCTGAGGCATCC 1740  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
Db 1741 GGCAGGACTGTGGGCAGCGGAAGGTGTATCCACCGTGCACACCAAGCCCTCCACCGGAG 1800  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
Db 1801 ACCTGAAGGAGAAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCCCTCAC 1860  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db 1861 AGCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAAGCTGTGGAGACAGAGT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
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QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
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QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
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QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
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QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
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QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProphe 800  
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QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820  
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QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
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QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
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QY 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
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QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140  
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DB 3592 GGGGATGACGGCGATGACGAGGGCAACCTGAGCAAGGGAAACGGTCCGCGGTGATC 3651  
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QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
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DB 3832 GACCCCCACAGCGCTGAACGCATCTCTGTGACCTCTCCAAATTACATCTTACCGCAGTC 3891  
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340  
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QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
DB 4192 GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4251  
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
DB 4252 TGCCAGGGCGAGGATACCAGGAACATCACCAATAATCGACTGTGCCGAGGCCAGTTAC 4311  
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
DB 4312 CGGTGGTCCGGCACAAAGTACAACTTTGACAACCTTGGCAGGCCCTGATGTCCCTGTTC 4371  
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QY 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu 1560  
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DB 4612 CGAAGACTGGAGAAAAAGAGGAATCTAATGCTGGACGATGTAATTGCTTCCGGCAGC 4671  
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DB 4672 TCAGCCAGCGCTGCGTCAGAAGGCCAGTGCAAACCTTACTCTCGACTACTCCCGCTTC 4731  
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QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622  
DB 4792 ATCGGGCTGAACGTTGGTACCATGGCCATGGAGCACTACAGCAGCCCCAGATTCTGGAT 4851  
QY 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642  
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DB 5452 GTGCTAGTCAACGTGGTGATCGCGTGTGATGAAGCACCTGGAGGAGAGCAACAAGGAG 5511  
QY 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862  
DB 5512 GCCAAGGAGGAGGCCGAGCTAGAGGTGAGCTGGAGCTGGAGATGAAGACCCCTCAGCCCC 5571  
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DB 5692 TTTTCCCTGGAGCACCCCCACGATGCAGCCCCCCCCCGAGCTGCCAGGACCCAGACTTA 5751  
QY 1923 LeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMet 1942

Db	5752	CTGACTGTGCGGAAGTCTGGGGTCAGCCGAAACGCACTCTCTGCCCAATGACAGCTACATG	5811
QY	1943	CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLys	1962
Db	5812	TGTCGGATGGGAGCACTGCCAGGGGCCCTGGGACACAGGGCTGGGGCTCCCAA	5871
QY	1963	AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeu	1982
Db	5872	GCTCAGTCAGGCTCGTCTTGCTTCACTCCAGCCAGCAGATACCAGTACATCCTG	5931
QY	1983	GlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThr	2002
Db	5932	CAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCAAGCCCACTGGGGCACC	5991
QY	2003	IleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGln	2022
Db	5992	ATCCCCAAAGTCCCCCACCAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAG	6051
QY	2023	AlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu	2042
Db	6052	GCAGCAATAAGGACTGACTCCTTGGACGTTTCAGGGTCTGGGAGCCCGGAAGACCTGCTG	6111
QY	2043	AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSer	2062
Db	6112	GCAGAGGTGAGTGGGCCCTCCCGGCCCTGGCCCGGCGCTACTCTTCTGGGCGCAGTCA	6171
QY	2063	SerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro	2082
Db	6172	AGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCG	6231
QY	2083	ProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrArgSer	2102
Db	6232	CCAGCCCCCTTGCCAGGCCCAAGACCCAACTGGGGCAAGGCCCTCCAGAGACCAGAAGC	6291
QY	2103	SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGly	2122
Db	6292	AGCTTAGAGTTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTCGCCCCCTGGCGGC	6351
QY	2123	GlnGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGlnSer	2142
Db	6352	CAGGAGGAGCCCCCATCCCCACGGACCTGAAGAAGTGCTACAGCGTGGAGGCCAGAGC	6411
QY	2143	CysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSer	2162
Db	6412	TGCCAGCGCGGCCACAGTCTCTGGCTGGATGAGCAGCAGGAGACACTCTATCGCCGTCAGC	6471
QY	2163	CysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGlyGln	2182
Db	6472	TGCTTGACAGCGGCTCCCAACCCCACTGGGCACAGACCCCTTAACCTTGGGGGCCAG	6531
QY	2183	ProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIleThrIle	2202
Db	6532	CCTCTTGGGGGCGCTGGAGCGCGCCCAAGAAACTCAGCCCGCTAGTATCACCATA	6591
QY	2203	AspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeuArgArg	2222
Db	6592	GACCCCCCGAGAGCCCAAGTCTCTCGAACCCCGCCAGCCCTGGTATCTGCCTCCGAGG	6651
QY	2223	ArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSerMetAla	2242
Db	6652	AGGGCTCCGTCACGCACTCCAAGGATCCCTTGGCCTCTGGCCCCCTTGACAGCATGGCT	6711
QY	2243	AlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAla	2262
Db	6712	GCCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCTCTGACCCAGCA	6771
QY	2263	AspLeuAspPro	2266
Db	6772	GACCTGGACCCC	6783

RESULT 13  
AF227746  
LOCUS

6897 bp mRNA linear PRI 06-MAR-2000

AF227746

DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform af (CACNA1G) mRNA, complete cds.

ACCESSION AF227746

VERSION AF227746.1 GI:7159264

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 6897) Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J. Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels J. Biol. Chem. 275 (9), 6090-6100 (2000)

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source

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ORIGIN

Alignment Scores:

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US-09-611-257A-37 (1-2266) x AF227746 (1-6897)

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DB	361	GATGACTTCATCTTTGCCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCTTGGC	420
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DB	481	ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACCTCAGCTTCTCAGCTGTGAGG	540
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AF227748				
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REFERENCE 1 (bases 1 to 6921)				
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.				
TITLE Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels				
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)				
MEDLINE 20158909				
PUBMED 10692398				
REFERENCE 2 (bases 1 to 6921)				
AUTHORS Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.				
TITLE Direct Submission				
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.) U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France				
FEATURES Location/Qualifiers				

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ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	6921
Score:	11703.00	Matches:	2241
Percent Similarity:	96.26%	Conservative:	1
Best Local Similarity:	96.22%	Mismatches:	1
Query Match:	98.31%	Indels:	86
DB:	9	Gaps:	3

US-09-611-257A-37 (1-2266) x AF227748 (1-6921)

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QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
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QY	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProphe	800
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QY	801	GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp	820
DB	2401	GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTTCATTTGGTTCATCAGCGTGTGG	2460
QY	821	GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg	840
DB	2461	GAGATCGTGGCCACGAGGGGGCGGCCCTGTCGGTGTCTCGGACCTTCCCGCCTGATGCGT	2520
QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
DB	2521	GTGCTGAAGCTGGTGGCTTCTGCCGGCGCTGCAGCGCAGCTGGTGGTGTCTCATGAAG	2580
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
DB	2581	ACCATGGACAAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTTCATCTTCATCTTCAGC	2640
QY	881	IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu	900
DB	2641	ATCCTGGGCATGCATCTCTTTCGGCTGCAAGTTTGGCTCTGAGCGGATGGGACACCCCTG	2700
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
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QY	921	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	940
DB	2761	ACCCAGGAGGACTGGAAACAAAGTCCTCTACAATGGTATGGCCTCCACGTCGTCCTGGCG	2820
QY	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal	960
DB	2821	GCCCTTTATTTTCATTGCCCCTCATGACCTTCGGCACTACGTGCTCTTCAATTTGCTGGTC	2880
QY	961	AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly	980
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QY	1001	SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu	1020
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QY	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle	1040
DB	2992	GCCTTGGTGTCCCTGGGAGAGACCCGGAGCTGCGGAAGAGCCTGCTGCCGCCCTCTCATC	3051
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
DB	3052	ATCCACACGGCCGCCACACCATGTCGTGCCCCAAGAGACACCGGCCCTGGGCGAG	3111
QY	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
DB	3112	CGCTGGGCCCTGCGTCCGCCCGCACCCAGCAGCAGCGGGTCCGCAGAGCCTGGGGCGGCC	3171
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
DB	3172	CACGAGATGAAGTCAACGCCCGACGCCCGCAGCTCTCCGCACAGCCCCCTGGAGCGCTGCA	3231
QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
DB	3232	AGCAGCTGGACCAGCAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG	3291

QY	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluSerGln	1144
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QY	1141	AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
DB	3352	GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTGCGGGCAGTACCACATCGCCAC	3411
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
DB	3412	AGGGGTCCCTGGAGCGGAGGCCAAGAGTTCCTTTGACCTGCCAGACACACTGCAGGTG	3471
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
DB	3472	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACACGAGACTGCAAT	3531
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
DB	3532	GGCAAGTCGGCTTCAGGGCGCCCTGGCCCGGGCCCTGCGGCCCTGATGACCCCCACTGGAT	3591
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
DB	3592	GGGATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGGAACGGGTCCGCGCTGGATC	3651
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QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
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QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
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DB	3892	TTTCTGGCTGAATGACAGTGAAGGTGGTGGCACTGGGTGGTGTCTCGGGAGCAGGCG	3951
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuValLeuIleSerValIleAsp	1360
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QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
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QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
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QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500



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RESULT 15					
AF134985					
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DEFINITION	Homo sapiens T calcium channel alpha1G subunit (CACNA1G) mRNA,				
	complete cds.				

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1 (bases 1 to 7030)  
Mittman, S., Guo, J. and Agnew, W.S.  
Structure and alternative splicing of the gene encoding alpha1G, a  
human brain T calcium channel alpha subunit  
Neurosci. Lett. 274 (3), 143-146 (1999)  
20014446  
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2 (bases 1 to 7030)  
Mittman, S., Guo, J. and Agnew, W.S.  
Direct Submission  
Submitted (15-MAR-1999) Anesthesiology/Critical Care Medicine, The  
Johns Hopkins University School of Medicine, 600 N. Wolfe Street,  
Meyer 297, Baltimore, MD 21287-7294, USA

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## ORIGIN

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: April 15, 2005, 23:55:55 ; Search time 2319 Seconds  
(without alignments)  
5784.448 Million cell updates/sec

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11877.5	99.8	7741	AAD04756	Aad04756 Human T-t
2	11874	99.7	6892	AAF31684	Aaf31684 Human alp
3	11815.5	99.3	7648	ADQ89063	Adq89063 Human uro
4	11815.5	99.3	7648	ADSL6298	Adsl6298 Human vol
5	11758.5	98.8	6729	AAX83484	Aax83484 Human T-t

6	11741	98.6	6750	2	AAX83481	Aax83481 Human T-t
7	11735.5	98.6	6783	2	AAX83482	Aax83482 Human T-t
8	11727	98.5	6804	2	AAX83483	Aax83483 Human T-t
9	11627.5	97.7	8002	4	AAH98402	Aah98402 Human EST
10	11111	93.3	7286	3	AAZ52309	Aaz52309 Rat pancr
11	10962.5	92.1	6741	2	AAX83488	Aax83488 Rat T-typ
12	10945	91.9	6762	2	AAX83485	Aax83485 Rat T-typ
13	10945	91.9	6942	13	ADSL6295	Adsl6295 Rat volta
14	10939.5	91.9	6795	2	AAX83486	Aax83486 Rat T-typ
15	10925	91.8	6816	2	AAX83487	Aax83487 Rat T-typ
16	10890.5	91.5	7540	5	AAF31677	Aaf31677 Rat alpha
17	6315.5	53.1	3993	4	AAS01624	Aas01624 Human T-t
18	6223	52.3	8447	5	AAF31678	Aaf31678 Rat alpha
19	6216.5	52.2	7898	2	AAX59081	Aax59081 Human act
20	6215.5	52.2	7898	8	ABZ58365	Abz58365 Human T-t
21	6214.5	52.2	7898	2	AAX59080	Aax59080 Human act
22	5902.5	49.6	6114	2	AAX83490	Aax83490 Human T-t
23	5892.5	49.5	6132	2	AAX83489	Aax83489 Human T-t
24	5713	48.0	6941	2	AAX59082	Aax59082 Human act
25	5496.5	46.2	6990	13	ADSL6296	Adsl6296 Human vol
26	5492.5	46.1	6816	6	AAS16826	Aas16826 Human T-t
27	5492.5	46.1	6816	8	ABX93560	Abx93560 Human CDN
28	5492.5	46.1	6816	12	ADH69264	Adh69264 Human TCC
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31	5484	46.1	6855	12	ADH69266	Adh69266 Human TCC
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34	5361.5	45.0	5469	2	AAX83491	Aax83491 Human T-t
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43	2140	18.0	3464	12	ADL31040	Adl31040 Full leng
44	1971.5	16.6	1669	2	AAX59083	Aax59083 Human act
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ALIGNMENTS

RESULT 1  
AAD04756  
ID AAD04756 standard; cDNA; 7741 BP.

AC AAD04756;

DT 17-JUL-2001 (first entry)

DE Human T-type low voltage activated calcium channel alpha1G-c cDNA.

XX Human T-type low voltage activated calcium channel alpha1G-c; stress; epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease; endocrine disorder; respiratory disorder; peripheral muscle disorder; muscle excitability; fertilisation; contraception; hypertension; neuronal firing regulation; cardiovascular disorder; gene therapy; forensic analysis; epidemiological study; neuroleptic; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 5'UTR 1..522

FT CDS 523..7344

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FT /tag= b

FT /product= "Human T-type low voltage activated calcium

FT channel alpha1G-c protein"

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FT /*tag= c
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PN 03-MAY-2001.
XX
PF 06-OCT-2000; 2000WO-US027761.
XX
PR 26-OCT-1999; 99US-00426998.
XX
PA (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX
DR WPI; 2001-300486/31.
DR P-PSDB; AAE01019.
XX
PT New nucleic acid encoding human calcium channel protein, useful for
PT identifying specific modulators and potential pharmaceuticals for
PT treating e.g. epilepsy.
XX
PS Claim 2; Page 76-81; 115pp; English.
XX
CC The invention relates to isoform of human T-type low voltage activated
CC calcium channel (alpha1G-c) cDNA and protein. Cells transformed with
CC calcium channel DNA to express calcium alpha1G-c channel protein are used
CC to identify specific modulators (antagonists or agonists). These
CC modulators are useful as therapeutic agents and are used for treating
CC wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress
CC epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
CC endocrine disorders, respiratory disorder, peripheral muscle disorder,
CC muscle excitability, fertilisation, contraception, disorders involving
CC hypertension, neuronal firing regulation, potentiation of synaptic
CC signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
CC hypertrophy, angina pectoris). Calcium alpha1G-c channel DNA is useful
CC for isolating and identifying related molecule mutations. It is also
CC optionally used as antisense sequences, in gene therapy. Calcium channel
CC alpha1G-c DNA, protein and antibodies are useful for forensic analysis,
CC diagnosis and epidemiological studies, by standard hybridisation or
CC immunological assays. The present sequence is T-type low voltage
CC activated calcium channel alpha1G-c cDNA. This sequence is isolated from
CC human thalamus cDNA library
XX
SQ Sequence 7741 BP; 1469 A; 2496 C; 2287 G; 1489 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 7741
Score: 11877.50 Matches: 2264
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.78% Indels: 7
DB: 4 Gaps: 1

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QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
DB 1903 CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGCCAGGAGACCCAGCCAGCAGC 1962  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
DB 1963 AGCTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACCTCGGTGCACCAACCACAC 2022  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
DB 2023 CATCACCACTTACCACCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGAG 2082  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
DB 2083 ATCCAGGACAGGATGCCAATGGGTCCCGCAGGCTCATGTGTCACCAACCCTCGACGCCT 2142  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
DB 2143 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2202  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
DB 2203 TGCCACTTAGAGCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCATCTGAGGCATCC 2262  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
DB 2263 GGCAGGACTGTGGGCAGCGGAAGGTGTATCCACCGTGCACACAGCCCTCCACCGGAG 2322  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
DB 2323 ACGCTGAAGGAGAAGGCACTAGTAGAGTGGCTGCCAGCTCTGGGCCCCCAACCCCTCAC 2382  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
DB 2383 AGCCTCAACATCCACCCCGGCCCTCAGACTCCATGCACAAAGTGTGGAGACACAGAT 2442  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
DB 2443 ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA 2502  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
DB 2503 GCCTGTGTTCCAGACAGCTGCCCTACTGTGCCGGGCCGGSCAGGGAGGTGGAGCTC 2562  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
DB 2563 GCCGACCGTGAATGCCTGACTCAGACAGGAGGCAGTTTATGAGTTACACAGGATGCC 2622  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
DB 2623 CAGCACAGGACCTCCGGGACCCCAACAGCCGGCGCAACGGAGCCTGGGCCAGATGCA 2682  
QY 721 GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleVal 740  
DB 2683 GAGCCCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2742  
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
DB 2743 GACAGCAAGTACTTTGGCCGGGGAATCATGATCGCCATCCTCGTCAACACACTCAGCATG 2802  
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
DB 2803 GGCATCGAATACCAGCAGCAGCCCGCAGGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2862  
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800  
DB 2863 GTCTTCACCAGCCTCTTTGGCCCTGGAGATGCTGTGAAGCTGCTGTGTATGGTCCCTTT 2922

QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820  
DB 2923 GGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTCAATGTGTTCATCAGCGTGTGG 2982  
QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
DB 2983 GAGATCGTGGGCCAGCAGGGGGCGGCTGTTCGGTGTCTCGGACCTTCCGCCTGATGCGT 3042  
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
DB 3043 GTGCTGAAGCTGGTGGCTTCTCTCGCGGCTGCAGGGCAGTGGTGTCTCATGAAG 3102  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
DB 3103 ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTTCAGC 3162  
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
DB 3163 ATCCTGGGCATGCATCTTCTCGGCTGCAAGTTTGCTCTGAGCGGATGGGACACCCCTG 3222  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu 920  
DB 3223 CCAGACCGGAAGAATTTTGACTCTCTGCTCTGGGCCATCGTCACTGTCTTTCAGATCCTG 3282  
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
DB 3283 ACCCAGGAGGACTGGAAACAAAGTCTCTACAATGGTATGGCTCCACGTCGTCTCTGGGCG 3342  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
DB 3343 GCCCTTTTATTCATTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTC 3402  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
DB 3403 GCCATTCTGGTGGAGGGCTTCCAGGCGGAGGAATCAGAAACGGGAAGATGCGAGTGA 3462  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
DB 3463 CAGTTAAGCTGTATTTCAGCTGCCTGTTCGACTCCAGGGGGGAGATGCCAACAAAGTCCGAA 3522  
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
DB 3523 TCAGAGCCCGATTCTTCTCACCCACCTGGATGGTGTGGGACAGGAAGAAGTGTCTTG 3582  
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040  
DB 3583 GCCTTGGTGTCCCTGGGAGAGCACCCGAGCTGCGGAAGAGCTGTGCCCTCTCATC 3642  
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
DB 3643 ATCCACACGCGCCACACCCCATGTGCTGCCAAGAGCACAGCACGGGCTTGGCGGAG 3702  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
DB 3703 GCGCTGGGCCCTGCGTCGCGCCGCACAGCAGCAGCGGTCGCGCAGAGCCTTGGGCGGCC 3762  
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
DB 3763 CACGAGATGAAGTCACCGCCCGCAGCCCGCAGCTCTCCGCACAGCCCTTGGAGCGCTGCA 3822  
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
DB 3823 AGCAGCTGGACACGACGCGGCTCCAGCCGGAACAGCCTCGGCGGTGCACCCAGCCTGAAG 3882  
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGln 1140  
DB 3883 CGGAGAAGCCCAAGTGGAGAGCGGCGTCCCTGTTGTTCGGGAGAAGGCCAGGAGGCCAG 3942  
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
DB 3943 GATGAAGAGGAGAGCTCAGAAGAGGACGGGCCAGCCCTTGGGGCAGTGACCATCGCCAC 4002  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180

Db	4003	AGGGGCTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCACACACTGCAGGTG	4062	5083	CTGCTCATTTGTGGCCTTCTTTGTCTCTGAACATGTTTGTGGGTGTGGTGGAGAACTTC	5142
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200	1541	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeu	1560
Db	4063	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTCTTGAGGACACGAGACTGCAAT	4122	5143	CACAACTGTCCGCAGCACACGAGGAGGAAGAGAGGCCCGCGCGGAGAGAAAGCGCCTA	5202
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp	1220	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
Db	4123	GGCAAGTCGGCTTCAGGGCGCCTGGCCGGGCCCTCGGCCCTGATGACCCCCACTGGAT	4182	5203	CGAAGACTGGAGAAAAGAGAAAGAGTAAGGAGAAGCAGATGGCTGAAGCCCAGTGCAA	5262
QY	1221	GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis	1593
Db	4183	GGGATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGGAACGGGTCCGCGCTGGATC	4242	5263	CCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTCGTCCACCACTTGTGCACCGCCAC	5322
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	4243	CGAGCCCGACTCCCTGCCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCT	4302	5323	TACCTGGACCTCTTCATCACAGGTGTCTATCGGGCTGAACGTGGTCACCATGGCCATGGAG	5382
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	4303	CCTCAGTCCAGGTTCGCCCTCCTGTGTACCGGATCATCACCCACAAGATGTCGACCAC	4362	5383	CACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT	5442
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	4363	GTGGTCTTGTTCATCATCTTCTTAACTGCATCACCATCGCATGGAGCGCCCAAAATT	4422	5443	GTCACTTTTGTCTTGGAGTCAGTTTTCAAACCTTGTGGCCTTGGTTTCCGTCCGTCTTC	5502
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320	1654	GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	4423	GACCCCCACAGCGCTGAACGCATCTTCTTGACCTCTCCAAATTACATCTTACCGCAGTC	4482	5503	CAGGACAGGTGGAACACAGCTGGACCTGGCCATTGTGCTGTCTCATCATGGGCATCAG	5562
QY	1321	PheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAla	1340	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	4483	TTTCTGGCTGAAATGACAGTGAAGGTGTGGCACTGGGCTGGTCTCATCTCCGTCTCGAC	4542	5563	CTGGAGGAAATCGAGTCAACGCCTCGCTGCCCATCAACCCACCATCATCCGCATCATG	5622
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuValLeuIleSerValIleAsp	1360	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	4543	TACCTGCGGAGCAGTTGGAACGTGTGGACCGGCTGTTGGTGTCTCATCTCCGTCTCGAC	4602	5623	AGGTGCTGCGCATTTGCCGAGTGTGAAGTGTGCTGAAGTGTGGCATGCGGCGG	5682
QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	4603	ATTCTGGTGTCCATGTCTCTGACAGCGGCACCAAGATCCTGGCGATGCTGAGGGTGTG	4662	5683	CTGCTGGACACGGTGATGACGGCCCTGCCCGAGGTGGGAACTCTTCTTCTCATG	5742
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	4663	CGGCTGCTGCGGACCCTGCGCCGCTCAGGGTGTATCAGCGGCGCAGGGGCTGAAGCTG	4722	5743	TTGTGTTTTTTCATCTTTGCAGCTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGAC	5802
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	4723	GTGGTGGAGACGCTGATGTCTCACTGAAACCCATCGGCAACATTGTAGTCATCTGCTGT	4782	5803	GAGACACACCCCTGTAGGGCCTGGGCGGTGTCACCTTTTCGGAACTTTGGCATGGCC	5862
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal	1440	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	4783	GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG	4842	5863	TTCTTAACCTCTTCCGAGTCTCCACAGGTGACAATTTGAATGGCATTATGAAGGACACC	5922
QY	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	4843	TGCCAGGGCGAGGATACCAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC	4902	5923	CTCCGGGACTGTGACCGAGGAGTCCACCTGCTACAAACACGGTCTCTCGCCTATCTACTTT	5982
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	4903	CGGTGGTCCGGCACAAGTACAACCTTGACAACCTTGGCCAGGCCCTGTATGTCCTGTTC	4962	5983	GTGTCTTCTGCTGACGGCCCCAGTTCTGTGTAGTCAACGTGGTGTATCGCGCTGTGATG	6042
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeu	1853
Db	4963	GTTTTGGCCTCCAAGGATGGTTGGGTGGACATCATGTACGATGGCTGGATGCTGTGGGC	5022	6043	AAGCACCTGGAGAGAGACAACAGGAGGCCAAGGAGGCCGAGCTAGAGGCTGAGCTG	6102
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
Db	5023	GTGGACAGAGGCCCATCATGAACCAACCCCTGGATGTGTGTACTTTCATCTCGTTC	5082	6103	GAGCTGGAGATGAAGACCTTCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCA	6162
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540	1874	TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro	1893
				6163	TGGCCTGGGTTCAGGGGCCCCGACAGCCCCCAGCCCCCAGCCCCCAGCCCCA	6222

Qy	1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis	1913
Db	6223	GCGGCCCCACGCGAGATCAGCCTCCCACTTTTCCTGGAGACCCCACGATGACGCCAC	6282
Qy	1914	ProThrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThr	1933
Db	6283	CCCACGGAGCTGCCAGACAGACTTACTGACTGTGCGGAAGTCTGGGGTCAGCGAAG	6342
Qy	1934	HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu	1953
Db	6343	CACCTCTTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCCGAGGGGCCCTG	6402
Qy	1954	GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer	1973
Db	6403	GGACACAGGGGCTGGGGCTCCCCAAGCTCAGTCAGGCTCCGTCTTGTCCGTTCACTCC	6462
Qy	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuGln	1993
Db	6463	CAGCCAGCAGATACCAGCTACATCCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAG	6522
Qy	1994	ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerPro	2013
Db	6523	CCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCACCAGGACGCTCCCT	6582
Qy	2014	LeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGln	2033
Db	6583	TTGGCTCAGAGGCCACTCAGGGCCAGGCAGCAATAAGGACTGACTCCTTTGAGCGTTGAG	6642
Qy	2034	GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProLeuAla	2053
Db	6643	GGTCTGGGCAGCCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCCCCGCCCTGGCC	6702
Qy	2054	ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis	2073
Db	6703	CGGGCCTACTCTTTCTGGGGCCAGTCAAGTACCAGGCACAGCAGCACTCCCGAGCCAC	6762
Qy	2074	SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp	2093
Db	6763	AGCAAGATCTCCAAGCAGCATGACCCCGCCAGCCCTTGCCAGGCCCAGAACCCAACTGG	6822
Qy	2094	GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle	2113
Db	6823	GGCAAGGGCCCTCCAGAGACCAGAGCAGCTTAGAGTTGGACACGGAGCTGAGTGGATT	6882
Qy	2114	SerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLys	2133
Db	6883	TCAGGAGACCTCCTGCCCCCTGGCGGCCAGGAGAGCCCCCATCCCCACGGGACCTGAAG	6942
Qy	2134	LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu	2153
Db	6943	AAGTGCTACAGCGTGGAGGCCCAGAGCTGCCAGCGCGGCCCTACGTCTCGCTGGATGAG	7002
Qy	2154	GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly	2173
Db	7003	CAGAGGAGACACTCTATCGCCGTGAGCTGCCTGGACAGCGGCTCCCAACCCCACTGGGC	7062
Qy	2174	ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLys	2193
Db	7063	ACAGACCCCTCTAACCTTGGGGGCCAGCCCTCTTGGGGGGCCCGGAGCCGGCCCAAGAAA	7122
Qy	2194	LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro	2213
Db	7123	AAACTCAGCCCCCTAGTATCACCATAGACCCCCCCGAGAGCCAAAGTCTCTCGGACCCCG	7182
Qy	2214	ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu	2233
Db	7183	CCCAGCCCTGGTATCTGCCTCCGGAGGAGGGCTCCGTCCAGCGACTCCAAGGATCCCTTG	7242
Qy	2234	AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer	2253
Db	7243	GCCTCTGGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCCAAAGAAAGAGTGTGAGT	7302

QY	2254	LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
Db	7303	CTCTCCGGTTTATCTCTGACCCAGACCTGGACCCC	7341
RESULT 2			
AAF31684			
ID	AAF31684	standard; cDNA; 6892 BP.	
XX			
AC	AAF31684;		
XX			
DT	09-APR-2001	(first entry)	
XX			
DE	Human	alpha-IG T-type calcium channel cDNA.	
XX			
KW	Human;	antiarrhythmic; anticonvulsant; hypotensive; c	
KW	T-type	calcium channel subunit; cardiac hypertrophy;	
KW	hypertension;	sleep disorder; epilepsy; alpha-IG T-ty	
KW	ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200102561-A2.		
XX			
PD	11-JAN-2001.		
XX			
PF	04-JUL-2000;	2000WO-CA000794.	
XX			
PR	02-JUL-1999;	99US-00346794.	
XX			
PA	(NEUR-) NEUROMED TECHNOLOGIES INC.		
XX			
PI	Snutch TP,	Baillie DL;	
XX			
DR	WPI; 2001-123111/13.		
XX	P-PSDB; AAB66481.		
XX			
PT	Novel T-type calcium channel alpha-1 subunit gene use		
PT	cardiac hypertrophy, cardiac arrhythmia, hypertension		
PT	epilepsy.		
XX			
PS	Example 3; Fig 6; 103pp; English.		
XX			
CC	The present sequence is given in a specification prov		
CC	partial sequences for three types of mammalian (human		
CC	calcium channel subunits. An expression cassette has		
CC	comprises a nucleotide sequence encoding a T-type cal		
CC	subunit operably linked to control sequences to effec		
CC	The novel calcium channel nucleic acids and proteins		
CC	treating conditions characterised by undesirable leve		
CC	channel activity such as cardiac hypertrophy, cardiac		
CC	hypertension, sleep disorder and epilepsy		
XX			
SQ	Sequence 6892 BP; 1315 A; 2223 C; 2017 G; 1337 T; 0 U		
Alignment Scores:			
Pred. No.:	0	Length:	6892
Score:	11874.00	Matches:	226
Percent Similarity:	99.82%	Conservative:	1
Best Local Similarity:	99.78%	Mismatches:	4
Query Match:	99.75%	Indels:	0
DB:	5	Gaps:	0
US-09-611-257A-37 (1-2266) x AAF31684 (1-6892)			
QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGly	
Db	51	ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCTGGGACA	
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGly	
Db	111	CGGCTCAACGACCTGCGGGGGCGCGGGGGCGCGGGGCCCGGGC	
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAla	

Db 171 CCGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTT 230  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
Db 231 TTCTTCTACTTGAGCCAGGACAGCCCGCCCGGAGCTGGTGTCTCCGCACGGTCTGTAAAC 290  
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 291 CCCTGGTTGAGCGCATCAGCATGTTGGTCACTCCTTCTCAACTGCGTGACCCCTGGGCATG 350  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 351 TTCGGGCCATGCGAGACATCGCCTGTGACTCCACGCGCTGCCGATCCTGCAGGCCCTTT 410  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
Db 411 GATGACTTCACTTTGCCCTTCTTTCGCGTGAGATGGTGGTGAAGATGGTGGCCTTGGGC 470  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160  
Db 471 ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 530  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 531 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACCTCAGCTTCTCAGCTGTCCAG 590  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 591 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATCCTT 650  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 651 GTCACGTTGCTGCTGGATACGCTGCCCATGCTGGCAACGCTCCTGCTGCTCTGCTTCTTC 710  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 711 GTCTTCTTCACTTTCGGCATCGCTGGCGCTCCAGCTGTGGCGAGGGCTGCTTCGGAACCGA 770  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
Db 771 TGCTTCTTACCTGAGAAATTTCAGCCTCCCCCTGAGCGTGGAACCTGGAGCGCTATTACCAG 830  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 831 ACAGAGACGAGGATGAGAGCCCTTTCATCTGTCTCCAGCCACGCCAGAACGGCATGGCG 890  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 891 TCCTGCAGAACGTCGCCACGCTGCGGGGACGGGGCGGTGGCCACCTTGGCGTCTG 950  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 951 GACTATGAGGCTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAAACCACTACTAC 1010  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
Db 1011 ACCAACTGCTCAGCGGGGAGCAACAACCCCTTCAAGSGCGCCATCAACTTGACAACATT 1070  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1071 GGCTATGCTGATGCCATCCTTCCAGTCACTACGCTGGAGGGCTGGTGGTGGCATCATG 1130  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
Db 1131 TACTTTGTGATGGATGCTCATTCCTTCTACAATTTCATCTACTTCACTCCTCATCATC 1190  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1191 GTGGGCTCCTTCTTCAATGATCAACCTGTGCTGGTGTGATGTCACGCGAGTTCTCAGAG 1250  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420

Db 1251 ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCTGTCCAACGCC 1310  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
Db 1311 AGCACCTTGGTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1370  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1371 GTGTACATCCTTCGTAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1430  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1431 CGGTTGGGCGTCTCAGCAGCCCGCAGCACCCCTCGGGGCCAGGAGACCCAGCCAGCAGC 1490  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
Db 1491 AGCTGCTCTGCTCCACCCGCGCCTATCCGTCCACCACTGTGTGCACCAACCAACCAC 1550  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1551 CATCACCACTACCACTGGCAATGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 1610  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Db 1611 ATCCAGGACAGGATGCCAATGGTCCCGCAGGCTCATCTGCCACCACTCGACGCCT 1670  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db 1671 GCCCTCTCCGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1730  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
Db 1731 TGCCACTTAGAGCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCCCATCTGAGGCATCC 1790  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600  
Db 1791 GGCGAGGACTGTGGCAGCGGGAAGGTGTATCCCAACCGTGACACCGCCCTCCACCGGAG 1850  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaAlaSerSerGlyProProThrLeuThr 620  
Db 1851 ACGCTGAAGGAGAGGACACTAGTAGAGTGGTGCCAGCTCTGGGCCCCCAACCCCTCACC 1910  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db 1911 AGCCTCAACATCCCCACCGGGCCCTACAGTCCATGCACAAGTCTGGAGACACAGAGT 1970  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1971 ACAGTGCCTGCCAAAGCTCTTCAAGATCTCCAGCTCCAGCCCTTGCTTGAAGCAGACAGTGA 2030  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db 2031 GCCTGTGTCAGACAGCTGCCCTTACTGTGCCGGGCCGGGCGGAGGGAGGCTC 2090  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2091 GCCGACCGTGAAATGCCTGACTCAGACAGCGAGGAGTTTATGATTTCACACAGGATGCC 2150  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Db 2151 CAGCACAGCAGCCTCCGGGACCCCCACAGCCCGCGGCAACGGAGCCTGGGCCAGATGCA 2210  
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740  
Db 2211 GAGCCCAGCTCTGTGTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2270  
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
Db 2271 GACAGCAAGTACTTTGGCCGGGGAATCATGATCGCCATCTGCTGTCACACACTCAGCATG 2330  
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Db 2331 GGCATCGAATACCAAGCAGCAGCCCGGAGGAGCTTACCACACGCCCTAGAAATCAGCAACATC 2390



QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800  
DB 2391 GTCTTACACAGCTCTTTGGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGTCCTTT 2450  
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820  
DB 2451 GGCTACATCAAGAATCCCTACAACATCTTCGATGTTGATGTTGATCAGCGTGTGG 2510  
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
DB 2511 GAGATCGTGGCCAGCAGGGGGCGGCTGTGCGTGTGCTGCGACCTTCGCGCTGATCGT 2570  
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
DB 2571 GTGCTGAAGCTGCTGCGCTTCTCGCGCGCTGCAGCGGAGCTGGTGTGCTCATGAAG 2630  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880  
DB 2631 ACCATGGACACGTGGCCACCTTCTGCATGCTGCTTATGCTTCTTCATCTTCAGC 2690  
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
DB 2691 ATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCTCTGGGCCATCGTCACTGTCTT 2750  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu 920  
DB 2751 CCAGACCGGAAGAAATTTTGACTCTCTGCTGCGCCATCGTCACTGTCTTTCAGATCCTG 2810  
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940  
DB 2811 ACCCAGGAGGACTGGAACAAAGTCTCTACAATGTTATGGCTCCACGTCCTCGGGCG 2870  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
DB 2871 GCCCTTTATTTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTC 2930  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980  
DB 2931 GCCATTCTGTGGAGGGCTTCCAGGCGGAGGAATCAGCAACGGGAAGATCGGAGTGGAA 2990  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
DB 2991 CAGTTAAGCTGTATTTCAGTGCCTGTGACTCCAGGGGGAGATGCCAACAGTCCGAA 3050  
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020  
DB 3051 TCAGAGCCCGATTCTTCTACCCAGCTGGATGGTGTGATGGGACAGGAAGAAGTCTTG 3110  
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProIle 1040  
DB 3111 GCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCTGTGCGCCCTCTCATC 3170  
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
DB 3171 ATCCACACGGCGCCACACCCATGTGCTGCCAAGAGCACAGCACGGGCTGGGCGGAG 3230  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
DB 3231 GCGCTGGGCCCTGCGTTCGCGCCGACAGCAGCAGCGGGTTCGGCAGAGCCCTGGGCGGCC 3290  
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
DB 3291 CACGAGATGAAGTCAACCCCGCCAGCGCGCAGCTCTCCGCACAGCCCTGGAGCGCTGCA 3350  
QY 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
DB 3351 AGCAGCTGGACAGCAGCGGCTCCAGCGGAAACAGCCTCGCGCGTGCACCCAGCCCTGAAG 3410  
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140  
DB 3411 CGGAGAAAGCCCAAGTGGAGAGCGGCGTCCCTGTTGTCCGGAGAGGCCAGGAGCCAG 3470

QY 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
DB 3471 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTGCGGCGAGTGACCATCGCCAC 3530  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
DB 3531 AGGGGTCCCTGGAGCGGAGGCCCAAGAGTTCTTTGACCTTGCCAGACACACTGCAGCTG 3590  
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
DB 3591 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACGAGGACTGCAAT 3650  
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
DB 3651 CGCAAGTCGGCTTCAGGGCGCCTGCGCCCGGCCCTGCGGCTGATGACCCCCACTGGAT 3710  
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyArgValArgAlaTrpIle 1240  
DB 3711 GGGGATGACGCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGGTCCGCGGTGGATC 3770  
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
DB 3771 CGAGCCCGACTCCCTGCCCTGCTACCTCGAGCGAGACTCCTGCTCACCTACATCTTCCCT 3830  
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
DB 3831 CCTCAGTCCAGGTTCCGCCCTCCTGTGTCAACGGATCATCACCAAGATGTTTCGACCAG 3890  
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
DB 3891 GTGGTCTTGTTCATCATCTTCTTAACTGCATCACCATCGGCATGGAGCGCCCCAAAT 3950  
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
DB 3951 GACCCCCACAGCGCTGAACGCATCTCTGACCCCTCTCCAATTACATCTTCACCGCAGTC 4010  
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340  
DB 4011 TTTCTGGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTGTCTTCGGGGAGCAGGCG 4070  
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
DB 4071 TACCTGGGAGCAGTTGGAACTGCTGGACGGGCTGTTGGTGTCTCATCTCCGTTCATCGAC 4130  
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380  
DB 4131 ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTG 4190  
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
DB 4191 CGGCTGCTGGGACCCCTGCGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTG 4250  
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420  
DB 4251 GTGGTGGAGACGCTGATGCTCTCACTGAACCCCATCGGCAACATTTAGTTCATCTGCTGT 4310  
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
DB 4311 GCCTTCTTCATCATTTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4370  
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
DB 4371 TGCCAGGGGAGGATACCAAGGAACATCACCAATAATCGGACTGTGCCGAGGCCAGTTAC 4430  
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
DB 4431 CGGTGGTCCGGCACAAGTACAACTTTGACAACCTTGGCAACCTTGGCCAGGCCCTGATGTCCCTGTT 4490  
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
DB 4491 GTTTTGGCCTCCAAGGATGGTGGGTGGACATCATGTACGATGGGTGGATGCTGTGGGC 4550  
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520

Db	4551	GTGGACGAGCAGCCCATCATGAACCAACCCCTGGATGCTGCTACTTTCATCTCGTTC	4610
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe	1540
Db	4611	CTGCTCAFTGTGGCCCTCTTTGTCTGAACATGTTGTGGGTGTGGTGGAGAACTTC	4670
QY	1541	HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu	1560
Db	4671	CACAAGTGTAGGCAGCACCCAGGAGGAAGAGGAGGCCGCGGGAGAGAAAGCGCCTA	4730
QY	1561	ArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580
Db	4731	CGAAGACTGGAGAAAAAGAGAGAGGAGGCCGCGGGAGAGAAAGCCAGTGC	4790
QY	1581	ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1600
Db	4791	CGCTTCCGGCTCCTCGTCCACCACCTGTGCACCGCACTACCTGGACCTTTCATCACA	4850
QY	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
Db	4851	GGTGTATCCGGCTGAACGTGGTCACCATGGCCATGGAGCACTACCGAGCAGCCAGATT	4910
QY	1621	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer	1640
Db	4911	CTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTATCTTTGTCTTGAGTCA	4970
QY	1641	ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeu	1660
Db	4971	GTITTCAAACTTGTGGCCTTTGGTTTCCGTCCGTTCTTCCAGGACAGGTGGAACCGACTG	5030
QY	1661	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1680
Db	5031	GACCTGGCCATTGTGCTGTCTCCATCATGGGCATCACGCTGGAGGAAATCGAGGTCAAC	5090
QY	1681	AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
Db	5091	GCCTCGCTGCCCATCAACCCACCATCATCCGCATCATGAGGGTGTGCGCATTGCCCCGA	5150
QY	1701	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln	1720
Db	5151	GTGCTGAAGCTGCTGAAGATGCTGTGGCATGCGGGCGCTGCTGGACACGGTGATGCAG	5210
QY	1721	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1740
Db	5211	GCCCTGCCCCAGGTGGGAACCTTGGACCTTCTCTCATGTTGTGTTTTTCATCTTTGCA	5270
QY	1741	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1760
Db	5271	GCTCTGGCGGTGAGACTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGC	5330
QY	1761	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1780
Db	5331	CTGGGCCGTGTCATGCCACCTTTCCGAACTTTGGCATGGCCCTTCTAACCCCTTCCGAGTC	5390
QY	1781	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu	1800
Db	5391	TCCACAGGTGACAAATTGGAATGGCATTATGAAGGACACCCCTCCGGGACTGTGACCAAGGAG	5450
QY	1801	SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla	1820
Db	5451	TCCACCTGCTACAACACGGTTCATCTCGCCTATCTACTTTGTGTCTTCTGCTGACGGCC	5510
QY	1821	GlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsn	1840
Db	5511	CAGTTCTGTAGTCAACGTGGTGTATCGCCGTGCTGATGAAGCACTGGAGGAGAGCAAC	5570
QY	1841	LysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu	1860
Db	5571	AAGGAGCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTTC	5630
QY	1861	SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro	1880

Db	5631	AGCCCCCAGCCCCCACTCGCCACTGGGCAGCCCCCTTCTCTGGCCTGGGGTCGAGGGCCCC	5690
QY	1881	AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla	1900
Db	5691	GACAGCCCCGACAGCCCCAAGCCTGGGCTCTGCACCCAGCGGCCCCACGCAGATCAGCC	5750
QY	1901	SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyPro	1920
Db	5751	TCCCACTTTTCCCTGGAGCACCCACGATGCAGCCCCACCCACGGAGCTGCCAGGACCA	5810
QY	1921	AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer	1940
Db	5811	GACTTACTGACTGTGCGAAGTCTGGGTTCAGCCGAAACGCACTCTCTGCCCAATGACAGC	5870
QY	1941	TyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeu	1960
Db	5871	TACATGTGTGGCATGGAGCACTGCCGAGGGCCCCCTGGGACACAGGGGTGGGGCTC	5930
QY	1961	ProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyr	1980
Db	5931	CCCAAAGCTCAGTCAGGCTCCGTCTTGTCCTGTTCACTCCAGCCAGCAGATACCACTAC	5990
QY	1981	IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrp	2000
Db	5991	ATCCTGCAGTTCCCAAGATGCACCTCATCTGTCCAGCCCCACAGCGCCCCAACCTGG	6050
QY	2001	GlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArg	2020
Db	6051	GGCACCATCCCAAACTGCCCCCAACAGGACGCTCCCCCTTGGCTCAGAGGCCACTCAG	6110
QY	2021	ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp	2040
Db	6111	CGCCAGGCAGCAATAAGGACTGACTCTCTGGACGTTTCAGGGTCTGGGCAGCGCGGAAGAC	6170
QY	2041	LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGly	2060
Db	6171	CTGTGGCAGAGGTAGTGGGCCCTCCCGCCCCCTGGCCGGGCCCTACTCTTTCTGGGGC	6230
QY	2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet	2080
Db	6231	CAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATG	6290
QY	2081	ThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThr	2100
Db	6291	ACCCGCCAGCCCCCTTGGCCAGGCCCAAGAACCCAACTGGGGCAAGGCCCTCCAGAGACC	6350
QY	2101	ArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProPro	2120
Db	6351	AGAAGCAGCTTAGAGTTGGACACGGAGCTGAGCTGGATTTTCAGGAGACCTCCTGCCCCCT	6410
QY	2121	GlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAla	2140
Db	6411	GGCGGCCAGGAGAGCCCCCATCCCCACGGGACCTGAAGAAAGTGTACAGCGTGGAGGCC	6470
QY	2141	GlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAla	2160
Db	6471	CAGAGCTGCCAGCGCGGCCCTACGTCTTGCTGGATGAGCAGAGGAGACACTCTATCGCC	6530
QY	2161	ValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGly	2180
Db	6531	GTCAGCTGCCTGGACAGCGGCTCCCAACCCCACTGGGCACAGACCCCTCTAACCTTGGG	6590
QY	2181	GlyGlnProLeuGlyProGlySerArgProLysLysLysLeuSerProProSerIle	2200
Db	6591	GGCCAGCCTCTTGGGGGCCCTGGAGCCGGCCCCAAGAAAAAACTCAGCCGCCCTAGTATC	6650
QY	2201	ThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeu	2220
Db	6651	ACCATAGACCCCCCGAGAGCCCAAGTCTCTCGGACCCCGCCAGCCCTTGGTATCTGCCTC	6710
QY	2221	ArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSer	2240
Db	6711	CGGAGGAGGGCTCCGTCCAGCGACTCCAAGGATCCCTTGGCCCTCTGGCCCCCTTGACAGC	6770

[illegible]

RESULT 3  
ADQ89063  
ID ADQ89063 standard; cDNA; 7648 BP.

WO2004065576-A2.

05-AUG-2004.

14-JAN-2004; 2004WO-US000750.

15--JAN-2003: 2003US-0440318P.

04-FEB-2003; 2003US-0444783P:

27-MAR-2003; 2003US-0457901P.

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19-MAY-2003; 2003US-0471614P.

16-JUN-2003; 2003US-0478742P.

18-JUL-2003; 2003US-0488529P.

30-JUL-2003; 2003US-0491156P.

02-SEP-2003; 2003US-0499594P.

26-SEP-2003; 2003US-0506332P.

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WPI: 2004-562167/54.

P-PSDB; ADQ89064.

Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological disorder.

Claim 1: SEQ ID NO 15: 542bp: English:

The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder

Db 841 TCCTGCAGAAAGCGTGCACCGTGCCTGGGGGACGGGGGGGGTGGCCACACCTTGGCGTCTG 900  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 901 GACTATGAGGCCTACAAACAGCTCCAGCAACACCACTGTGTCACTGGAAACCAAGTACTAC 960  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
Db 961 ACCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAACATT 1020  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360  
Db 1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCTATCACGCTGAGGGCTGGGTCCGACATCATG 1080  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
Db 1081 TACTTTGTGATGGATGCTCATCTCTTCTACAAATTTTCATCTTCAATCTCTCTCATCATC 1140  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGGTGTGATTCACCGCAGTCTTCAGAG 1200  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAGCAGCGGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCTCTGTCCAACGCC 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
Db 1261 AGCACCTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTGTCAAGTACCTG 1320  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1321 GTGTACATCCTTCGTAAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGCGCAGGAGACCCAGCCAGCAGC 1440  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 500  
Db 1441 AGCTGCTTCGCTCCCAACCGCGCCTATCCGTCCACCACTGCTGTCACCAACCAACCAAC 1500  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CATCACCACTACCACTGGGCAATGGGCTGGGCGCTCAGGGCCCCCGGGCCAGCCCGGAG 1560  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Db 1561 ATCCAGGACAGGATGCCAATGGGTCCCGCAGGCTCATGCTGCCACCACTCGACGCCT 1620  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db 1621 GCCCTCTCCGGGGCCCCCTGTTGGCGCAGAGTCTGTGACAGCTTCTACCATGCCGAC 1680  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
Db 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGGCCCCCTCCAGGTCCCCATCTGAGGCATCC 1740  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600  
Db 1741 GGCAGGACTGTGGGACGCGGAAGGTGTATCCACCGTGCACACCAAGCCCTCCACCGGAG 1800  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
Db 1801 ACGCTGAAGGAGAGGAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACC 1860  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db 1861 AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAGCTGTGGAGACACAGAGT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACAGGTGCCTGCCAAAGCTCTTGAAGATCTCCAGCCCTTGTGAAAGCAGACAGTGGGA 1980

QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db 1981 GCCTGTGTCCAGACAGTGCCTTACTGTGCCCGGGCGGGGAGGGAGGAGCTC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCGACCGTGAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTTCACACAGGATGCC 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Db 2101 CAGCACAGCGACCTCCGGGACCCCAACAGCGGGCGGCAACGAGACCTGGGCCAGATGCA 2160  
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740  
Db 2161 GAGCCAGCTCTGTGTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220  
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
Db 2221 GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTTGGTCAACACACTCAGCATG 2280  
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Db 2281 GGCAATCGAATACCAAGAGAGAGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340  
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPhe 800  
Db 2341 GTCTTCACCAAGCTTCTTGGCCTGGAGATGCTGCTGAAGCTGCTTGTGTATGTTCCCTTT 2400  
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr 820  
Db 2401 GGCTACATCAAGAATCCCTACAAATCTTCGATGGTGTCTTGTGTCATCAGCGTGTGG 2460  
QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
Db 2461 CAGATCGTGGGCGCAGCAGGGGGCGGCTGTGCGTGTGCGGACCTTCCGCTGATGCGT 2520  
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
Db 2521 GTGCTGAAGCTGGTGGCTTCTTCCGCGCGCTGCAGCGGAGCTGGTGTGTCATGAAG 2580  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880  
Db 2581 ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTTCTCATCTTCTCATC 2640  
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
Db 2641 ATCCTGGGATGCATCTCTCGGCTGCAAGTTGCTTCTGAGCGGATGGGACACCCCTG 2700  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
Db 2701 CCAGACCGGAAGAAATTTTGACTCTTGTCTTGGGCCATCGTCACTGTCTTTCAGATCCTG 2760  
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
Db 2761 ACCCAGGAGACTGGAACAAAGTCTCTACAATGATGATGGCTCCACGTCGTCCTGGGCG 2820  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
Db 2821 GCCCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTCGCTCTTCAATTGCTGTC 2880  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980  
Db 2881 GCCATTTCTGGTGGAGGGCTTCCAGCGGAGGAAATCAGAAACGGGAAGATGCGAGTGA 2940  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
Db 2941 CAGTTAAGCTGTATTCAGCTGCCTGTGACTCCAGGGGGAGATGCCAACAAAGTCCGAA 3000  
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020  
Db 3001 TCAGAGCCCGATTCTTCTCACCCAGCCTGGATGGTGTGAGGAGCAGGAAGAGTCTTG 3060



QY	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProLeuIle	1040
DB	3061	GCCTTGGTGTCCCTGGAGAGACCCGGAGCTGCGAAGAGCCTGCTGCCGCTCTCATC	3120
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
DB	3121	ATCCACACGGCCGCCACACCCATGTGCTGCCCAAGAGACACAGCACGGGCTTGGGCGAG	3180
QY	1061	AlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
DB	3181	CGCTGGGCCCTGCTGCGCCGCACACAGCAGCAGCGGTTCGGCAGAGCCTGGGGCGGC	3240
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
DB	3241	CACGAGATGAAGTACCGGCCAGCGCCAGCGCCAGCCTCGGCCGTGCACCCAGCCTGAAG	3300
QY	1101	SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
DB	3301	AGCAGCTGGACCAAGCAGCGGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG	3360
QY	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln	1140
DB	3361	CGGAGAACCCAAAGTGAGAGCGGCGGTCCCTGTTGTGGGAGAAAGCCAGGAGCCAG	3420
QY	1141	AspGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
DB	3421	GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTCGGGCAGTGACCATCGCCAC	3480
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
DB	3481	AGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG	3540
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
DB	3541	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAAGACTGCAAT	3600
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProLeuAsp	1220
DB	3601	GGCAAGTCGGCTTCAGGGCGCCTGGCCCGGCCCTGCGGCCTGATGACCCCGACTGGAT	3660
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
DB	3661	GGGGATACGCCGATACGAGGGCAACCTGAGCAAAAGGGAACGGGTCCGGCGTGGATC	3720
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
DB	3721	CGAGCCCGACTCCCTGCCTGCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCT	3780
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
DB	3781	CCTCAGTCCAGGTTCCGCTCCTGTGTACCGGATCATCACCACAAGATGTTGACCCAC	3840
QY	1281	ValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
DB	3841	GTGGTCTTGTATCATCTTCTTAACATGCATCACCATCGCCATGGAGCGGCCCAAAATT	3900
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
DB	3901	GACCCCCACAGCGCTGAACGCATCTTCTCTGACCCCTCTCCAATTACATCTTACCCGAGTC	3960
QY	1321	PheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGlnAla	1340
DB	3961	TTTCTGGCTGAATGACAGTGAAGGTGGTGGCTGGGTGGTGTCTTCGGGAGCAGGCG	4020
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
DB	4021	TACCTGGGAGCAGTTGGAACGTGCTGGACGGGCTGTTGGTGTCTCATCTCCCTCATCGAC	4080
QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
DB	4081	ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGTGCTG	4140
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400

Db	4141	CGGCTGCTGGGACCCCTGGCCCGCTCAGGGTGATCAGCCGGGCGCAGGGGCTGAAGCTG	4200
Qy	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys	1420
Db	4201	GTGGTGGAGACGCTGATGTCTCACTGAACCCATCGGCAACATTGTAGTCATCTGCTGT	4260
Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
Db	4261	GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTG	4320
Qy	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4321	TGCCAGGGCGAGGATACCAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC	4380
Qy	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4381	CGGTGGTCCGGCACAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTTCCTGTTC	4440
Qy	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4441	GTTTTGGCCCTCCAAGGATGGTTGGTGGACATCATGTACGATGGGCTGGATGCTGTGGGC	4500
Qy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4501	GTGGACCAGCAGCCCATCATGAACCAACCAACCCCTGGATGCTGTGTACTTCATCTCGTTC	4560
Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4561	CTGCTCATTTGTGGCCTTCTTTGTCTGAACATGTTTGTGGTGTGGTGTGGAGAACTTC	4620
Qy	1541	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu	1560
Db	4621	CACAAGTGTCCGCAGCACCCAGGAGGAAGAGGAGGCCCGCGCGGAGAGAAGCGCCTA	4680
Qy	1561	ArgArgLeuGluLysLysArgArg	1568
Db	4681	CGAAGACTGGAGAAAAAGAGAAGGAATCTAATGCTGGACGATGTAATTGTTCCGGCAGC	4740
Qy	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1582
Db	4741	TCAGCCAGCGTGGCTCAGAAGCCCGAGTGCAAACTTACTACTCCGACTACTCCCGCTTC	4800
Qy	1583	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
Db	4801	CGGCTCCTCGTCCACCACCTGTGCAACGACCTACCTGGACCTCTTCATCACAGGTGTC	4860
Qy	1603	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1622
Db	4861	ATCGGGCTGAACGTGGTCACCATGGCCATGAGCACTACCAGCAGCCCCAGATTCTGGAT	4920
Qy	1623	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
Db	4921	GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCACTCTTTGTCTTGGAGTCAGTTTTC	4980
Qy	1643	LysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeu	1662
Db	4981	AAACTTGTGGCCTTGGTTTCCGTCCGTTCTTCAGGACAGGTGGAACAGCTGGACCTG	5040
Qy	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682
Db	5041	GCCATTGTGCTGTCTCCATCATGGGCATCACGCTGGAGGAATCGAGGTCAACGCCTCG	5100
Qy	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702
Db	5101	CTGCCCATCAACCCACCATCATCCGCATCATGAGGGTGTGCGCATTGGCCGAGTGCTG	5160
Qy	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5161	AAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGACACGGTGATGCAGGCCCTG	5220
Qy	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaLeu	1742

Db 5221 CCCAGGTGGGAACCTGGACTTCTCTTCAITGTTGTTGTTTTTTCATCTTTGCAGCTCTG 5280

QY 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762

Db 5281 GGCCTGGAGCTCTTTGGAGACCTGGAGTGTACGAGACACACCCCTGTGAGGGCCTGGGC 5340

QY 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782

Db 5341 CGTCATGCCACCTTTCGGAACCTTGGCATGGCCCTTCTTAACCTCTTCCGAGTCTCCACA 5400

QY 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802

Db 5401 GGTGACAAATGGAAATGGCAATTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGTCCACC 5460

QY 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822

Db 5461 TGCTACAAACACGGTTCATCTCGCCTATCTACTTTGTGTCTTCTGTGCTGACGGCCAGTTC 5520

QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842

Db 5521 GTGCTAGTCAACGTGGTGATCGCCGTCTGATGAAGCACCTGGAGGAGAGCAACAAGGAG 5580

QY 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862

Db 5581 GCCAAGGAGGAGCCGAGCTAGAGCTGAGCTGAGTGAAGACCCCTCAGCCCC 5640

QY 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882

Db 5641 CAGCCCCACTCGCCACTGGGCAGCCCTTCTCTGGCTGGGTCGAGGGCCCCGACAGC 5700

QY 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902

Db 5701 CCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACCGGAGATCAGCCTCCAC 5760

QY 1903 PheSerLeuGluHisProThr----- 1909

Db 5761 TTTTCCCTGGAGCACCCACGGACAGCAGCTGTTTGACACCATATCCCTGTGATCCAG 5820

QY 1909 ----- 1909

Db 5821 GGCTCCCTGGAGTGGGAGCTGAAGCTGATGACGAGCTGGCAGGCTGGCAGGCCAGGCC 5880

QY 1909 ----- 1909

Db 5881 TCTGCCTTCCCTTCTGTGACGTCAGAGATTGTGTCTGAACCGTCTGTCTCTAGCTCTG 5940

QY 1909 ----- 1909

Db 5941 ATGGAGGCTCTGTCTGTGACGTCAGAGATTGTGTCTGAACCGTCTGTCTCTAGCTCTG 6000

QY 1909 ----- 1909

Db 6001 ACGGATGACTCTTTCCTGTATGACATGCACACACTCTTACTTAGTGCCTGGAGAGCAAT 6060

QY 1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929

Db 6061 ATGCAGCCCCACCCACGGAGCTGCCAGGACCAAGACTTACTGACTGTGCGGAAGTCTGGG 6120

QY 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949

Db 6121 GTCAGCCGAACGCACTCTCTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCC 6180

QY 1950 GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu 1969

Db 6181 GAGGGGCCCTGGGACACAGGGGCTGGGGCTCCCCAAGCTCAGTCAGGCTCCGCTCTTG 6240

QY 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989

Db 6241 TCCGTTCACTCCAGCCAGCAGATACCAAGCTACATCTCTGCAGCTTCCCAAAGATGCACCT 6300

QY 1990 HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2009

Db 6301 CATCTGCTCCAGCCCCACAGCGCCCCCAACCTGGGGCACCATCCCCAAACTGCCCCCACCA 6360

QY 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029

Db 6361 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGGGCCAGGAGCAATAAGACTGACTCC 6420

QY 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049

Db 6421 TTGGACGTTTCAAGGTTCTGGCAGCCCGGGAAGACCTGTGGCAGAGTGTAGTGGCCCTCC 6480

QY 2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069

Db 6481 CCGCCCTGGCCCGGGCTACTCTTTCTGGGCCAGTCAAGTACCCAGGCACAGCAGCAC 6540

QY 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089

Db 6541 TCCCGCAGCCACAGCAAGATCTCAAGCACATGACCCCGCCAGCCCTTGTCCAGGCCCA 6600

QY 2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109

Db 6601 GAACCAACTGGGGCAAGGGCCCTCCAGAGACCAAGAGCAGCTTAGAGTTGGACACGGAG 6660

QY 2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerPro 2129

Db 6661 CTGAGCTGGATTTACGAGAGACCTCTCTGCCCTCTGGCGCCAGGAGGCCCTCATCCCCA 6720

QY 2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149

Db 6721 CGGACCTGAAGAAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCGGCTACGTCC 6780

QY 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169

Db 6781 TGGCTGGATGAGCAGAGAGACACTCTATCGCCGTGAGTGCCTGGACAGCGGCTCCCA 6840

QY 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySer 2189

Db 6841 CCCACCTGGGCACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTGGGGGCTGGGAGC 6900

QY 2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209

Db 6901 CGGCCCAAGAAAAAACTCAGCCCGCTAGTATACCATAGACCCCCCGAGAGCAAGGT 6960

QY 2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229

Db 6961 CCTCGACCCCGCCCGCCAGCCCTGTATCTGCTCCGAGGAGGGCTCCGTCACGAGCTCC 7020

QY 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249

Db 7021 AAGGATCCCTTGGCCTCTGGCCCCCTGACAGCATGGTGCCTCGCCCTCCCAAGAAA 7080

QY 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266

Db 7081 GATGTGCTGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 7131

RESULT 4

ADS16298

ID ADS16298 standard; DNA; 7648 BP.

XX

AC ADS16298;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human voltage-dependent alpha 1G subunit calcium channel (CACNA1G) DNA.

XX

KW Voltage-dependent ion channel; drug candidate;

KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;

KW anticonvulsant; antiarrhythmic; human; alpha 1G subunit; ds.

XX

OS Homo sapiens.

OS

XX US2004175761-A1.

PN

XX 09-SEP-2004.

PD

XX

PF 01-MAR-2003; 2003US-00377139.  
XX  
PR 01-MAR-2003; 2003US-00377139.  
XX  
PA (MACK/) MACKINNON R.  
PA (MACK/) MACKINNON A L.  
PA (JIAN/) JIANG Y.  
PA (RUTA/) RUTA V.  
XX  
PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;  
XX  
DR WPI; 2004-642122/62.  
DR REFSEQ; NM\_018896.  
XX  
PT Screening drug candidates that target voltage dependent ion channel  
PT protein, involves contacting screening protein with chemical compound,  
PT which is drug candidate and determining whether chemical compound binds  
PT to screening protein.  
XX  
PS Disclosure; SEQ ID NO 10; 61bp; English.  
XX  
CC The invention relates to the composition of matter suitable for use in  
CC identifying chemical compounds that bind to voltage-dependent ion channel  
CC proteins. The composition comprises a screening protein that consists of  
CC an ion channel voltage sensor domain of the ion channel protein  
CC immobilised on a solid support. The invention is useful for identifying  
CC chemical compounds (drug candidate) that bind to voltage-dependent ion  
CC channel proteins. The drug candidate of the invention is utilised for  
CC treating a condition mediated by aberrant electrical activity that  
CC initiates uptake or release of neurotransmitters and contraction of  
CC muscles. The drug candidate of the invention is also utilised for  
CC treating epilepsy and arrhythmia. The present sequence is a voltage-  
CC dependent calcium channel DNA.  
XX  
SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 7648  
Score: 11815.50 Matches: 2264  
Percent Similarity: 95.29% Conservative: 1  
Best Local Similarity: 95.25% Mismatches: 1  
Query Match: 99.26% Indels: 111  
DB: 13 Gaps: 2  
  
US-09-611-257A-37 (1-2266) x ADS16298 (1-7648)  
  
QY 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20  
DB 1 ATGGACGAGGAGGATGGAGCGGGCCGAGGAGTCGGGACAGCCCCGGAGCTTCATG 60  
  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
DB 61 CGGCTCAACGACTGTTCGGGGCCGGGGCCGGGGCCGGGGTCAGCAGAAAGGAC 120  
  
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
DB 121 CCGGGCAGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTT 180  
  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrPheGlyLeuArgThrValCysAsn 80  
DB 181 TTCCTTCTACTTGAGCCAGGACAGCCCGCCGGGAGCTGGTGTCTCCGACCGGTCTGTAA 240  
  
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
DB 241 CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTCTCAACTGCGTACCCCTGGGCATG 300  
  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
DB 301 TTCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCTT 360  
  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
DB 361 GATGACTTCATCTTGCCTTCTTTGCGGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC 420

QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160  
DB 421 ATCTTTGGGAAAAAGTGTATTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 480  
  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 481 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTTCAGG 540  
  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 541 ACAGTCCGTGCTGCTGCAGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTT 600  
  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
DB 601 GTCACGTTGCTGCTGGATACGCTGCCCATGCTGGGCAACGCTCTGCTGCTCTGCTTCTTC 660  
  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240  
DB 661 GTCTTCTTTCATCTTTCGGCATCGCTCGCGCTCCAGCTGTGGGCGAGGGCTGCTTCGGAACCG 720  
  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
DB 721 TGCTTCTTACTGAGAATTTTACGCTCCCTCCCTGAGCGTGGAGCTGGAGCGCTATTACCGAG 780  
  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
DB 781 ACAGAGAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCAGCGAGAACGCGCATGCGG 840  
  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
DB 841 TCCTGCAAGAGCGTGCACCGCTGCGCGGGGACGGGGGGCGGTGGCCCACTTGGCGGTCTG 900  
  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr 320  
DB 901 GACTATGAGGCCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCACTACTAC 960  
  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
DB 961 ACCAACTGCTCAGCGGGGAGGACAAACCCCTTCAAGGGCGCATCAACTTTGACAAACATT 1020  
  
QY 341 GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360  
DB 1021 GGCTATGCTGGATCGCCATCTTCCAGGTTCATCACGCTGGAGGGCTGGGTGACATCATG 1080  
  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
DB 1081 TACTTTGTGATGGATGCTCATCTCTTCTACAATTTCTACTTCTCTCTCTCTCTCTCTCT 1140  
  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
DB 1141 GTGGGCTCTTCTTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1200  
  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
DB 1201 ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGG 1260  
  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440  
DB 1261 AGCACCTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1320  
  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
DB 1321 GTGTACATCTCTCGTAAGGAGCCCGCAGGCTGGCTAGGTCTCTCGGGCAGCAGGTGTG 1380  
  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
DB 1381 CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGGCGCAGGAGACCCAGCCAGCAG 1440  
  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
DB 1441 AGCTGCTCTCGCTCCCAACCGCGCCTATCCGTCACCACTGGTGGTGGTGGTGGTGGTGG 1500





Db 3661 GGGGATACGCCGATGACGAGGGCAACCTGAGCAAAGGGGAACGGGTCCGGCGGTGGATC 3720

Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260

Db 3721 CGAGCCCGACTCCCTGCCTGCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTCCCT 3780

Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280

Db 3781 CCTCAGTCCAGGTCCGCCTCCTGTGTACCCGGATCATCACCAAGATGTTCCAGCAC 3840

Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300

Db 3841 GTGGTCCCTGTGCATCATCTCTTAACTGCATCACCATCGGCATGGAGCGCCCAAAAT 3900

Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320

Db 3901 GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAAATACATCTTCAACGCAGTC 3960

Qy 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340

Db 3961 TTTCTGGCTGAATGACAGTGAGGTGTGGCACTGGGCTGGTCTTCCGGGAGCAGCG 4020

Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360

Db 4021 TACCTGCGGAGCAGTTGGAACGTGCTGGACGGGCTGTTGGTGTCTATCTCCGTCTCGAC 4080

Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380

Db 4081 ATTTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTCTG 4140

Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400

Db 4141 CGGCTGCTGCGGACCTCGGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGTGAAGCTG 4200

Qy 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420

Db 4201 GTGGTGGAGACGTGATGCTCTCACTGAAACCCCATCGGCAACATTTAGTCACTCTGTGT 4260

Qy 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440

Db 4261 GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTG 4320

Qy 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460

Db 4321 TGCCAGGGCGAGGATACAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC 4380

Qy 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480

Db 4381 CGGTGGTCCGGCACAAAGTACAACATTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTT 4440

Qy 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500

Db 4441 GTTTTGGCCTCCAAGGATGTTGGGTGGACATCATGTACGATGGGCTGGATGCTGTGGGC 4500

Qy 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520

Db 4501 GTGGACCGACGCCCATCATGAACCAACCCCTGGATGCTGTGTACTTTCATCTCGTTC 4560

Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540

Db 4561 CTGCTCATTTGTGGCTTCTTTGTCTGAAACATGTTTGTGGGTGTGGTGGAGAACTTC 4620

Qy 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLeu 1560

Db 4621 CACAAGTGTCCGAGCACCCAGGAGGAAGAGGAGGCCCGGGCGGGAGGAGAAGCGCTTA 4680

Qy 1561 ArgArgLeuGluLysLysArgArg----- 1568

Db 4681 CGAAGACTGGAGAAAAAGAGAGGAATCTAATGCTGGACGATGTAATTGCTTCCGGGAGC 4740

Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582

Db 4741 TCAGCCAGCGGTGCGTCAAGAAGCCCCAGTGCAACCTTACTACTCCGACTACTCCCGCTTC 4800

Qy 1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602

Db 4801 CGGCTCCTCGTCCACCACATTGTGCACGAGCCACTACCTGGACCTCTTTCATCACAGGTGC 4860

Qy 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622

Db 4861 ATCGGGCTGAACGTGGTCACCATGGCCATGGAGCACTACCAAGAGCCCCAGATTCTGGAT 4920

Qy 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642

Db 4921 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTTCTTGTCTTGGAGTCAGTTTC 4980

Qy 1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu 1662

Db 4981 AAACCTTGCGCCTTTGGTTTCCGTCGGTCTTCCAGGACAGGTGGAACCAAGCTGGACCTG 5040

Qy 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682

Db 5041 GCCATTGTGTGCTGTCTCATCATGGGCATCACGCTGGAGGAAATCGAGGTCAACGCCTCG 5100

Qy 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702

Db 5101 CTGCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGCTCGCATTTGCCGAGTGTG 5160

Qy 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722

Db 5161 AAGCTGTGAAGATGGCTGTGGGCATCGGGCGCTGTCTGCACCGGTGATGCAGGCCCTG 5220

Qy 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742

Db 5221 CCCCAGGTGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGCAGCTCTG 5280

Qy 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762

Db 5281 GCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCCCTGGC 5340

Qy 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782

Db 5341 CGTCATGCCACCTTTTCGAACTTTGGCATGGCCTTCCCTAACCCCTCTTCCGAGTCTCCACA 5400

Qy 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802

Db 5401 GGTGACAAATTGGAATGGCATTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGTCCACC 5460

Qy 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822

Db 5461 TGCTACAACACGCTCATCTCGCCTATCTACTTTGTGTCTTCGTGTCGCGGCCCAAGTTC 5520

Qy 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842

Db 5521 GTGCTAGTCAACGTGGTGTATCGCCGTGCTGATGAAGCACCTGGAGGAGAGCAACAAGGAG 5580

Qy 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862

Db 5581 GCCAAGGAGAGGCCGAGCTAGAGCTGAGCTGGAGCTGGAGATGAAGACCCCTCAGCCCC 5640

Qy 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882

Db 5641 CAGCCCCACTCGCCACTGGGCAGCCCTTCTCTGGCCTGGGCTCGAGGGCCCCGACAGC 5700

Qy 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902

Db 5701 CCCGACAGCCCCAAGCCTGGGGCTGTGCACCCAGCGGCCCGCGAGATCAGCCTCCAC 5760

Qy 1903 PheSerLeuGluHisProThr----- 1909

Db 5761 TTTTCCCTGGAGCACCCCAACGACAGGCAGCTGTTTGTACACCATATCCCTGTGTATCCAG 5820

Qy 1909 ----- 1909

Db 5821 GGCTCCCTGGAGTGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCCAGGGGGCCAGCCC 5880

QY 1909 ----- 1909  
Db 5881 TCTGCCTTCCCTTCTGCCCCCAGCCTGGAGGCTCCGACCCACAGATCCCTCTAGCTGAG 5940  
QY 1909 ----- 1909  
Db 5941 ATGGAGGCTCTGTCTCTGACGTCAGAGATTGTGTCTGAACCGTCTCTGTCTCTAGCTCTG 6000  
QY 1909 ----- 1909  
Db 6001 ACGGATGACTCTTTGCTGTGATGATGACATGCACACACTTTACTTAGTGCCCTGGAGAGCAAT 6060  
QY 1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929  
Db 6061 ATGCAGCCCCACCCACGAGCTGCCAGGACCCAGACTTACTGACTGTGCGGAAGTCTGGG 6120  
QY 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949  
Db 6121 GTCAGCCGAACGCACTCTCTGCCCCAATGACAGCTACATGTGTGGCATGGGAGCACTGCC 6180  
QY 1950 GluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeu 1969  
Db 6181 GAGGGGCCCCCTGGGACACAGGGGCTGGGGGCTCCCCAAGCTCAGTCAGGCTCGTCTTG 6240  
QY 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989  
Db 6241 TCCGTTCACTCCAGCCAGCAGATACAGCTACATCTCTGAGCTTCCCCAAGATGCACCT 6300  
QY 1990 HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro 2009  
Db 6301 CATCTGCTCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCAACTGCCCCCACC 6360  
QY 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029  
Db 6361 GGACGCTCCCCCTTGGCTCAGAGGCCACTCAGGCGCCAGGACGACAAATAGGACTGACTCC 6420  
QY 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049  
Db 6421 TTGGACGTTTCCGGGCTGGGCAGCCGGAGACCTGTGTGGCAGAGGTGAGTGGGCCCTCC 6480  
QY 2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069  
Db 6481 CCGCCCCCTGGCCCGGCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCAC 6540  
QY 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089  
Db 6541 TCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGCCCGAGGCCA 6600  
QY 2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109  
Db 6601 GAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAGAGCAGCTTAGAGTTGGACACGGAG 6660  
QY 2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlnGluGluProProSerPro 2129  
Db 6661 CTGAGCTGGATTTCAGGAGACCTCTGCCCCCTGGCGGCCAGGAGGCCCTCCATCCCCA 6720  
QY 2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149  
Db 6721 CGGGACCTGAAGAAGTGCTACAGCGTGGAGGCCCCAGAGCTGCCAGCGCGGCCTACGTCC 6780  
QY 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169  
Db 6781 TGGCTGGATGAGCAGAGGAGACACTCTATCGCCGTCAGCTGCCTGGACAGCGGCTCCCA 6840  
QY 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySer 2189  
Db 6841 CCCCACCTGGCAGCAGACCCCTCTAAACCTTGGGGGCCAGCCTCTTGGGGGCCCTGGGAGC 6900  
QY 2190 ArgProLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209  
Db 6901 CGGCCCCAAGAAAAAATCAGCCCGCTAGTATCACCATAGACCCCCCGAGAGCCAAAGGT 6960  
QY 2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229

Db 6961 CCTCGGACCCCGCCAGCCCTGTATCTGCTCCGGAGGAGGCTCCGTCCAGCACTCC 7020  
QY 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249  
Db 7021 AAGGATCCCTTGGCCTCTGGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAAA 7080  
QY 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 7081 GATGTGCTGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 7131  
RESULT 5  
AAX83484  
ID AAX83484 standard; cDNA; 6729 BP.  
XX  
AC AAX83484;  
XX 07-DEC-1999 (first entry)  
DT  
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavT1d) cDNA.  
DE  
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
KW  
XX Homo sapiens.  
OS  
XX WO9929847-A1.  
PN  
XX 17-JUN-1999.  
PD  
XX 30-OCT-1998; 98WO-US023161.  
PF  
XX 05-DEC-1997; 97US-00985809.  
PR  
XX (LOYO ) UNIV LOYOLA CHICAGO.  
PA  
XX Perez-Reyes E, Cribbs LL;  
PI WPI; 1999-394972/33.  
XX P-PSDB; AAY14589.  
DR  
XX New T-type voltage-gated calcium channels.  
XX Disclosure; Page 58-67; 138pp; English.  
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1d. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 6729 BP; 1283 A; 2168 C; 1975 G; 1303 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0 Length: 6729  
Score: 11758.50 Matches: 2242  
Percent Similarity: 98.94% Conservative: 0  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.78% Indels: 23  
Gaps: 1  
DB:

US-09-611-257A-37 (1-2266) x AAX83484 (1-6729)		
QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db	1	ATGGACGAGGAGGATGGAGCGGGCCGCGAGGAGTCGGGACAGCCCCCGGAGCTTCATG 60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40
Db	61	CGGCTCAACGACCTGTCGGGGCCGGGGCGCGCGCTGCCGTACCCCGCGCTGGCCCCGGTGGTT 120
QY	41	ProGlySerAlaAspSerGluAlaGlyLeuProTyrProAlaLeuAlaProValVal 60
Db	121	CCGGGCAGCGCGACTCCGAGCGGAGGGGCTGCCGTACCCCGCGCTGGCCCCGGTGGTT 180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db	181	TTCTTCTACTTGAGCCAGGACAGCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db	241	CCCTGGTTTGAGCGCATCAGCATGTTGGTCATCTTCTCAACTGGGTGACCCCTGGGCATG 300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db	301	TTCCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGATCCTGCGGCCTTT 360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db	361	GATGACTTCATCTTGGCTTCTTTGGCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC 420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160
Db	421	ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGAACCGGCTTGACTTTTTCATCGTC 480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db	481	ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACCTCAGCTTCTCAGCTGTGAG 540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db	541	ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATCCTT 600
QY	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db	601	GTCACGTTGCTGTGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTCTGCTTCTTC 660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
Db	661	GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCGAGGCTGCTTCGGAACCGA 720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db	721	TGCTTCTTACCTGAGAAATTTACGCTCCCTGAGCGTGGACTGGAGCGCTATTACCAG 780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db	781	ACAGAGAACGAGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGG 840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db	841	TCCTGCAGAACGCTGCCACGCTGCGGGGACGGGGCGGTGGCCCCACCTTTCGGGTCTG 900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db	901	GACTATGAGGCCCTACAAACAGCTCCAGCAACACCACCTGTGTCACTTGAACCACTACTAC 960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db	961	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGGCCATCACTTTGACAAATT 1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360

Db	1021	GGCTATGCTGGATCGCCATCTTCCAGGTTCATCACGCTGGAGGGTGGTTCGACATCATG 1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db	1081	TACTTTGTGATGGATGCTCATCTCTTCTACAATTTTCATCTACTTCATCTCCTCATCATC 1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db	1141	GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGAATGCGCACGCAGTTCTCAGAG 1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db	1201	ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCTGTCCAACGCC 1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db	1261	AGCACCTGGCTAGCTTCTCTGAGCCCGGCAGCTGCTATGAGGAGTGTCTCAAGTACCTG 1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db	1321	GTGTACATCTTCGTAAGGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db	1381	CGGGTTGGGCTGCTCAGCAGCCCCAGCACCCCTCGGGGGCCAGAGACCCAGCCAGCAGC 1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 500
Db	1441	AGCTGCTCTCGTCTCCACCGCCGCTATCTCCACCCCTGGTGACCCACCACCACCCAC 1500
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db	1501	CATCACCACTACTACCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db	1561	ATCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGTGTGCACCCACCCTCGACGCT 1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db	1621	GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCACAGTCTCCCATCTGAGGCGATCC 1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
Db	1741	GGCAGGACTGTGGGCAGCGGGAAGGTGTATCCACCGTGCACACAGCCCTCCACCGGAG 1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db	1801	ACGCTGAAGGAGAGGCACTAGTAGAGGTGGTGCAGCTTCCAGCTCTGGGGCCCCCAACCTCAC 1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db	1861	AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAGCTGTGGAGACACAGAGT 1920
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db	1921	ACAGGTGCTGCCAAAGCTCTTGCAGATCTCCAGCCCTTGTGAAAGCAGACAGTGA 1980
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db	1981	GCCTGTGTCCAGACAGTGCCTTACTGTGCCCGGGCCGGGGCAGGGGAGGTGGAGCTC 2040
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db	2041	GCCGACCGTGAAATGCCTGACTCAGACAGCGAGGAGTATTATGAGTTTACACAGGATGCC 2100
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db	2101	CAGCACAGCGACCTCCGGGACCCCCCACAGCCGGCGGCAACGAGAGCTTGGGCCCATGCA 2160

QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740  
 Db 2161 GAGCCAGCTCTGTGCTGGCCCTCTCTGGAGGCTAATCTGTGACACCTTCGGAAGATTGTG 2220  
 QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
 Db 2221 GACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCATG 2280  
 QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
 Db 2281 GGCATCGAATACACAGCAGCGCCGAGGAGCTTACCAAGCCCTAGAAATCAGCAACATC 2340  
 QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800  
 Db 2341 GTCTTACACAGCTCTTTGCCCTGGAGATGCTGCTGAAGTCTTGTGTATGTTCCCTTT 2400  
 QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820  
 Db 2401 GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTCTATTTGGTTCATCAGCGTGTGG 2460  
 QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
 Db 2461 GAGATCGTGGCCAGCAGGGGGCGGCTGTCGGTGTGCGGACCTTCCGCCCTGATCGCT 2520  
 QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
 Db 2521 GTGCTGAAGCTGTGCGCTTCTCGCGCGCTGCAGCGGAGTGGTGTCTCATGAAG 2580  
 QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
 Db 2581 ACCATGGACAACTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTTCATCTTCAGC 2640  
 QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
 Db 2641 ATCTGGGCATGCATCTCTTCGGCTGCAAGTTGCTCTGAGCGGATGGGACACCTG 2700  
 QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
 Db 2701 CCAGACCGGAAGAAATTTTGACTCTTGTCTGGGCCATCGTCACTGTCTTTCAGATCTCG 2760  
 QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
 Db 2761 ACCAGGAGGACTGGAAACAAAGTCCTCTACAAATGGTATGGCTCCACGTCGTCCTGGCG 2820  
 QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
 Db 2821 GCCCTTATTTTATTGCTTTCATGACCTTCGGCAACTACGTGCTCTCAATTTGCTGCTC 2880  
 QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
 Db 2881 GCCATTCTGGTGGAGGGCTTCCAGGCGGAG-----GGAGATGCCCAACAAAGTCCGAA 2910  
 QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
 Db 2911 -----GGAGATGCCCAACAAAGTCCGAA 2931  
 QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
 Db 2932 TCAGAGCCCGGATTTCTTCTCACCAGCCTGGATGGTGGTGGGACAGGAAGAAGTCTTG 2991  
 QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040  
 Db 2992 GCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCCTGCTGCCGCTCTCATC 3051  
 QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
 Db 3052 ATCCACACGGCGCCACACCCATGTCTGCTGCCAAGAGCACCAGCAGCGGCGCTGGCGAG 3111  
 QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAlaAla 1080  
 Db 3112 GCGCTGGGCCCTTGGCTCGCGCCGACAGCAGCGGGGTGCGGACAGCCTGGGGCGGCC 3171

QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
 Db 3172 CACGAGATGAAGTCAACGCCAGCGCCCGAGCTCTCCGACAGCCCCCTGGAGCGCTGCA 3231  
 QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
 Db 3232 AGCAGCTGACACAGCAGCGCGCTCCAGCCGGAACAGCTCGGCCGTGCACCCAGCCTGAAG 3291  
 QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnLeuSerGln 1140  
 Db 3292 CGGAGAAGCCCAAGTGGAGAGCGCGGTCCCTGTGTTCGGGAGAGGCCAGAGAGCCAG 3351  
 QY 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
 Db 3352 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCAGCCCTCGGGCAGTGACCATCGCCAC 3411  
 QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
 Db 3412 AGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3471  
 QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
 Db 3472 CCAGGGCTGCATCGACTGCCAGTGGCCGAGGCTCTGCTTCTGAGCACCCAGGACTGCAAT 3531  
 QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProProLeuAsp 1220  
 Db 3532 GGCAAGTCGGCTTCAGGGCGCTGGCCCGGCCCTCGGGCTGATGACCCCGCTGATGAT 3591  
 QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
 Db 3592 GGGGATGACGCCGATGACGAGGGCAACTGAGCAAGGGGAACGGGTCCCGCGCTGGATC 3651  
 QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
 Db 3652 CGAGCCGACTCCCTGCTGCTGCTCGACGAGACTCCTCGGTGAGCTGCTGCTGCTGCTGCT 3711  
 QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
 Db 3712 CCTCAGTCCAGGTTCGGCTCCTGTGTCTGATCAGGATCATCACCACAAAGATGTTTCGACCCAC 3771  
 QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
 Db 3772 GTGGTCTTGTTCATCATCTTCTTAACGTGATCACCATCGCCATGAGCGGCCCAAAAT 3831  
 QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
 Db 3832 GACCCCAACAGCGCTGAACGATCTTCTGACCGGCAACCAAGATCCTGGCATGCTGAGGGTGTG 3891  
 QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340  
 Db 3892 TTTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACTGGCTGGTGTGCTCGGGGAGCAGCG 3951  
 QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
 Db 3952 TACCTGGGAGCAGTTGGAACTGTGACGCGGCTGTTGGTGTGCTCATCTCCGTTCATCGAC 4011  
 QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380  
 Db 4012 ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGCATGCTGAGGGTGTG 4071  
 QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
 Db 4072 CGGCTGCTGCGGACCTTGGCCCGCTCAGGGTGTATCAGCGGCGCAGGGGCTGAAGCTG 4131  
 QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420  
 Db 4132 GTGGTGGAGACGCTGATGCTCTCACTGAAACCCATCGGCAACATTTGTAGTCTATCTGCTGT 4191  
 QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
 Db 4192 GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTG 4251  
 QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460



Db 4252 TGGCAGGGCGAGGATACCGAGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC 4311  
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
Db 4312 CGGTGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTC 4371  
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
Db 4372 GTTTTGGCCTCCAAGGATGGTTGGTGGACATCATGTACGATGGCTGGATGCTGTGGGC 4431  
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520  
Db 4432 GTGGACCAGCGCCCATCATGAACCAACCCCTGGATGCTGCTGTACTTTCATCTCGTTC 4491  
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe 1540  
Db 4492 CTGCTCATTTGGCCTTCTTTGCTCCTGAACATGTTTGTGGGTGGTGGAGAACTTC 4551  
QY 1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu 1560  
Db 4552 CACAAGTGTCCGAGCACCAGGAGGAAGAGGAGGCCCGCGCGGAGGAGAAAGCGCTA 4611  
QY 1561 ArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580  
Db 4612 CGAAGACTGGAGAAAAGAGNAGAAAGCCAGTGCAAACTTACTACTCCGACTACTCC 4671  
QY 1581 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600  
Db 4672 CGCTTCCGGCTCCTCGTCCACCACCTTGTGCACCAGCCACTACTTGGACCTCTTCATCACA 4731  
QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620  
Db 4732 GGTGTCAATCGGGTGAACTGTGGTCAACATGGCCATGGAGCACTACCAGCAGCCCCAGATT 4791  
QY 1621 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer 1640  
Db 4792 CTGGATGAGGCTCTGAAAGATCTGCAACTACATCTTCACTGTCTATCTTTGTCTGGAGTCA 4851  
QY 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660  
Db 4852 GTTTTCAAACCTTGTGGCCTTTGGTTTCCGTCCGTCTTCCAGACAGGTGGAACCAAGCTG 4911  
QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1680  
Db 4912 GACCTGGCCATTGTGCTGCTGTCATCGGCATCACGCTGGAGGAATCGAGGTCAAC 4971  
QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700  
Db 4972 GCCTCGCTGCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGTGCGCATTTGCCGA 5031  
QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720  
Db 5032 GTGCTGAAGCTGTGAAGATGGCTGTGGGCATCGGGCGCTGCTGGACACACGGTGATGCAG 5091  
QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPhePheMetLeuLeuPhePheAla 1740  
Db 5092 GCCCTGCCCCAGTGGGGAACCTGGGACTTCTTTTCATGTTGTGTTTTCATCTTTGCA 5151  
QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760  
Db 5152 GCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTACGAGACACACCCCTGTGAGGGC 5211  
QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780  
Db 5212 CTGGGCCGTGTCACCTTTCGGAACCTTGGCATGGCCCTTCTTAACCTCTTCCGAGTC 5271  
QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800  
Db 5272 TCCACAGGTGACAATTGGAATGGCATTATGAAGGACACCCCTCCGGACTGTGACCAGGAG 5331  
QY 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820

Db 5332 TCCACCTGCTACAACACGGTCACTCTCGCCTATCTACTTTGTGTCTCTGCTGCTGACGGCC 5391  
QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluSerAsn 1840  
Db 5392 CAGTTTCGTCTAGTCAACGTTGGTGTATCGCGTGTCTGATGAAGCACCTGGAGGAGCAAC 5451  
QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeu 1860  
Db 5452 AAGGAGGCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTC 5511  
QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880  
Db 5512 AGCCCCCAGCCCACTCGCCACTGGCAGCCCTTCTCTGTGGCTGGGGTCGAGGGGCC 5571  
QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900  
Db 5572 GACAGCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACGCGAGATCAGCC 5631  
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyPro 1920  
Db 5632 TCCCACTTTTCCCTGGAGCACCCCAAGATGCAGCCCCACCCACGAGCTGCCAGGACCA 5691  
QY 1921 AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer 1940  
Db 5692 GACTTACTGACTGTGCGAAGTCTGGGTGAGCCGAAACGCACTCTCTGCCCAATGACAGC 5751  
QY 1941 TyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeu 1960  
Db 5752 TACATGTGTCCGCATGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGCTGGGGGCTC 5811  
QY 1961 ProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyr 1980  
Db 5812 CCCAAAGCTCAGTCAGGCTCCGTCTGTCTCGTTCACTCCAGCCAGCAGATACCAGCTAC 5871  
QY 1981 IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrp 2000  
Db 5872 ATCCTGTCAGCTTCCAAAGATGCACCTCATCTGCTCCAGCCCCACAGCGCCCAACCTGG 5931  
QY 2001 GlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArg 2020  
Db 5932 GGCACCATCCCCAAACTGCCCCCCACAGGACGCTCCCCCTTTGGCTCAGAGGCCACTCAGG 5991  
QY 2021 ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040  
Db 5992 CGCCAGGCAGCAATAAGGACTGACTCTTGGACGTTTCCAGGGTCTGGGCAGCCGGGAAGAC 6051  
QY 2041 LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGly 2060  
Db 6052 CTGCTGGCAGAGGTGAGTGGGCCCTCCCCCGCCCTTGGCCCGGGCTACTCTTTCTGGGGC 6111  
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080  
Db 6112 CAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATG 6171  
QY 2081 ThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThr 2100  
Db 6172 ACCCCGCCAGCCCTTGGCCAGGCCCAGAACCCAACTGGGGCAAGGGCCCTCCAGAGACC 6231  
QY 2101 ArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProPro 2120  
Db 6232 AGAAGCAGCTTAGAGTTGGACACGGAGCTGAGTGGATTTTTCAGGAGACCTCTCTGCCCT 6291  
QY 2121 GlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAla 2140  
Db 6292 GCGGGCCAGGAGGAGCCCCCATCCCCACGGGACCTGAAGAAGTGTACAGCGTGGAGGCC 6351  
QY 2141 GlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAla 2160  
Db 6352 CAGAGCTGCCAGCGCCGGCCTACGTCCTGGTGGATGAGCAGGAGACACTCTATCGCC 6411  
QY 2161 ValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGly 2180  
Db 6412 GTCAGCTGCTGGACAGCGGCTCCCCAACCCCACTGGGGCACAGACCCCTCTAACCTTGGG 6471

QY 2181 GlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIle 2200  
Db 6472 GGCCAGCCTCTTGGGGGGCTGGGAGCCGCCCAAGAAAAACTCAGCCCGCCTAGTATC 6531  
QY 2201 ThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeu 2220  
Db 6532 ACCATAGACCCCCCGAGAGCAAGGTCTCTGGACCCCGCCAGCCCTGGTATCTGCCTC 6591  
QY 2221 ArgArgAlaProSerSerSerLysAspProLeuAlaSerGlyProProAspSer 2240  
Db 6592 CGGAGGAGGCTCCGTCCAGCGACTCCAAGGATCCCTTGGCCTCTGGCCCTTGACAGC 6651  
QY 2241 MetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAsp 2260  
Db 6652 ATGGCTGCCTCGCCCTCCCCAAGAAAGATGTCTCGGTATCTCTCGGTATCTCTGAC 6711  
QY 2261 ProAlaAspLeuAspPro 2266  
Db 6712 CCAGCAGACCTGGACCCC 6729

RESULT 6

AAX83481

ID AAX83481 standard; cDNA; 6750 BP.

XX AAX83481;

DT 07-DEC-1999 (first entry)

XX Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a) cDNA.

DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX Homo sapiens.

PN WO9929847-A1.

XX 17-JUN-1999.

XX 30-OCT-1998; 98WO-US023161.

XX 05-DEC-1997; 97US-00985809.

XX (LOYO ) UNIV LOYOLA CHICAGO.

PA Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

DR P-PSDB; AAY14586.

XX New T-type voltage-gated calcium channels.

PT Disclosure; Page 31-40; 138pp; English.

XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX SQ Sequence 6750 BP; 1290 A; 2170 C; 1984 G; 1306 T; 0 U; 0 Other;  
Alignment Scores: 0 Length: 6750  
Pred. No.: 11741.00 Matches: 2241  
Score: 11741.00  
Percent Similarity: 98.64% Conservative: 1  
Best Local Similarity: 98.59% Mismatches: 1  
Query Match: 98.63% Indels: 30  
DB: 2 Gaps: 2  
US-09-611-257A-37 (1-2266) x AAX83481 (1-6750)  
QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
Db 1 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCCGGAGCTTCATG 60  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
Db 61 CGGCTCAACGACCTGTCCGGGGCCCGGGGGCGGGCGGGGGTCCAGCAGAAAAAGGAC 120  
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
Db 121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCCGGTGTT 180  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
Db 181 TTCTTCTACTTGAGCCAGGACAGCCCGCGCGGAGGTGGTGTCTCCGACCGGTCTGTAAAC 240  
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 241 CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCACTGCGTGACCCCTGGGCATG 300  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 301 TTCCGGCCATGCGAGGACATCGCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTT 360  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
Db 361 GATGACTTTCATCTTTGCCCTTCTTTGCCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC 420  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160  
Db 421 ATCTTTGGGAAAAAGTGTACTCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 480  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 481 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCCAGG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACCGGGTCCCGCAGCATGGCATCCTT 600  
QY 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCACGTTGCTGTGGATACGCTGCCCATGTGGGCAACGTCCTGTGCTGTGCTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCGAGGGCTGCTTCGGAACCGA 720  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrGln 260  
Db 721 TGCTTCTTACTGAGAAATTCAGCTCCCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 781 ACAGAGAACGAGGATGAGAGCCCTTTCATCTGTCTCCAGCCACGCGAGAACGGCATCGG 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCCTGCAGAACGCTGCCACGCTGCGGGGACCGGGGGCGGTGGCCACCTTGGCGTCTG 900

QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
|||  
Db 901 GACTATAGGCCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCACTACTAC 960  
|||  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnPropheLysGlyAlaIleAsnPheAspAsnIle 340  
|||  
Db 961 ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTTGACAAACATT 1020  
|||  
QY 341 GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
|||  
Db 1021 GGCTATGCCTGGATCGCCATCTTCCAGGTTCATCAGCTGGAGSGTGGTGCACATCATG 1080  
|||  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
|||  
Db 1081 TACTTTGTGATGGATGCTCATCTTCTTACAATTTTCATCTACTTCTCTCATCATC 1140  
|||  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
|||  
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGAATGGCCACGCAGTTCTCAGAG 1200  
|||  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
|||  
Db 1201 ACCAAGCAGCGGAAAGCCAGCTGATCGGGAGCAGCGTGTGCGTTCCTGTCCAAACGCC 1260  
|||  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
|||  
Db 1261 AGCACCTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGTGTCTCAAGTACCTG 1320  
|||  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
|||  
Db 1321 GTGTACATCCTTCGTAAGGCAGCCCGCAGCGTGGCTCAGGTTCTCGGGCAGCAGGTGTG 1380  
|||  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
|||  
Db 1381 CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGCCAGGAGACCCAGCCAGCAGC 1440  
|||  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
|||  
Db 1441 AGCTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACCTGGTGCACCAACCACCCAC 1500  
|||  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
|||  
Db 1501 CATCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCCGGAG 1560  
|||  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
|||  
Db 1561 ATCCAGGACAGGATGCCAATGGGTCCGCGGCTCATGTGCGCACCACTCGACGCCT 1620  
|||  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
|||  
Db 1621 GCCCTCTCCGGGCCCCCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCGGAC 1680  
|||  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
|||  
Db 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGSGCCCCCTCCAGGTCCCCATCTGAGGCATCC 1740  
|||  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
|||  
Db 1741 GGCAGGACTGTGGCAGCGGGAAGGTGTATCCACCGTGCACACAGCCCTCCACCCGAG 1800  
|||  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
|||  
Db 1801 ACGCTGAAGGAGAAGGCACTAGTAGGTGGTGGCTGCCAGCTTGGGCCCCCAACCTTCACC 1860  
|||  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
|||  
Db 1861 AGCCTCAACATCCACCCCGGCCCTACAGCTCCATGCACAAAGCTGCTGGAGACACAGAT 1920  
|||  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
|||  
Db 1921 ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA 1980  
|||  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
|||

Db 1981 GCCTGTGGTCCAGACAGTGCCTACTGTGCCCGGGCAGGGAGGTGGAGCTC 2040  
|||  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
|||  
Db 2041 GCCGACCGTGAAATGCCTGACTCAGACAGCGAGGAGTTTATAGTTTACACAGGATGCC 2100  
|||  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
|||  
Db 2101 CAGCACAGCGACTCCGGGACCCCAAGCCCGGGCAACGGAGCTGGGCCAGATGCA 2160  
|||  
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740  
|||  
Db 2161 GAGCCCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220  
|||  
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
|||  
Db 2221 GACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAACACACTCAGCATG 2280  
|||  
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
|||  
Db 2281 GGCATCGAATACCAAGCAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340  
|||  
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProphe 800  
|||  
Db 2341 GTCTTACCAGCTCTTTGCCCTGGAGATGCTGTGAAGCTGCTGTGTATGTTCCCTTT 2400  
|||  
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820  
|||  
Db 2401 GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTCAATGTTGGTTCATCAGCGTGTGG 2460  
|||  
QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
|||  
Db 2461 GAGATCGTGGCCAGCAGGGGGGGCGCTGTGCGTGTGCGGACCTTCCGCTGATGCGT 2520  
|||  
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
|||  
Db 2521 GTGCTGAAGCTGGTGGCTTCTGCGCGCGCTGCAGCGGCGAGTGGTGGTGCATGAAG 2580  
|||  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
|||  
Db 2581 ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTTCAGC 2640  
|||  
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
|||  
Db 2641 ATCCTGGGCATGCATCTTTCGGCTGCAAGTTTGCTCTGAGCGGATGGGACACCCCTG 2700  
|||  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
|||  
Db 2701 CCAGACCCGGAAGAATTTTGACTCTTCTGCTGCGCCATCGTCACTGTCTTTCAGATCCTG 2760  
|||  
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
|||  
Db 2761 ACCCAGGAGACTGGAAACAAAGTCTCTACAATGGTATGGCTCCACGTCGTCCTGGCG 2820  
|||  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
|||  
Db 2821 GCCCTTTTATTCATTTGCCCTCATGACCTTCCGCAACTACGTCCTTCAATTTGCTGGTC 2880  
|||  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
|||  
Db 2881 GCCATTCTGGTGGAGGGCTTCCAGCGGAG----- 2910  
|||  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000  
|||  
Db 2911 -----GGAGATGCCAACCAAGTCCGAA 2931  
|||  
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
|||  
Db 2932 TCAGAGCCCGATTCTTCTCACCCAGCCTGGATGGTGTATGGGACAGGAAGATGCTTG 2991  
|||  
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040  
|||

Db	2992	GCCTTGGTGTCCCTGGGAGAGACACCCGGAGCTGCGGAAGAGCCCTGCTGCCGCTCTCATC	3051
Qy	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
Db	3052	ATCCACACGGCCGCCACACCCATGTGCTGCTGCCAAGACACAGCACGGGCTGGGGCAG	3111
Qy	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
Db	3112	CGCTGGGCCCTGCTGCGCGCCACACAGCAGCAGCGGGTGGCAGAGCCCTGGGGCGGCC	3171
Qy	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
Db	3172	CACGAGATGAAGTCACCGCCCGAGCGCCCGCAGCTCTCCGACAGCCCTGGAGCGCTGCA	3231
Qy	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
Db	3232	AGCAGCTGGACCAGCAGCGGCTCCAGCCGGAACAGCCTCGGCCGTGCACCAGCCTGAAG	3291
Qy	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln	1140
Db	3292	CGGAGAACCCCAAGTGGAGAGCGGGCGTCCCTGTTGTGCGGAGAAGGCCAGAGAGCCAG	3351
Qy	1141	AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3352	GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTCGGGCAGTGACCATCGCCAC	3411
Qy	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3412	AGGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACATGCGAGTG	3471
Qy	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3472	CCAGGGCTGCATCGCACTGCCAGTGGCGGAGGGTCTGCTTCTGAGCACCAAGGACTGCAAT	3531
Qy	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3532	GGCAAGTCGGCTTCAGGGCGCCTGGCCGGGCCCTGCGGCCCTGATGACCCCCACTGGAT	3591
Qy	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
Db	3592	GGGGATGACGCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGGTCCGCGCGTGGATC	3651
Qy	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
Db	3652	CGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCT	3711
Qy	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	3712	CCTCAGTCCAGGTTCCGCTCCTGTGTACCGGATCATCACCCACAAGATGTTCCGACCAC	3771
Qy	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	3772	GTGCTCCTTGTATCATCTTCTTAACCTGATCACCATCGCCATGGAGCGCCCCAAAT	3831
Qy	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Db	3832	GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAAATTACATCTTCACCGCAGTC	3891
Qy	1321	PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla	1340
Db	3892	TTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTCGGGAGCAGGCG	3951
Qy	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
Db	3952	TACCTGGGAGCAGTTGGAACTGCTGGACGGGCTGTTGGTGTCTCATCTCCGTATCGAC	4011
Qy	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4012	ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTG	4071
Qy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	4072	CGGCTGCTGGGACCCCTGCGCCCGCTCAGGGTGTATCAGCGGGCGCAGGGGCTGAAGCTG	4131
Qy	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4132	GTGGTGGAGACGCTGATGTCTCTACTGAAACCCATCGGCAACATTGTAGTCTATCTGTGT	4191
Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
Db	4192	GCCTTCTTCATCTTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG	4251
Qy	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4252	TGCCAGGGCGAGATACCAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC	4311
Qy	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4312	CGGTGGGTCCGGCACAAGTACAACCTTTGACAACCTTTGGCCAGGCCCTGATGTCCCTGTT	4371
Qy	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4372	GTTTGGCCTCCAAAGGATGGTTGGGTGGACATCATGTACGATGGCTGGATGTGTGGGC	4431
Qy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4432	GTGGACCAGCAGCCCATCATGAACCAACACCCCTGGATGCTGCTGTACTTCTATCTCGTTC	4491
Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4492	CTGCTCATTTGGCCCTTCTTGTCTGAACATGTTTGTGGTGTGGTGGTGGAGAACTTC	4551
Qy	1541	HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu	1560
Db	4552	CACAAGTGTCCGACGACACAGGAGGAAGAGAGGCCCGCGGGAGGAGAGCGCCTA	4611
Qy	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
Db	4612	CGAAGACTGGAGAAAAGAGAAGAGAGTAAGGAGAAGCAGATGGCTGAAGCCAGTGCAAA	4671
Qy	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis	1593
Db	4672	CCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTCGTCCACCACCTGTGCACCAGCCAC	4731
Qy	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	4732	TACCTGGACCTTTCATCACAGGTGTATCGGGCTGAACGTGGTCAACCATGGCCATGGAG	4791
Qy	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	4792	CACATACCAGCAGCCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT	4851
Qy	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	4852	GTCATCTTGTCTTGGAGTCACTTTTCAAACCTTGTGGCCTTTGGTTTCCGTCGGTCTTTC	4911
Qy	1654	GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	4912	CAGGACAGGTGGAAACCAGCTGGACCTGGCCATTGTGCTGTGCTGTCCATCATGGGCATCACG	4971
Qy	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	4972	CTGGAGGAAATCGAGGTCAACGCTCGCTGCCCATCAACCCACCATCATCCGCATCATG	5031
Qy	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5032	AGGGTGTCTGCCATTGGCCGAGTGTGAAGTGTGCTGAAGATGGCTGTGGGCATCGGGCG	5091
Qy	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5092	CTGCTGGACACGGTGATCAGGCCCTGCCCCAGGTGGGGAACCTTGGGACTTCTCTTCATG	5151
Qy	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5152	TTGTTGTTTTTTCATCTTTTGACGCTTGGGCGTGGAGCTCTTTGGAGACCTTGGAGTGTGAC	5211



QY 1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773  
DB 5212 GAGACACACCCCTGTGAGGGCCTGGCGCTCATGCCACCTTTCGGAACCTTTGGCATGCCC 5271  
QY 1774 PheLeuThrLeuPheArgValSerThrGlyAspAsnTyrAsnGlyIleMetLysAspThr 1793  
DB 5272 TTCCTAACCCCTCTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATTATGAAGGACACC 5331  
QY 1794 LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe 1813  
DB 5332 CTCGGGACTGTGACCAGGAGTCCACCTGCTACAACACGGTCACTTCGCCCTATCTACTTT 5391  
QY 1814 ValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMet 1833  
DB 5392 GTGTCTTCGTGTCAGCGGCCAGTTTCGTGCTAGTCAACGTTGTGATCGCGTGTGATG 5451  
QY 1834 LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeu 1853  
DB 5452 AAGCACCTGGAGGAGAGCAACAAGGAGGCCAAGGAGGAGGCCAGCTAGAGGCTGAGCTG 5511  
QY 1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873  
DB 5512 GAGCTGGAGATGAAGACCCCTCAGCCCCCAGCCCCACTCGCCACTGGGCAGCCCCCTTCCTC 5571  
QY 1874 TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro 1893  
DB 5572 TGGCCTGGGGTCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCA 5631  
QY 1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913  
DB 5632 GCGGCCACGCGAGATCAGCCTCCCACTTTTCCCTGGAGCACCCACGATGCAGCCCCAC 5691  
QY 1914 ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr 1933  
DB 5692 CCCACGGAGCTGCCAGGACCAGACTTACTGACTGTGCGGAAGTCTGGGTTCAGCCGAACG 5751  
QY 1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu 1953  
DB 5752 CACTCTCTGCCAATGACAGCTACATGTGTGCGCATGGGACTGGGAGCTGCCGAGGGCCCTG 5811  
QY 1954 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973  
DB 5812 GGACACAGGGGTGGGGCTCCCCAAAGCTCAGTCAGGCTCGTCTGTGTCGGTTCACTCC 5871  
QY 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993  
DB 5872 CAGCCAGCAGATACCAGCTACATCTCGAGCTTCCCAAAGATGCACCTCATCTGTCTCCAG 5931  
QY 1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProProGlyArgSerPro 2013  
DB 5932 CCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCACACGAGACGCTCCCT 5991  
QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033  
DB 5992 TTGGCTCAGAGGCCACTCAGGCGCCAGGAGCAATAAGGACTGACTCCTTGGACGTTTCCAG 6051  
QY 2034 GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla 2053  
DB 6052 GGTCTGGGCAGCGGGAAGACCTGTGTCAGAGGTGAGTGGGCCCTCCCCCGCCCTGGCC 6111  
QY 2054 ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSerHis 2073  
DB 6112 CGGGCCTACTCTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCAC 6171  
QY 2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp 2093  
DB 6172 AGCAAGATCTCCAAGCACATGACCCCCGCGAGCCCCCTTGCCCCAGGCCCAGAACCCACTGG 6231  
QY 2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113  
DB 6232 GGCAAGGGCCCTCAGAGACCAGAGCAGCTTAGAGTTGGACAGGAGCTGAGCTGGATT 6291  
QY 2114 SerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLys 2133

DB 6292 TCAGGAGACCTCTGCCCCCTGGCGCCAGGAGAGCCCCCATCCCCACGGACCTGAAG 6351  
QY 2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153  
DB 6352 AAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGGCTTACGTCTTGGTGGATGAG 6411  
QY 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173  
DB 6412 CAGAGGAGACACTCTATCGCCGTAGCTGCCTGGACAGCGGCTCCCAACCCACCTGGGC 6471  
QY 2174 ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2193  
DB 6472 ACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTGGGGGCCCTGGAGCCGGCCCAAGAAA 6531  
QY 2194 LysLeuSerProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213  
DB 6532 AAACCTCAGCCCGCCTAGTATCACCATAGACCCCCCCGAGAGCAAGGTCTCTCGGACCCCG 6591  
QY 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233  
DB 6592 CCCAGCCCTGGTATCTGCTCCGGAGAGGGCTCCGTCCAGCGACTCCAAGGATCCCTTG 6651  
QY 2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer 2253  
DB 6652 GCCTCTGGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAAAGATGTGCTGAGT 6711  
QY 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
DB 6712 CTCTCCGGTTATCTCTGACCCAGCAGACCTGGACCCC 6750

RESULT 7

AAx83482  
ID AAX83482 standard; cDNA; 6783 BP.  
XX  
AC AAX83482;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1b) cDNA.  
XX  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
XX  
OS Homo sapiens.  
XX  
PN W09929847-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
DR P-PSDB; AAY14587.  
XX  
PT New T-type voltage-gated calcium channels.  
XX  
PS Disclosure; Page 40-49; 138pp; English.  
XX  
CC This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type

CC channels include short current time, slow activation kinetics near  
CC threshold, fast inactivation kinetics and slow tail current. The  
CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel  
CC genes from humans and rats. Each of the novel Ca-channels contains a  
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells  
CC expressing the T-type voltage-gated calcium channel proteins can be used  
CC to screen for drugs which affect calcium channels. Methods are also  
CC disclosed for treating a disease or disorder associated with a deficiency  
CC in a native T-type calcium channel nucleic acid, e.g. to treat  
CC cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0 Length: 6783  
Score: 11735.50 Matches: 2241  
Percent Similarity: 98.16% Conservative: 1  
Best Local Similarity: 98.12% Mismatches: 1  
Query Match: 98.58% Indels: 41  
DB: 2 Gaps: 2

US-09-611-257A-37 (1-2266) x AAX83482 (1-6783)

QY	1	MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
DB	1	ATGGACGAGGAGGATGGAGCGGGCGCGGAGGAGTCGGGACAGCCCGGAGCTTCATG	60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
DB	61	CGGCTCAACGACTGTGGGGCGCGGGCGCGGGCGGGGTCAGCAGAAAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	121	CGGGCAGCGCGGACTCCGAGCGGGGCGGGCGGGCGGGGTCGCGCGCTGGCGGTGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	181	TTCTTCTACTTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	241	CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCCTTCTCACTCGGTGACCCCTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTCCGGCCATCGGAGGACATCGCCTGTGACTCCAGCGGTGCCGATCCTGCAGGCCCTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTCATCTTTGCTTCTTTGCGGTGGAGATGGTGGTGAAGATGGTGGCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
DB	421	ATCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	481	ATCGAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCAAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	601	GTCACGTTGCTGTGGATACGCTGCCATGCTGGGCAACGTCCTGTGCTCTGCTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	661	GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCAGGGCTGCTTCGGAACCGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260

DB	721	TGCTTCTACTGAGAAATTTACGCTCCCTTGAGCGTGGACCTGGAGCGCTATTACCAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	781	ACAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCACGCCGAGAACGGCAATGCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
DB	841	TCCTGCAGAACGCTGCCACGCTGGCGGGGACGGGGGGGTGGCCACCTTGGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr	320
DB	901	GACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	961	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGGCATCAACTTTGACAACAT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
DB	1021	GGCTATGCCTGGATGCCATCTTCCAGGTATCAGCTGGAGGGTGGTGGTGGTGGTGGT	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1081	TACTTTGTGATGATGCTCATCTCTTCTACAAATTCATCTACTTCTCTCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu	400
DB	1141	GTGGGCTCCTTCTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1201	ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGGGTTCCTGTCCAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
DB	1261	AGCACCTTGGCTAGCTTCTGTAGCCCGGAGCTGCTATGAGGAGTGTCTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1321	GTGTACATCTTCGTAAAGCAGCCCGCAGGTGGTCTCAGGTCTCTCGGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerProAlaProLeuGlyGlyGlnGlnThrGlnProSerSer	480
DB	1381	CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
DB	1441	AGTGCTCTCGTCCACCGCGGCTATCCGTCACCACTGGTGGTGGTGGTGGTGGTGGTGGT	1500
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
DB	1501	CATCACCACTACTACCACTGGGCAATGGACGCTCAGGGCCCCCGGGGGCAGCCCGGAG	1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
DB	1561	ATCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCACTCGACGCCT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
DB	1621	GCCCTCTCGGGGGCCCCCTTGGTGGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer	580
DB	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCATCTCTGAGGCATCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
DB	1741	GGCAGGACTGTGGGCAGCGGGAAGGTGTATCCACCCGTGCACACAGCCCTCCACCGGAG	1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
DB	1801	ACGCTGAAGAGGAGGCACTAGTAGAGGTGGTGGCTGCCAGTCTTGGGGCCCCCAACCTCACC	1860

QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
DB 1861 AGCTCAACATCCACCCGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
DB 1921 ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
DB 1981 GCCTGTGTCCAGACAGCTGCCCTACTGTGCCGGCCGGGCGAGGGAGGTGGAGCTC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
DB 2041 GCCGACCGTGAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTACACAGGATGCC 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
DB 2101 CAGCACAGCGACTCCGGGACCCCCACAGCCGGCGCAACGGAGCCTGGGCCAGATGCA 2160  
QY 721 GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleVal 740  
DB 2161 GAGCCCGACTGTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220  
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
DB 2221 GACAGCAAGTACTTGGCCGGGAATCATGATCGCCATCTCGGTCAACACACTCAGCATG 2280  
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
DB 2281 GGCATCGAATACCAGCAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCACATC 2340  
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProphe 800  
DB 2341 GTCTTCACCAAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGTTGTATGGTCCCTTT 2400  
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820  
DB 2401 GGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTATGTGGTTCATCAGCGTGG 2460  
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgGlnArgLeuMetArg 840  
DB 2461 GAGATCGTGGGCAGCAGGGGGCGGCTGTGCGTGTGCGACCTTCCGCTGATGCGT 2520  
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
DB 2521 GTGCTGAAGCTGGTGCCTTCTCGCGCGCTGCAGCGCAGCTGGTGTCTCATGAAG 2580  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
DB 2581 ACCATGGACACGTGGCCACCTTCTGCATGCTGCTTATGCTTTCATCTTTCATCTTCAGC 2640  
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
DB 2641 ATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCCCTCTGAGCGGGATGGGACACCCCTG 2700  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
DB 2701 CCAGACCGGAAGAATTTTGACTCTCTGCTGGGCCATCGTCACTGTCTTTCAGATCCTG 2760  
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
DB 2761 ACCCAGGAGGACTGGAACAAAGTCTCTACAATGGTATGGCTCCACGTCGTCTCGGCG 2820  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 960  
DB 2821 GCCCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTC 2880  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
DB 2881 GCCATTCTGGTGAGGGCTTCCAGGCGGAG----- 2910

QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
DB 2911 -----GGAGATGCCAACAAGTCCGAA 2931  
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020  
DB 2932 TCAGAGCCCGATTCTTCTCACCCAGCCTGGATGGTGTATGGGACAGGAAGTGTGTG 2991  
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040  
DB 2992 GCCTTGGTGTCCCTGGGAGAGCACCGGAGCTGGGAAGAGCCTGTGCCGCTCTCATC 3051  
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlu 1060  
DB 3052 ATCCACACGGCCGCCACACCCATGTGCTGCCAAGAGCAGCAGCGGCTGGGCGGAG 3111  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
DB 3112 GCGCTGGGCCCTGCGTCGCGCCGACACAGCAGCAGCGGCTGGCAGAGCCTGGGCGGCGC 3171  
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
DB 3172 CACGAGATGAAGTCAACGCCCCAGCCCGCAGCTCTCCGACAGCCCTGGAGCGCTGCA 3231  
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
DB 3232 AGCAGCTGGACACAGCGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3291  
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnGlnGln 1140  
DB 3292 CGGAGAAAGCCCAAGTGGAGAGCGCGGTCCCTGTTGTCCGGAGAAGGCCAGGAGCCAG 3351  
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
DB 3352 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTCGGGGAGTGACCATCGCCAC 3411  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
DB 3412 AGGGGGTCCCTGGAGCGGAGGCGCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3471  
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
DB 3472 CCAGGGTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCCAGGACTGCAAT 3531  
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
DB 3532 GGCAAGTCGGCTTCAGGGCGCTTGGCCCGGCTGCGGCTGATGACCCCCCACTGGAT 3591  
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
DB 3592 GGGGATGACGCCGATACGAGGGCAACCTGAGCAAAGGGGAACGGGTCCGCGCGTGGATC 3651  
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
DB 3652 CGAGCCCGACTCCCTGCTGCTGCTGCTCGAGCGAGACTCCTGGTTCAGCCTACATCTCCCT 3711  
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
DB 3712 CCTCAGTCCAGGTTCCGCCCTCCTGTGTCAACCGGATCATACCCACAAGATGTTCCGACCAC 3771  
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
DB 3772 GTGGTCTTGTTCATCATCTTCTTAACTGCATCACCATCGCCATGGAGCGCCCCAAAATT 3831  
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
DB 3832 GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATTACATCTTACCCGAGTC 3891  
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340  
DB 3892 TTTTCTGCTGAAATGACAGTGAAGGTGGTGGCAGTGGGCTGGTGTCTTCGGGGAGCAGGCG 3951  
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360

Db 3952 TACCTGGGAGCAGTTGGAACTGCTGGACGGGCTGTGGTGCTCATCTCCGTCATCGAC 4011  
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380  
Db 4012 ATTCTGGTGTCATGGTCTCTGACAGCGGCACCAAGATCTCTGGGCATGCTGAGGGTGCTG 4071  
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
Db 4072 CGGCTGCTGGCGACCCCTGCGCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTG 4131  
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420  
Db 4132 GTGGTGGAGACGCTGATGCTCCTCACTGAAACCCCATCGGCAACATTGTAGTCATCTGCTGT 4191  
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
Db 4192 GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4251  
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
Db 4252 TGCCAGGGCGAGGATACCAGGAACATCACCAATAAATCGACTGTGCCGAGGCCAGTTAC 4311  
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
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QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
Db 4372 GTTTTGGCCTCCAAGGATGGTTGGTGGACATCATGTACATGGGCTGGATGCTGTGGGC 4431  
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520  
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QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540  
Db 4492 CTGCTCATTTGTGGCTTCTTTGTCTGAACATGTTTGTGGTGTGGTGGAGAACTTC 4551  
QY 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu 1560  
Db 4552 CACAAGTGTCCGGACACACCAGGAGGAAGAGGAGGCCCGCGCGGGAGGAGAGCGCCTA 4611  
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568  
Db 4612 CGAAGACTGGAGAAAAGAGAAAGGAATCTAATGCTGGACGATGTAATTGCTTCCGSCAGC 4671  
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582  
Db 4672 TCAGCCAGCGCTCGCTCAGAACCCAGTGCAAACCTTACTACTCCGACTACTCCCGCTTC 4731  
QY 1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602  
Db 4732 CGGCTCCTCGTCCACCACTTGTGCACCACTACCTGGACCTACCTGGACCTTTCATCACAGGTGTC 4791  
QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622  
Db 4792 ATCGGGCTGAACGTGTCACCATGGCCATGGAGCACTACCAGAGCCCCAGATTCTGGAT 4851  
QY 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642  
Db 4852 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTTCATCTTGTCTTGGAGTCAGTTTTC 4911  
QY 1643 LysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeu 1662  
Db 4912 AAACCTGTGGCCTTTGGTTTCCGTCGGTCTTCCAGGACAGGTGGAACCACTGGACCTG 4971  
QY 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682  
Db 4972 GCCATTGTGCTGTGTCATCATGGGCATCAGCTGGAGGAATCGAGGTCAACGCCTCG 5031  
QY 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702

Db 5032 CTGCCCCATCAACCCACCACCATCATCCGCAATCATGAGGGTGCTGGCATTTGCCGAGTGCTG 5091  
QY 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722  
Db 5092 AAGCTGCTGAAGATGGCTGTGGGCATCGGGCGCTGCTGGACACGGTGATGCAGGCCCTG 5151  
QY 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeu 1742  
Db 5152 CCCAGGTGGGAACTGGGACTTCTCTTCATGTTGTTGTTTTTCATCTTTGCAGCTCTG 5211  
QY 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762  
Db 5212 GCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCCTGGGC 5271  
QY 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782  
Db 5272 CGTCATGCCACCTTTCGGAACCTTTGGCATGGCCTTCTTAACCCCTCTTCCGAGTCTCCACA 5331  
QY 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802  
Db 5332 GGTGACAAATTGGAATGGCATTTATGAAGGACACCCCTCCGGACTGTGACGAGGTCCACC 5391  
QY 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822  
Db 5392 TGTACAACACGGTTCATCTCGCCTATCTACTTGTGTCTTCTGCTGACGGCCAGTTTC 5451  
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842  
Db 5452 GTGCTAGTCAACGTGGTGATCGCCGTGCTGATGAAGCACCTGGAGGAGAGACAACAAGGAG 5511  
QY 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862  
Db 5512 GCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTCAGCCCC 5571  
QY 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882  
Db 5572 CAGCCCCACTCGCCACTGGGCAGCCCCCTTCTCTGCTGGCTGGGTGAGGGCCCCGACAGC 5631  
QY 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902  
Db 5632 CCCGACAGCCCCAAGCCTGGGCTCTGCACCCAGCGGCCACCGGAGATCAGCCTCCCAC 5691  
QY 1903 PheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyProAspLeu 1922  
Db 5692 TTTTCCCTGGAGCACCCCGACGATGCAGCCCCACCCACCGAGCTGCCAGGACCAGACTTA 5751  
QY 1923 LeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMet 1942  
Db 5752 CTGACTGTGCGGAAGTCTGGGTCAGCCGACGCACTCTCTGCCCAATGACAGCTACATG 5811  
QY 1943 CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLys 1962  
Db 5812 TGTCGGCATGGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGTGGGGGCTCCCCAAA 5871  
QY 1963 AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeu 1982  
Db 5872 GCTCAGTCAGGCTCCGCTCTTGTCTCGTTCACTCCAGCCAGCAGATACCAGCTACATCCTG 5931  
QY 1983 GlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThr 2002  
Db 5932 CAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCAACAGCGCCCCAACCTGGGGCACC 5991  
QY 2003 IleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGln 2022  
Db 5992 ATCCCCAAACTGCCCCCAACCCAGGACGCTCCCCCTTTGGCTCAGAGGCCACTCAGGGCCAG 6051  
QY 2023 AlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu 2042  
Db 6052 GCAGCAATAAGGACTGACTCTCTGGACGTTTCAGGGTCTGGGCAGCCGGGAAGACCTGCTG 6111  
QY 2043 AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSer 2062  
Db 6112 GCAGAGGTGAGTGGGGCCCTCCCGCCCTTGGCCCGGGGCTACTCTTTCTGGGGCCAGTCA 6171





QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTT 600  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCACGTTGCTGTGATACGCTGCCATGCTGGCAACGTCCTGCTGCTCTGCTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCCTTCTCATCTTCGGCATCGTCGGCTCCAGCTGTGGCAGGGCTGCTTCGGAACCGA 720  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
Db 721 TGCTTCTTACTAGAAATTTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 781 ACAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCACGCGAGAACGGCATGCGG 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCCTGCAGAACGCTGCCACGCTGCGGGGACGGGGGGGTGGCCCACTTGGGTCTG 900  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 901 GACTATGAGGCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCCAGTACTAC 960  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
Db 961 ACCAACTGCTCAGCGGGGGAGCAACCCCTTCAAGGGGCCCATCAACTTTGACAACATT 1020  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1021 GGCTATGCCTGGATGCCCATCTTCCAGGTCAACGCTGGAGGGCTGGGTGCACATCATG 1080  
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QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAGCAGCGGGAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTTCCTGTCCAACGCC 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
Db 1261 AGCACCCCTGGTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1320  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
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QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGGTTGGGCTGCTCAGCAGCCCCAGCACCCCTCGGGGGCAGGAGACCCAGCCAGCAGC 1440  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
Db 1441 AGTGCTCTCGCTCCACCGCGCCTATCCGTCCACCACCTGGTGCACCACCACCACCAC 1500  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CATCACCACTACTACCCTTGGGCAATGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 1560  
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Db 1621 GCCCTCTCGGGGCCCCCCTGGTGGCGCAGAGTGTGCACAGCTTCTACCATGCCGAC 1680  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580  
Db 1681 TGCCACTTAGAGCCAGTCCGTGCCAGGGCCCCCTCCAGGTCCCCATCTGAGGCATCC 1740  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
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QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACAGTGCCTGCCAAAGCTTTGCAAGATCTCCAGCCCTTGTCTTGAAGACAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db 1981 GCCTGTGGTCCAGACAGCTGCCCTACTGTGCCCGGGCCGGGAGGGGAGGTGGAGCTC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
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QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
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QY 721 GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleVal 740  
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QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
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QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProphe 800  
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QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
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QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
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QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880  
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QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
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QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920

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Qy 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
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Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
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Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
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Db 4612 CGAAGACTGGAGAAAAAGAGAGGAGTAAGGAGAGCAGATGGCTGATCTAATGCTGGAC 4671  
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QY 1756 HisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu 1775  
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QY 1896 HisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHisProThr 1915  
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QY 1916 GluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSer 1935  
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QY 2056 TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLys 2075  
Db 6172 TACTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAG 6231  
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QY 2196 SerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSer 2215  
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QY 2236 GlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSer 2255  
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Db 6772 GGTATTATCTCTGACCCAGCAGACCTGGACCCC 6804  
RESULT 9  
AAH98402  
ID AAH98402 standard; cDNA; 8002 BP.  
XX XX  
AC AAH98402;  
XX XX  
DT 12-OCT-2001 (first entry)  
XX XX  
DE Human EST-derived coding sequence SEQ ID NO: 259.  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
KW gene therapy; nutrition; ss.





Db 1936 AGTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACTGGTGCAACCACCACCAC 1995

QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520

Db 1996 CATCACCACTACCACTGGGCAATGGGACGCTCAGGCCCCCGGGCCAGCCGGAG 2055

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QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580

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Db 3406 -----GGAGATGCCAACAAAGTCCGAA 3426

QY 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020

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QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080

Db 3607 GCGCTGGGCCCTGCGTCGCGCGGCACACGAGCAGAGCGGTGCGCAGAGCCTGGGCGCGGCC 3666

QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100

Db 3667 CACGAGATGAAGTCAACCGCCAGCGCCCGCAGCTCTCCGACACAGCCCCCTGGAGCGCTGCA 3726

QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120

Db 3727 AGCAGCTGGACCAGCAGGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCACGCTGAAG 3786

QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGluGlnGlnSerGln 1140

Db 3787 CGGAGAAGCCCAAGTGGAGAGCGGCGGTCCCTGTTGTCGGGAGAAGGCCAGGAGAGCCAG 3846

QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160

Db 3847 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCAGCCCTCGGGCAGTGACCATCGCCAC 3906

QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180

Db 3907 AGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3966

QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGln-AspCysAs 1200

Db 3967 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCCAGGACTGCAA 4026

QY 1200 nGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAs 1220

Db 4027 TGGCAAGCTGGGCTTCAGGGCGCTGGCCCCGGGCCCCCTGGCGCCTGATGACCCCCCACTGGA 4086



Db 6247 CTTACTGACTGTGCGGAAGTCTGGGGTCAGCCGAACGCACTCTCTGCCCCAATGACAGCT 6306

QY 1941 YrMetCysArgHis-GlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeu 1960

Db 6307 ACATGTGTGGCATGGGAGACACTGCCGAGGGGCCCTGGGACACAGGGGCTGGGGGCTC 6366

QY 1961 ProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyr 1980

Db 6367 CCCAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCAGCCAGCAGATACCAGCTAC 6426

QY 1981 IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrp 2000

Db 6427 ATCCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCAAGCCGCCCCAACCTGG 6486

QY 2001 GlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArg 2020

Db 6487 GGCACCATCCCAAACTGCCCCCAACAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGG 6546

QY 2021 ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040

Db 6547 CGCCAGGCAGCAATAAGGACTGACTCTTGGACGTTTCAGGGTCTGGGCAGCCGGGAAGAC 6606

QY 2041 LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGly 2060

Db 6607 CTGCTGGCAGAGGTGAGTGGGCCCTCCCGCCCTGGCCCGGGCTACTCTTTCTGGGGC 6666

QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080

Db 6667 CAGTCAAGTACCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATG 6726

QY 2081 ThrProProAlaProCysProGlyProGluProAsnTrp-GlyLysGlyProProGluTh 2100

Db 6727 ACCCGCCAGCCCTTGCCAGGCCCAAGCAACCACTGGGGCAAGGGCCCTCCAGAGAC 6786

QY 2100 rArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProPr 2120

Db 6787 CAGAAGCAGCTTAGAGTTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTGCCCC 6846

QY 2120 oGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAl 2140

Db 6847 TGGCGGCCAGGAGGAGCCCCCATCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGC 6906

QY 2140 aGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAl 2160

Db 6907 CCAGAGCTGCCAGCGCCGGCCCACTCCCGCTGGCTGGATGAGCAGAGGAGACACTCTATCGC 6966

QY 2160 aValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuG1 2180

Db 6967 CGTCAGCTGCCTGGACAGCGGCTCCCAACCCCACTGGGCAAGACCCCTCTAACCTGG 7026

QY 2180 YGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerI1 2200

Db 7027 GGGCCAGCCTCTTGGGGGCTTGAGAGCGGGCCCAAGAACTCAGCCCGCTAGTAT 7086

QY 2200 eThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLe 2220

Db 7087 CACCATAGACCCCGGAGAGCCCAAGTCTCGGACCCCGCCAGCCCTGGTATCTGCCT 7146

QY 2220 uArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSe 2240

Db 7147 CCGGAGGAGGGCTCGTCCAGGACTCCAAGGATCCCTTGGCTCTGGCCCCCTTGACAG 7206

QY 2240 rMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAs 2260

Db 7207 CATGGCTGCCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCCTCTGA 7266

QY 2260 pProAlaAspLeuAspPro 2266

Db 7267 CCCAGCAGACCTGGACCCC 7285

RESULT 10

AAZ52309

ID AAZ52309 standard; cDNA; 7286 BP.

XX AAZ52309;

XX AC

DT 18-JUL-2000 (first entry)

XX Rat pancreatic T-type calcium channel cDNA.

DE

XX Rat; pancreatic T-type calcium channel alpha subunit; insulin;

XX pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;

KW antidiabetic; calcium influx; L type calcium channel; NIDDM;

KW type II diabetes; non-insulin dependent diabetes mellitus; ss.

XX Rattus sp.

XX

FH Key Location/Qualifiers

FT misc\_feature 1. .157

FT /\*tag= b

FT /note= "Region upstream to the coding region of

FT pancreatic T-type calcium channel protein"

FT 2. .7285

FT /\*tag= a

FT /product= "Pancreatic T-type calcium channel alpha1

FT subunit"

FT /transl\_except= (pos:11. .13, aa:Xaa)

FT /transl\_except= (pos:7022. .7024, aa:Xaa)

FT /transl\_except= (pos:7112. .7114, aa:Xaa)

FT /note= "Xaa corresponds to in-frame stop codon. This

FT region includes sequence upstream to the coding region of

FT pancreatic T-type calcium channel protein. Does not

FT include stop codon"

FT /partial

FT 158. .7285

FT /\*tag= c

FT /product= "Pancreatic T-type calcium channel alpha1

FT subunit"

FT /note= "This region is claimed as SEQ ID NO: 1"

XX

PN WO200015845-A1.

XX

PD 23-MAR-2000.

XX

PF 26-AUG-1999; 99WO-US019675.

XX

PR 26-AUG-1998; 98US-0098004P.

PR 27-JAN-1999; 99US-0117399P.

XX

PA (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.

XX

PI Li M;

XX

DR WPI; 2000-271475/23.

DR P-PSDB; AAY70720.

XX

PT Novel nucleic acids encoding pancreatic T-type calcium channels used for

PT regulation of T-type calcium channels and treatment of type II diabetes.

XX

PS Example 1; Page 114-119; 124pp; English.

XX

CC The present cDNA encodes a protein that includes pancreatic T-type

CC calcium channel alpha1 subunit derived from rat insulin secreting beta

CC cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-

CC type calcium channel alpha1 subunit (alpha1G). The T-type Ca2+ channel

CC from INS-1 (alpha1G-INS) and neuronal alpha1G are alternative splice

CC isoforms of the same gene. The INS-1 isoform is also expressed in brain,

CC neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+

CC channel belongs to the family of low voltage activated Ca2+ channels. The

CC present sequence is used for treating diseases associated with abnormal

CC expression or function of T-type calcium channels. They are especially

CC used for treating type II diabetes. Modulators of pancreatic T-type Ca2+

CC channel e.g. antisense oligonucleotides, ribozymes and inhibitors are

CC used in methods for modifying insulin secretion by pancreatic beta cells,

CC basal calcium levels, potential L type calcium channel activity,

CC pancreatic cell death, pancreatic beta cell proliferation and calcium



CC influx through L type calcium channels in cells

XX Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7286  
Score: 11111.00 Matches: 2135  
Percent Similarity: 94.80% Conservative: 35  
Best Local Similarity: 93.27% Mismatches: 95  
Query Match: 93.34% Indels: 24  
DB: 3 Gaps: 5

US-09-611-257A-37 (1-2266) x AAZ52309 (1-7286)

QY 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
DB 158 ATGACGAGGAGGATGGAGCGGGCCGAGGAGTCGGGACAGCCCGTAGCTTCACG 217  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
DB 218 CAGCTCAACGACCTGTCCGGGGCCGGGGCCGGCAGGGCCGGGGTCGACCGGAAAGGAC 277  
QY 41 ProGlySerAlaAspSerGluAlaGlyGlyLeuProTyrProAlaLeuAlaProValVal 60  
DB 278 CCGGGCAGCGGACTCCGAGCGGAGGGGCTGCCGTACCCCGCGCTAGCCCCGGTGGTT 337  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
DB 338 TTCTTCTACITGAGCCAGGACAGCCGCCGGGAGCTGGTGTCTCCGACGGTCTGTAAAC 397  
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
DB 398 CCGTGGTTCGAGCGAGTCAGTATGCTGCTATTCTTCTCAACTGTGTGACTCTGGGTATG 457  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
DB 458 TTCAGGCGGTGTGAGGACATTGCCCTGTGACTCCAGCGCTCCGGATCCTGCAGGCCCTC 517  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
DB 518 GATGACTTCATCTTTGCCCTTCTTTGCTGTGAAATGGTGGTGAAGATGGTGGCTTGGGC 577  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160  
DB 578 ATCTTTGGGAAGAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATGTG 637  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 638 ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACCTGAGCTTCTCCGCACTCAGG 697  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 698 ACAGTCCGTGTGCTGCGACCGCTCAGGSCCATTAACCGGGTGGCCAGCATGCGCATCTC 757  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
DB 758 GTCACATTACTGTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 817  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240  
DB 818 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGAGGACTGCTTCCGCAACCGA 877  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
DB 878 TGCTTCTCCCGAGAACTTCAGCCTCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 937  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
DB 938 ACAGAGAATGAGGACGAGAGCCCTTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATGAGA 997  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
DB 998 TCCTGCAGGAGTGTGCCACACACTCGCTGGGGAAGCGGTGTGTGGCCCAACCTTCAGTCTG 1057

QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
DB 1058 GACTATGAGACCTATAACAGTTCAGCAACACCACCTGTGTCAACTGGAACCACTACTAT 1117  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
DB 1118 ACCAACTGCTCTGCGGGCGAGCACAACACCCCTTCAAAGGCGCATCAACTTTGACAACATT 1177  
QY 341 GlyTyrAlaTyrPileAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360  
DB 1178 GGCTATGCTGGATCGCCATCTTCCAGGTTCATCACACTGGAGGCTGGGTGACATCATG 1237  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
DB 1238 TACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCACTTCACTTCTTCTCATCATC 1297  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
DB 1298 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1357  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
DB 1358 ACCAAACAGCGGAGAGTCAGTGTATCGGGAGCAGCGTGTATGAGGAGCTACTCAAGTACCTG 1417  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440  
DB 1418 AGCACCTTGGCAAGCTTCTCTGAGCCAGGAGCTGCTATGAGGAGCTACTCAAGTACCTG 1477  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
DB 1478 GTGTACATCCTCCGAAAGCAGCCCGAAGGCTGGCCAGGCTCTTAGGGCTATAGGCGTG 1537  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
DB 1538 CGGGCTGGGCTGCTCAGCAGCCCACTGGCCCGTAGTGGGCGAGGAGCCCGCCAGTGGC 1597  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 500  
DB 1598 AGCTGCACCTCGCTCACACCGCTGCTGTCTGTCCACACCTGGTCCACCATCACAC 1657  
QY 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
DB 1658 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAG 1717  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerProSerPro 540  
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QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
DB 1778 ACTCCCTCTGGGGGCCCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCATGTGAC 1837  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
DB 1838 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 1897  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
DB 1898 GGTTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCACTCCAGCCCTCCAGAG 1957  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
DB 1958 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACC 2017  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer 640  
DB 2018 AGCTTCAACATCCCACTGGGCCCTTCACTCCATGCACAAGCTCTCTGGAGACACAGAT 2077  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
DB 2078 ACGGAGGCTGCCATAGTCTCCTGCAAAATCTCCAGCCCTTGCTCCAGGCGACAGAGTGA 2137

QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Dbb 2138 GCCTGGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGAGTCC 2197  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Dbb 2198 GCTGACCATGTCTATGCTGACTCAGACAGCGAGGCTGTGTATGATTACACAGGACGCT 2257  
QY 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719  
Dbb 2258 CAGCACAGTGACCTCCGGGATCCCAACAGCCGGCGGACAGCGGAGCTTGGGCCCAGAT 2317  
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739  
Dbb 2318 GCAGAGCCTAGTTCTGTGCTGGCTTCTGGAGGCTGATCTGTGACACATTCGGGAAGATC 2377  
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759  
Dbb 2378 GTAGATAGCAAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2437  
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Dbb 2738 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTTCTCATCTTCTTC 2797  
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Dbb 2978 GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGTG 3037  
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QY 1139 SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158  
Dbb 3578 AGTCAGGATGAGGAGGAAAGTTCAGAAAGAGGACCGGGCCAGCCAGCAGGAGTACCAT 3637  
QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178  
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Dbb 3698 CAGTCCCGGGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCCTCTGAGCACCAAGAC 3757  
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Dbb 3938 TTTCTCTCTCAGTCAAGTTTCGTCTCTGTGTCACTGATCATCACCAAGATGTTT 3997  
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298  
Dbb 3998 GACCATGTGGTCTCTGTCATCATCTTCTCAACTGATCATCATCGCTATGAGCGCCCC 4057  
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Dbb 4118 GCAGTCTTTTAGTGAATGACAGTGAAGTGGTGGTGGCTGGCTGGTGGTGGGAG 4177  
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Dbb 4238 ATCGACATCTGGTCTCCATGTCTCCGACAGCGGCACCAAGATCTCTTGGCATGCTGAGG 4297  
QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398

Db 4298 GTGCTGGCTGTGCGGACCCCTGCGTCCACTCAGGGTCATCAGCGGGCCCCAGGGACTG 4357  
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Db 4358 AAGCTGGTGTAGAGACTCTGATGTATCCCTCAAACCCCAATTGGCAACATTGTGGTCATT 4417  
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Db 4478 TTCGTGTGTACGGGTGAGGACACCCAGGAACATCACTAACAATCCGACTCGCTGAGGCC 4537  
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Db 4538 AGCTACCGATGGGTCCGGGCACAAAGTACAACCTTGACAACCTGGGCCAGGCTCTGATGTCC 4597  
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Db 4718 TCCTTCTCTCATCGTGGCCCTTCTTTGTCTGAACATGTTTGTGGCGTGGTGGAG 4777  
Qy AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys 1558  
Db 4778 AACTTCCATAAGTGCAGACAGCACCCAGGAGGAGGAGGCGGCGGTGAGGAAG 4837  
Qy ArgLeuArgArgLeuGluLysLysArgArg----- 1568  
Db 4838 CGACTACGGAGGTGGAGAAAAGAGAAGGAATCTAATGTTGGACGATGTAATTGCTTCC 4897  
Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580  
Db 4898 GGCAGCTCAGCCAGCGCTGCGTCAGAAAGCCAGTGCAAGCCCTACTACTCTGACTACTCG 4957  
Qy ArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThr 1600  
Db 4958 AGATTCCGGCTCTTGTCCACCACCTGTGTACCAGCCACTACTGGACCTCTTTCATCACT 5017  
Qy GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620  
Db 5018 GGTGTATCGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATC 5077  
Qy LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer 1640  
Db 5078 CTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCCTCATCTTTGTCTTTGAGTCA 5137  
Qy ValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeu 1660  
Db 5138 GTTTTCAAACCTTGTGGCCTTTGGCTTCGCGCTTCTTCCAGGACAGGTGGAACCACTG 5197  
Qy AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1680  
Db 5198 GACCTGGCTATTGTCTTCTTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAAT 5257  
Qy AlaSerLeuProIleAsnProThrIleIleArgIleMetArgAlaLeuLeuAspThrValMetGln 1700  
Db 5258 GCTTCGCTGCCATCAACCCCAACCATCATCCGTATCATGAGGGTGTCCGCTTGTGTCGA 5317  
Qy ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720  
Db 5318 GTTCTGAAGCTGTTGAAGATGGCTGTGGGCATCGGGCACTGTGGACACGGTGTATGCAG 5377  
Qy AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740  
Db 5378 GCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTTTCATCTTTGCA 5437

Qy 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760  
Db 5438 GCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTATGAGACACACCCCTTGTGAGGC 5497  
Qy LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780  
Db 5498 TTGGGTGGCATGCCACCTTTAGAACTTTGGTATGGCCTTCTGACCCCTCTTCCGAGTC 5557  
Qy SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800  
Db 5558 TCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCCTCCGGACTGTGACCAAGGAG 5617  
Qy SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820  
Db 5618 TCCACCTGTACAACACTGTTCATCTCCCTATCTACTTTGTGTCTTCTGCTGACGGCC 5677  
Qy GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840  
Db 5678 CAGTTTGTGTGTCACCGTGGTCTATAGCTGTCTGATGAAGCACCTGGAAGAAAGCAAC 5737  
Qy LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrIleu 1860  
Db 5738 AAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGTGAAGATGAAGACGCTC 5797  
Qy SerProGlnProHisSerProLeuGlySerPropheLeuTrpProGlyValGluGlyPro 1880  
Db 5798 AGCCCGCAGCCCACTCCCGCTGGCAGCCCTTCTCTGCCCCGGGTGGAGGGTGTCTC 5857  
Qy AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900  
Db 5858 AACAGTCTTGACAGCCCTAAGCCCTGGGGCTCCACACACCACTGCCACATTTGGAGCAGCC 5917  
Qy SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918  
Db 5918 TCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCCGAGGAGGTGCCAGTCCCC 5977  
Qy 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937  
Db 5978 CTAGGACCAGACCTGTGCTGACTGTGAGGAAGTCTGGTGTGACCGGACGCACTCTCTGCC 6037  
Qy AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957  
Db 6038 AATGACAGCTACATGTGCCGAATGGGAGCACTGTCTGAGAGATCCCTAGGACACAGGGC 6097  
Qy TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977  
Db 6098 TGGGGGTCCCCAAAGCCAGTCAGGCTCCATCTTGTCTCGTTCACTCCCAACCAAGCAGAC 6157  
Qy ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997  
Db 6158 ACCAGCTGCATCTACAGCTTCCAAAGATGTGCACTATCTGTCTCCAGCCTCATGGGGCC 6217  
Qy ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017  
Db 6218 CCCACCTGGGGCGCCATCCCTAAACTACCCCACTGGCGCTCCCTCTGGCTCAGAGG 6277  
Qy ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037  
Db 6278 CCTCTCAGCGCGCCAGGAGCAATAAGGACTGACTCCCTGGATGTGAGGGCTGGGTAGC 6337  
Qy ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057  
Db 6338 CGGGAAGACCTGTGTTCAGAGGTGAGTGGGCCCTCTCTGCTCTGACCCGCTCTCATCC 6397  
Qy PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077  
Db 6398 TTCTGGGGCGGGTTCGAGCATCCAGGTGCAGCAGCGCTTCCGGCATCCAGAGCAAGTCTCC 6457  
Qy LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyGlyPro 2097  
Db 6458 AAGCACATCCGCTTGCCAGGCCCTTGCCAGGCCCTGGAACCCAGCTGGGCCAAGACCCCT 6517

QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117  
|||||  
Db 6518 CCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGAGACCTC 6577  
  
QY 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSer 2137  
||| |||  
Db 6578 CTT---CCAGCAGCCAGGAAGAACCCCTGTCCCCACGGGACCTGAAGAAGTGCTACAGT 6634  
  
QY 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHis 2157  
|||||  
Db 6635 GTAGAGACCAGAGCTGCAGGCGCAGGCTGGTCCCTGGCTAGATGAACAGCGGAGACAC 6694  
  
QY 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177  
|||||  
Db 6695 TCCATTGCTGTCTGTGGACAGCGGCTCCCAACCCCGCCTATGTCCCAAGCCCTCA 6754  
  
QY 2178 AsnLeuGlyGlyGlnProLeuGlyProGlySerArgProLysLysLysLeuSerPro 2197  
: : : : :  
Db 6755 AGCCTCGGGGCCAACCTCTTGGGGTCTCTGGGAGCCGGCCTAAGAAAAAATCAGCCCA 6814  
  
QY 2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217  
|||||  
Db 6815 CCCAGTATCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAATGCTCTGGT 6874  
  
QY 2218 IleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237  
: : : : :  
Db 6875 GTCTGCCTCAGGAGGAGGCGCGCGCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCC 6934  
  
QY 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257  
|||||  
Db 6935 CTTGACAGCAGGCTGCCTCACCCCTCCCAAGAAAGACACGCTGAGTCTCTCTGTTG 6994  
  
QY 2258 SerSerAspProAlaAspLeuAspPro 2266  
: : : : :  
Db 6995 TCTTCTGACCCACAGACATGGACCCC 7021

RESULT 11

AX83488  
ID AAX83488 standard; cDNA; 6741 BP.  
XX  
AC AAX83488;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d) cDNA.  
XX  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
XX  
OS Rattus sp.  
XX  
PN WO9929847-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
XX (LOYO ) UNIV LOYOLA CHICAGO.  
PA  
XX Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.  
DR P-PSDB; AAY14593.  
XX  
PT New T-type voltage-gated calcium channels.  
XX  
PS Disclosure; Page 94-103; 138pp; English.  
XX

CC This sequence represents the coding region for a rat T-type voltage-gated  
CC calcium (Ca) channel alpha-1-G designated rCavT1d. Voltage gated channels  
CC are membrane bound glycosylated proteins formed of several subunits. The

CC large alpha subunits form a pore in the membrane that is selective for a  
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III  
CC and IV) and each domain contains 6 putative transmembrane helical  
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage  
CC than L- or N-type channels. Characteristics of T-type channels include  
CC short current time, slow activation kinetics near threshold, fast  
CC inactivation kinetics and slow tail current. The sequences AAX83481-  
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans  
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region  
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type  
CC voltage-gated calcium channel proteins can be used to screen for drugs  
CC which affect calcium channels. Methods are also disclosed for treating a  
CC disease or disorder associated with a deficiency in a native T-type  
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6741  
Score: 10962.50 Matches: 2108  
Percent Similarity: 94.28% Conservative: 33  
Best Local Similarity: 92.82% Mismatches: 101  
Query Match: 92.09% Indels: 29  
DB: 2 Gaps: 5

US-09-6111-257A-37 (1-2266) x AAX83488 (1-6741)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20  
|||||  
Db 1 ATGGACGAGGAGGAGGATGGAGCGGGCCGCGGAGTGGGACAGCCCCGTAGCTTCACG 60  
  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
: : : : :  
Db 61 CAGCTCAACGACCTGTCCGGGCGGGGGCCGGCAGGGGCGGGGTCCAGCGAAAGGAC 120  
  
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60  
|||||  
Db 121 CCGGCAGCGCGGACTCCGAGCGGAGGGGTGCGGTACCCGCGCTAGCCCCGGTGGTT 180  
  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
|||||  
Db 181 TTTCTTCTACTTGAGCCAGGACAGCCCGCCCGGAGTGGTGTCTCCGACGGTCTGTAAAC 240  
  
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
|||||  
Db 241 CCGTGGTTCGAGCGAGTCACTATGCTGGTCACTTCTCAACTGTGTACTTGGGTATG 300  
  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
|||||  
Db 301 TTCAGCGCGTGTGAGGACATGCTGTGACTCCAGCGCTGCCGGATCCTCGAGGCTTC 360  
  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
|||||  
Db 361 GATGACTTCATCTTTGCCCTTCTTTGTGTGGAATGGTGGTGAAGATGGTGGCTTGGGC 420  
  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160  
|||||  
Db 421 ATCTTTGGGAAGAAATGTTACTTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTC 480  
  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
|||||  
Db 481 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGACGTGAGAACTCTCCGAGTCAGG 540  
  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
|||||  
Db 541 ACAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTC 600  
  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
|||||  
Db 601 GTCACATTACTGTGGACACCTTGCCCTATGCTGGGCAACGCTCCTGCTGCTGTTTCTTC 660  
  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
|||||



Db 661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGCGAGGACTGCTTCGCAACCGG 720

Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260

Db 721 TGCTTCTCCCGAGAACTTCAGCCTCCCTGAGCGTGAGCCTGGAGCCTTATTACCAG 780

Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280

Db 781 ACAGAGAATGAGCAGAGAGCCCTTCATCTGCTCTCAGCCCTCGGGAGAAATGGCATGAGA 840

Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300

Db 841 TCCTGCAGGAGTGTGCCACACTGCTGGGGAAGCGGTGGTGGCCCAACCTTCAGTCTG 900

Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320

Db 901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAAACCACTAT 960

Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340

Db 961 ACCAACTGCTCTGGGGCGAGCACAAACCCCTTCAAAGGGCGCCATCAACTTTGACAACTT 1020

Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360

Db 1021 GGCTATGCCTGGATGCCATCTTCCAGTCAACACTGAGGGCTGGTGCACATCATG 1080

Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380

Db 1081 TACTTCGTATGAGCGCTCACTCCTTTACAACCTTCACTTCACTTCTTCTCATCATC 1140

Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400

Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTGAATGCCACGCAGTTCTCCGAG 1200

Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420

Db 1201 ACCAAACAGCGGAGAGTCACTGATGCGGAGCAGCGTGATGATTCCTGTCCAACTGCT 1260

Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440

Db 1261 AGCACCTGGCAAGCTTCTCTGAGCCAGGAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460

Db 1321 GTGTACATCTCCGAAAGCAGCCCGAAGGCTGGCCCCAGGTCTCTAGGGCTATAGCGTG 1380

Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480

Db 1381 CGGGCTGGGCTGCTCAGCAGCCCCAGTGGCCCCGTAGTGGGCGAGGAGCCCCAGCCAGTGGC 1440

Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500

Db 1441 AGCTGCACTCGCTCACACCGTCTGTCTGTGTCCACCACCTGTGTCCACCACCATCACAC 1500

Qy 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520

Db 1501 CACCATCACCACTACCACCTGGGTATGGGACGCTCAGAGTTCCTCCGGGCGAGCCAGAG 1560

Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540

Db 1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTCTACCACCACTCTACACCC 1620

Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560

Db 1621 ACTCCCTCTGGGGCCCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCATGTGAC 1680

Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580

Db 1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 1740

Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600

Db 1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCTACACAGCCCTCCACCAGAG 1800

Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620

Db 1801 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCAC 1860

Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640

Db 1861 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660

Db 1921 ACGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGA 1980

Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680

Db 1981 GCCTGGGGCCGGACAGTTGTCTCTACTGTGCCCGGACAGGAGCAGGAGCCAGAGTCC 2040

Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700

Db 2041 GCTGACCATGTCTGCTGACTCAGACAGGAGGCTGTATGAGTTACACAGGACGCT 2100

Qy 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719

Db 2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGACAGCGGAGCCTGGGCCAGAT 2160

Qy 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739

Db 2161 GCAGAGCCTAGTTCTGTGTGGCTTCTGGAGGCTGATCTGTGACACATTCGGAAGATC 2220

Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759

Db 2221 GTAGATAGCAATACTTTGGCCGGGAATCATGATCGCCCATCTTGGTCAATACACTCAGC 2280

Qy 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779

Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340

Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799

Db 2341 ATCGTCTTCACCAGCCTCTTCGCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819

Db 2401 TTTGGCTACATTAAAGATCCCTACAACATCTTTGATGGTGTCAATTTGGTTCATCAGTGTG 2460

Qy 820 TrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839

Db 2461 TGGGAGATTGTGGCCAGCAGGGAGGTGGCCTGTGCGTGTGCGGACCTTCCGCTGATG 2520

Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859

Db 2521 CGGGTGTGAAGCTGGTGGCTTCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCATG 2580

Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879

Db 2581 AAGACCATGACAACTGGGCCACTTCTGCATGCTCCTCATGTGTTCATCTTCATCTTC 2640

Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899

Db 2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTTCGATCTCGAATCGGATGGGACAG 2700

Qy 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919

Db 2701 TTGCCAGACCGGAAGAAATTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

Qy 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939

Db 2761 CTGACTCAGGAAGACTGGAAATAAAGTCTCTACAACGGCATGGCCTCCACATCGTCTTGG 2820

Qy 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959

Db 2821 GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGTCTCTTTAACCTGTG 2880

QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979  
Db 2881 GTGGCCATTCTTGTGAAGGATTCCAGGCAGAG----- 2913  
QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999  
Db 2914 -----GGAGATGCCACCAAGTCT 2931  
QY 1000 GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019  
Db 2932 GAGTCAGAGCCTGATTCTTTTCGCCCAAGTGTGGATGGTGAGAGGAGAGAGCGC 2991  
QY 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu 1039  
Db 2992 TTGGCCCTGGTGGCTTTGGGAGAACACGCGGAACCTACGAAAGAGCCTTTTGGCACCCCTC 3051  
QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059  
Db 3052 ATCATCCATACAGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGG 3111  
QY 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079  
Db 3112 GAAGCACTGGGCTCTGGCTCTCGACGTACCAAGTACAGTAGCAGTGGTCCGCTGAGCTGGAGCT 3171  
QY 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098  
Db 3172 GCCCACCATGAGATGAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGT 3231  
QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118  
Db 3232 GCGGCAAGCAGCTGGACCAAGCGGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGC 3291  
QY 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlu 1138  
Db 3292 CTAAGCGGAGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGCGCAGGAG 3351  
QY 1139 SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158  
Db 3352 AGTCAGGATGAGGAGGAAAGTTTCAAGAGAGGACCGGGCCAGCCCGCAGCAGGCACTGACCAT 3411  
QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178  
Db 3412 CGCCACAGGGGTCTTGGACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTG 3471  
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198  
Db 3472 CAGGTGCCGGGTGCACCGCACAGCGCGCGCGAGCTGCTCCTCTGAGCACCAAGAC 3531  
QY 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspPro 1218  
Db 3532 TGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCCCTGAGGACTGATGACCCCAA 3591  
QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238  
Db 3592 CTGGATGGGGATGATGACAAATGATGAGGGAATCTGAGCAAGGGGAACGCATACAGCC 3651  
QY 1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258  
Db 3652 TGGGTGAGATCCCGGCTTCTGCCTGTGCGGAGAGCGAGATTCTGTGCGGCCTATATC 3711  
QY 1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278  
Db 3712 TTTCTCTCAGTCAAGGTTTTCGTCTCCTGTGTACCCGGATCATCACCCAGATGTTT 3771  
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298  
Db 3772 GACCATGTGTCCTCGTCATCATCTTCTCAACTGTATCACCCTGTATCACCCTATGGAGCGCCC 3831  
QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318  
Db 3832 AAAATTGACCCCAAGCGCTGAGCGCATCTTCTGACCCCTCTCCAACCTACATCTTCACG 3891  
QY 1319 AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGlu 1338

Db 3892 GCAGTCTTTCTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTTGGGGAG 3951  
QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358  
Db 3952 CAGGCCTACCTGCGCAGCAGCTGGAATGTGTGGACGGCTTGTGTGTCTCATCTCCGTC 4011  
QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378  
Db 4012 ATCGACATCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGG 4071  
QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398  
Db 4072 GTGCTGCGGCTGCTGCGGACCCCTGCGTCCACTCAGGGTTCATCAGCCGGGCCAGGACTG 4131  
QY 1399 LysLeuValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValIle 1418  
Db 4132 AAGCTGGTGTAGAGACTCTGATGTCTATCCCTCAAAACCCATTGGCAACATTGTGTCTATT 4191  
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438  
Db 4192 TGCTGTGCTTCTTCATCATTTTGGAAATCTCGGGGTGCAGCTCTTCAAAAGGAAGTTC 4251  
QY 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458  
Db 4252 TTCGTGTGTGAGGTGAGGACACAGGAACATCACTAACAATCCGACTGCGCTGAGGCC 4311  
QY 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478  
Db 4312 AGTACCGATGGTCCGACAAAGTACAACTTGACAACTTGGCCAGGCTCTGATGTCC 4371  
QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498  
Db 4372 CTGTTGTGTGGCTTCCAAGGATGGTGGTGTGACATCATGTATGATGGGCTGGATGCT 4431  
QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518  
Db 4432 GTGGTGTGGATCAGCAGCCCATCATGAACCAACCAACCCCTGGATGCTATATACTTTCATC 4491  
QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538  
Db 4492 TCCTTCCTCCTCATCGTGGCTTCTTTGTCTGAACATGTTTGTGGCGTGGTGGTGAG 4551  
QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys 1558  
Db 4552 AACTCCATAAGTGCAGACAGCACCGAGGAGGAGGAGGAGGCGGCGGTGAGGAGAAG 4611  
QY 1559 ArgLeuArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAsp 1578  
Db 4612 CGACTACGGAGGCTGGAGRAAAGAGAGGAAGCAAGCCAGTGAAGCCCTACTACTCTGAC 4671  
QY 1579 TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe 1598  
Db 4672 TACTCGAGATTCCGGCTCCTGTGCCACCACTGTGTACCAAGCCACTACCTGGACCTCTTC 4731  
QY 1599 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1618  
Db 4732 ATCACTGGTGTTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCC 4791  
QY 1619 GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeu 1638  
Db 4792 CAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCACTTTGTCTTT 4851  
QY 1639 GluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsn 1658  
Db 4852 GAGTCAGTTTCAAACCTGTGGCTTTGGCTTCCGCGTCTTCTCCAGGACAGGTGGAAC 4911  
QY 1659 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu 1678  
Db 4912 CAGCTGACCTGGCTATTGTGTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAG 4971  
QY 1679 ValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle 1698

Db 4972 GTCAATCTGTGCTGCCCATCAACCCCAACCATCATCCGTATCATGAGGGTGTCTCCGCATT 5031

Qy 1699 AlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrVal 1718

Db 5032 GCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGCATCGGGCACTGCTGCACACGGTG 5091

Qy 1719 MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle 1738

Db 5092 ATGAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATC 5151

Qy 1739 PheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCys 1758

Db 5152 TTTGCAGCTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTGT 5211

Qy 1759 GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe 1778

Db 5212 GAGGGCTTGGGTCCGCATGCCACCTTTAGGAACCTTTGGTATGGCCTTTCTGACCCCTCTC 5271

Qy 1779 ArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAsp 1798

Db 5272 CGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCCTCCGGGACTGTGAC 5331

Qy 1799 GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu 1818

Db 5332 CAGGAGTCCACTGCTACAACACTGTCTATCTCCCTATCTACTTGTGTCTTCTGCTG 5391

Qy 1819 ThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGlu 1838

Db 5392 ACGGCCAGTTTGTGCTGCTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTGGGAAGA 5451

Qy 1839 SerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluMetLys 1858

Db 5452 AGCAACAAAGAGGCCAAGGAGGAGGCGGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAG 5511

Qy 1859 ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlu 1878

Db 5512 ACGCTCAGCGCGCAGCCCCACTCCCGCTGGCAGCCCCCTCTCTGCCCCGGGTGGAG 5571

Qy 1879 GlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArg 1898

Db 5572 GGTGTCAACACTACTGACAGCCCTAAGCCTGGGCTCCACACACCACTGCCACATTGGA 5631

Qy 1899 SerAlaSerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro 1918

Db 5632 GCAGCCTCGGGCTTCTCCCTTGAGCACCCCAACGATGGTACCCCAACCCCGAGGAGTGCCA 5691

Qy 1919 -----GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer 1935

Db 5692 GTCCCCCTTAGCACACAGACCTGTGCTGAGTGTGAGGAAGTCTGGTGTGAGCCGACACTCT 5751

Qy 1936 LeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHis 1955

Db 5752 CTGCCCAATGACAGCTACATGTGCCGAATGGGAGCACTGTGTGAGAGATCCCTAGGACAC 5811

Qy 1956 ArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnPro 1975

Db 5812 AGGGGCTGGGGCTCCCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACCA 5871

Qy 1976 AlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHis 1995

Db 5872 GCAGACACCAAGTGCATCCTACAGCTTCCCAAGATGTGCACTATCTGTCTCCAGCCTCAT 5931

Qy 1996 SerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAla 2015

Db 5932 GGGGCTCCACCTGGGGCGCCCATCCCTAAACTACCCCACTGGCCGCTCCCTCTGGCT 5991

Qy 2016 GlnArgProLeuArgArgGlnAlaIleArgThrAspSerLeuAspValGlnGlyLeu 2035

Db 5992 CAGAGGCCTCTCAGGCGCCAGGCAAGCAATAAGGACTGACTCCCTGGATGTGCAGGCGCTG 6051

Qy 2036 GlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAlaArgAla 2055

Db 6052 GGTAGCCGGGAAGACCTGTTGTTCAGAGGTGAGTGGGGCCCTCTGCCCCTCTGACCCGGTCC 6111

Qy 2056 TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLys 2075

Db 6112 TCATCCTTCTGGGGCGGGTCCGAGCATCCAGGTGCAGACGGTTCGGGCATCCAGAGCAAA 6171

Qy 2076 IleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLys 2095

Db 6172 GTCTCCAAGCACATCCGCTGCCAGCCCTTGTCCCAGGCTTGAACCCAGCTGGGCCAAG 6231

Qy 2096 GlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGly 2115

Db 6232 GACCCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGGA 6291

Qy 2116 AspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCys 2135

Db 6292 GACCTCCTT---CCCAGCAGCCAGGAAGAACCCCTGTTCACACGGGACCTGAAGAAGTGC 6348

Qy 2136 TyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArg 2155

Db 6349 TACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGGGTCTGGCTAGATGAACACGGCG 6408

Qy 2156 ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAsp 2175

Db 6409 AGACACTCCATTGCTGTGAGCTGTCTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGC 6468

Qy 2176 ProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeu 2195

Db 6469 CCCTCAAGCCTCGGGGCCAACCTCTTGGGGTCTCTGGGAGCCGGCCTAAGAAAAAATC 6528

Qy 2196 SerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSer 2215

Db 6529 AGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGT 6588

Qy 2216 ProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSer 2235

Db 6589 CCTGGTGTCTGCCTCAGGAGGAGGGCGCGCCGAGTACTCTAAGGATCCCTCGGTCTCC 6648

Qy 2236 GlyProProAspSerMetAlaSerProSerProSerProLysLysAspValLeuSerLeuSer 2255

Db 6649 AGCCCCCTTGACAGCACGGCTGCTCACCCCTCCCAAGAAAGACACGCTGAGTCTCTCT 6708

Qy 2256 GlyLeuSerSerAspProAlaAspLeuAspPro 2266

Db 6709 GGTGTGTCTCTGACCAACAGACATGGACCCC 6741

RESULT 12

AAx83485

ID AAx83485 standard; cDNA; 6762 BP.

XX AC AAx83485;

DT 07-DEC-1999 (first entry)

XX DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavTla) cDNA.

XX KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX OS Rattus sp.

XX PN WO9929847-A1.

XX PD 17-JUN-1999.

XX PF 30-OCT-1998; 98WO-US023161.

XX PR 05-DEC-1997; 97US-00985809.

XX PA (LOYO ) UNIV LOYOLA CHICAGO.

XX PI Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

DR P-PSDB; AAY14590.

XX New T-type voltage-gated calcium channels.

PT Disclosure; Page 67-76; 138pp; English.

XX This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCav1.1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-x83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX Sequence 6762 BP; 1362 A; 2044 C; 1917 G; 1439 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:	0	Length:	6762
Score:	10945.00	Matches:	2107
Percent Similarity:	93.99%	Conservative:	34
Best Local Similarity:	92.49%	Mismatches:	101
Query Match:	91.94%	Indels:	36
DB:	2	Gaps:	6

US-09-611-257A-37 (1-2266) x AAX83485 (1-6762)

QY	1	MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
DB	1	ATGGACGAGGAGGAGGATGGAGCGGGCGCGGAGGATCGGGACAGCCCCGTAGCTTCACG	60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
DB	61	CAGCTCAACGACCTGTCCGGGGCCGGGGCCGGCAGGGGCCGGGGTTCGACGGAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	121	CCGGCAGCGCGGACTCCGAGCGGAGGGCTGCCGTACCCGGCGTAGCCCCGGTGGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	181	TTCTTCTACTTGACCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACCGTCTGTAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	241	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCACTTCTCACTGTGTGACTCTGGGTATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTACGGCCGTGTGAGGACATTGGCTGTGACTCCAGCGCTCCGGATCCTGCAGGCTTC	360
QY	121	AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTCATCTTGGCTCTTTTGTGTGAAATGGTGGTGAAGATGGTGGCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal	160
DB	421	ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTGACTTTTTCATTGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	481	ATTGCAGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGACGAGG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200

DB	541	ACAGTCCCGTGTGTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATTTCTC	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	601	GTCAATTACTGTGGACACCTTGCTATGCTGGGCAACGCTCCTGCTGCTGCTGTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	661	GTCTTTTTCATCTTTGGCATCGTGGCGTCCAGCTGTGGCAGGACTGCTCGCAACCGG	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	721	TGCTTCTCTCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCTTATTACCAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	781	ACAGAGAAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu	300
DB	841	TCCTGCAGGAGTGTGCCACACTGCGTGGGAAAGCGGTGGTGGCCACCTGCAGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
DB	901	GACTATGAGACCTATAACAGTTCCAGCAACACCACTGTGTCACTGGAACCACTACTAT	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	961	ACCAACTGCTCTGCGGGGAGACACACCCCTTCAAAGGCGCCATCAACTTTGACAACATT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet	360
DB	1021	GGCTATGCTGGATCGCCATCTTCCAGGTCACTACACTGGAGGGCTGGGTGACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle	380
DB	1081	TACTTCGTAATGAGCGCTCACTCCTTCTACAACTTCACTTCTTCTTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu	400
DB	1141	GTGGGCTCCTTCTTCATGATCAACCTGTGCCCTGGTGGTATTGCCACGCACTTCTCCG	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1201	ACCAACAGCGGGAGAGTCAGCTGATCGGGAGCAGCGTGTACGATTCTCTGCAATGCT	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
DB	1261	AGCACCTGGCAAGCTTCTCTGAGCCAGGAGCTGTGTATGAGGAGCTACTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1321	GTGTACATCTCCGAAAGAGAGCCCGAAGGCTGGCCAGGTCTCTAGGGCTATAGCGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
DB	1381	CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCCGTAGTGGGAGGAGCCCCAGCCAGTGGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
DB	1441	AGCTGCACTCGCTCACACCGCTGTGTCTGTCCACACCTGGTCCACCACTACCCAC	1500
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
DB	1501	CACCATCACCACTACCACTGGGTAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAG	1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
DB	1561	ATCCAGGACAGGATGCCAATGGGTCTCGCCGGCTCATGTACCACTACCCCTCTACACC	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560



Db 1621 ACTCCCTCTGGGGCCCTCCGAGGGGTGCGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy 561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580

Db 1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGACCCCTCCAGATGCCCATCGGAGGCATCT 1740

Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600

Db 1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACAGCCCTCCACCAGAG 1800

Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620

Db 1801 ATACTGAAGATAAAGCACTAGTGGAGGTGGCCCTCCAGCCCTGGGCCCTCCACCTCAC 1860

Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640

Db 1861 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660

Db 1921 ACGGAGCCTGCCATAGCTCTGTCAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGA 1980

Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680

Db 1981 GCCTGGGGCCGGACAGTTGTCCCTACTGTGCCGGACAGGAGGAGGACAGAGTCC 2040

Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700

Db 2041 GCTGACCATGTATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTACACAGGACGCT 2100

Qy 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719

Db 2101 CAGCACAGTACCTCCGGGATCCCCACAGCGCGGCGACAGCGAGCCTGGGCCAGAT 2160

Qy 720 AlaGluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIle 739

Db 2161 GCAGAGCCTAGTTCTGTCTGGCTTTCTGGAGGCTGATCTGTGACACATTCGGAAGATC 2220

Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759

Db 2221 GTAGATAGCAATACTTTGGCCGGGGAAATCATGATCGCCATCTGGTCAATACACTCAGC 2280

Qy 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779

Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340

Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799

Db 2341 ATCGTCTTACCAGCCTCTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal 819

Db 2401 TTTGGCTACATTAAAGATCCCTACAACATCTTTGATGGTGTCTATTTGGTTCATCAGTGTG 2460

Qy 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839

Db 2461 TGGGAGATTGTGGCCAGCAGGAGGTGGCTGTGGTGTCTGCGGACCTTCCGCCCTGATG 2520

Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859

Db 2521 CGGGTGTGAAGTGGTGGCTTCTTCCGCGGCCCTGCAGCGCCAGCTCGTGGTGTCTATG 2580

Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879

Db 2581 AAGACCATGGACACAGTGGCCACCTTCTGCATGCTCCTCATGTGTTCATCTTCATCTTC 2640

Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899

Db 2641 AGCATCTCTGGGCATGCATCTCTTTGGTTGCAAGTTCCGATCTCATGTGTTCATCTTC 2700

Qy 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919

Db 2701 TTGCCAGACCCGGAAGAATTTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGATT 2760

Qy 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939

Db 2761 CTGACTCAGGAAGACTGGAATAAAGTCTCTACAACGGCATGGCTCCACATCGTCTTGG 2820

Qy 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959

Db 2821 GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

Qy 960 ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer 979

Db 2881 GTGGCCATTCTTGTGAAGGATTCCAGGCAGAG----- 2913

Qy 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999

Db 2914 -----GGAGATGCCACCAAGTCT 2931

Qy 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019

Db 2932 GAGTCAGAGCCTGATTTCTTTTCGCCAGTGTGGATGGTGTGGGACAGAAAGAACGCGC 2991

Qy 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu 1039

Db 2992 TTGGCCCTGTGGCTTTGGGAGAACACGCGGAACACTACGAAGAGACCTTTTGCCACCCCTC 3051

Qy 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059

Db 3052 ATCATCCATACGGCTCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGG 3111

Qy 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079

Db 3112 GAAGCACTGGGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCT 3171

Qy 1080 Ala--HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098

Db 3172 GCCCACCATGAGATGAATGTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAGT 3231

Qy 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118

Db 3232 CGGGCAAGCAGCTGGACCAGCAGCGGCTCCAGCAGGAACAGCTGGGCGGGCCCCCAGC 3291

Qy 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlu 1138

Db 3292 CTAAAGCGGAGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAG 3351

Qy 1139 SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158

Db 3352 AGTCAGGATGAGGAGGAAAGTTTCAAGAGGACCGGGCCAGCCAGCAGGCGAGTGACCAT 3411

Qy 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178

Db 3412 CGCCACAGGGGTTCCTTGGAACTGAGGGCCAAGAGTTCTTTGACCTGCCTGACACTCTG 3471

Qy 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198

Db 3472 CAGGTGCCGGGCTGCACCCGACAGCCAGCGCGGAGCTCTGCTCTTGAGCACCAAGAC 3531

Qy 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProPro 1218

Db 3532 TGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCTTGAGGACTGATGACCCCCAA 3591

Qy 1219 LeuAspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238

Db 3592 CTGGATGGGATGATGACAAATGATGAGGGAATCTGAGCAAAAGGGGAACGCATACAAGCC 3651

Qy 1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258

Db 3652 TGGGTACAGATCCCGGCTTCTGCTGCTGTGTCGAGAGCGAGATCTGCTGGCCTATATC 3711

Qy 1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278

Db 3712 TTTCTCCTCAGTCAAGGTTTCGTCTCTCTGTGTACCCGGATCATCACCCACAAGATGTT 3771

QY	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1299
DB	3772	GACCATGTGTCCTCGTCATCATCTTCTCACTGATCACCATCGCTATGGAGCGCC	3831
QY	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
DB	3832	AAAATTGACCCCCACAGCGCTGAGCGCATCTTCTCACTGATCACCATCGCTATGGAGCGCC	3891
QY	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGlu	1338
DB	3892	GCAGTCTTTCTAGCTGAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTGGGGAG	3951
QY	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
DB	3952	CAGGCCTACCTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGTGGTGTCTCATCTCCGTC	4011
QY	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
DB	4012	ATCGACATCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGTGAGG	4071
QY	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
DB	4072	GTGCTGCGGCTGCTGCGGACCTGCGTCCACTCAGGTCATCAGCGGCCAGGACTG	4131
QY	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle	1418
DB	4132	AAGCTGGTGGTAGAGACTCTGATGTCTCCCTCAAAACCATTTGGCAACATTTGTGTCTATT	4191
QY	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
DB	4192	TGCTGTGCCCTTCTTTCATCATTTTTTGGAAATTTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTC	4251
QY	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
DB	4252	TTCTGTGTGTGAGGGTGAGGACACAGGAACATCACTAAACAAATCCGACTGCGCTGAGGCC	4311
QY	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
DB	4312	AGCTACCGATGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCC	4371
QY	1479	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498
DB	4372	CTGTTTGTGCTGGCCTCCAAGGATGGTTGGTTGACATCATGTATGATGGCTGGATGCT	4431
QY	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
DB	4432	GTGGGTGTGGATCAGCAGCCCATCATGAACCAACCCCTGGATGCTGCTATACTTTCATC	4491
QY	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu	1538
DB	4492	TCCTTCTCTCATCGTGGCTTCTTTGTCTTGAAACATGTTTGTGGCGTGGTGGTGAG	4551
QY	1539	AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLys	1558
DB	4552	AACTTCCATAAGTGCAGACAGACACAGGAGGAGGAGGAGGCGGCGGTGAGGAGAAG	4611
QY	1559	ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln	1571
DB	4612	CGACTACGGAGGCTGGAGAAAAAGAGAGAGTAAGGAGAAGCAGATGGCCGAGCCAG	4671
QY	1572	CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr	1591
DB	4672	TGCAAGCCCTACTACTCTGACTACTCGAGATTCCGGCTCTTGTCCACCACCTGTGTACC	4731
QY	1592	SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla	1611
DB	4732	AGCCACTACCTGGACCTCTTTCATCACTGGTGTCACTCGGCTGAACGTGTCACTATGGCC	4791
QY	1612	MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle	1631
DB	4792	ATGGAACATTACCAGCAGCCCCAGATCTTGGACGAGGCTCTGGAAGATCTGCAATTACATC	4851
QY	1632	PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg	1651

Db	4852	TTTTACCGTCATCTTTGTCTTTGAGTCAGTTTCAAACCTTGTGGCCTTTGGCTTCCGCCGT	4911
QY	1652	PhePheGlnAspArgTirAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly	1671
Db	4912	TTCTTCCAGGACAGGTGGAACACAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGC	4971
QY	1672	IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg	1691
Db	4972	ATCACACTGGAGGAGATTGAGGTCAATCTGTGCTGCCCATCAACCCACCATCATCCGT	5031
QY	1692	IleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMet	1711
Db	5032	ATCATGAGGGTGCTCCGCAATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATG	5091
QY	1712	ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu	1731
Db	5092	CGGGCACTGCTGCACACGGTGATGAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTC	5151
QY	1732	PheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlu	1751
Db	5152	TTTCATGTTATTGTTTTTCATCTTTCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAG	5211
QY	1752	CysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGly	1771
Db	5212	TGTGATGAGACACACCCCTTGTGAGGGCTTGGGTGGGCATGCCACCTTTAGGAACCTTGGT	5271
QY	1772	MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys	1791
Db	5272	ATGGCCTTCTGACCCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAG	5331
QY	1792	AspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIle	1811
Db	5332	GACACCCCTCCGGGACTGTGACCGAGGTCCACCTGCTACAACACTGTCTATCTCCCTATC	5391
QY	1812	TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal	1831
Db	5392	TACTTTGTGCTCTCGTGTACGCCCCAGTTTGTGCTGGTCAACGCTGGTCAAGCTGTG	5451
QY	1832	LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAla	1851
Db	5452	CTGATGAAGCACCTGGAAGAAAGCAACAAGAGGCCAAGGAGGCCGAGCTCGAGGCC	5511
QY	1852	GluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro	1871
Db	5512	GAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGGCAGCCCC	5571
QY	1872	PheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeu	1891
Db	5572	TTCTCTGGCCCCGGGGTGGAGGCTGTCACAGCTACTGACAGCCCTAAGCCTGGGGCTCCA	5631
QY	1892	HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln	1911
Db	5632	CACACCACTGCCACATTTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTA	5691
QY	1912	ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer	1928
Db	5692	CCCCACCCGAGGAGGTGCCAGTCCCCCTAGGACCCAGACCTGTGACTGTGAGGAAGTCT	5751
QY	1929	GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr	1948
Db	5752	GGTGTACGCCGACGCACCTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACT	5811
QY	1949	AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerVal	1968
Db	5812	GCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCAGTCAGGCTCCATC	5871
QY	1969	LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla	1988
Db	5872	TTGTCCGTTCACTCCCAACCAGACACACAGCTGCATCCTACAGCTTCCCAAGATGTG	5931
QY	1989	ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro	2008

Db 5932 CACTATCTGCTCCAGCCTCATGGGGTCCACCTGGGGCGCCATCCCTAAACTACCCCA 5991

Qy 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp 2028

Db 5992 CCTGGCCGCTCCCTCTGGCTCAGAGGCTCTCAGGCGCCAGGCAATAAGGACTGAC 6051

Qy 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyPro 2048

Db 6052 TCCCTGGATGTGCAGGCGCTGGGTAGCCGGGAAGACCTGTTGTGAGAGGTGAGTGGGCC 6111

Qy 2049 SerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068

Db 6112 TCCTGCCCTCTGACCCGGTCTCTCATCTTCTGGGGCGGTCCAGCATCCAGGTGCAGCAG 6171

Qy 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088

Db 6172 CGTTCGGGCATCCAGAGCAAGTCTCCAAGCACATCCGCTTCCAGCCCTTGCCAGGC 6231

Qy 2089 ProGluProAsnTrpGlyLysGlyProGluThrArgSerSerLeuGluLeuAspThr 2108

Db 6232 CTGGAACCCAGCTGGGCCAAGGACCTCCAGAGACCAGAGCAGCTTAGAGCTGGACAG 6291

Qy 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSer 2128

Db 6292 GAGCTGAGCTGGATTCAGGAGACCTCTT--CCCAGCAGCCAGGAAGAACCCCTGTTTC 6348

Qy 2129 ProArgAspLeuLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148

Db 6349 CCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAGAGTGCAGGCGCAGGCTGGG 6408

Qy 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168

Db 6409 TTCTGGCTAGTAGAACAGCGGAGACCTCCATTGTCTGCTGAGTGTCTGGACAGCGGCTCC 6468

Qy 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyProGly 2188

Db 6469 CAACCCCGCCTATGTCCAAGCCCTCAAGCCTCGGGGCCAACCTCTTGGGGTCTCTGGG 6528

Qy 2189 SerArgProLysLysLeuSerProProSerIleThrIleAspProProGluSerGln 2208

Db 6529 AGCCGGCCTAAGAAAAAATCAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAG 6588

Qy 2209 GlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAsp 2228

Db 6589 GGCTCTCGGCCCCATGCAGTCTCTGGTGTCTGCTCAGGAGGAGGGCGCGCCAGTGAC 6648

Qy 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248

Db 6649 TCTAAGGATCCCTCGGTCTCCAGCCCTTGACAGCACGGCTGCCTCACCTCCCAAG 6708

Qy 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266

Db 6709 AAAGACACGCTGAGTCTCTCTGGTTGTCTTCTGACCCCAACAGACATGGACCCC 6762

RESULT 13

ADS16295

ID ADS16295 standard; DNA; 6942 BP.

XX AC ADS16295;

XX DT 02-DEC-2004 (first entry)

XX DE Rat voltage-dependent T type alpha 1G subunit calcium channel DNA.

XX KW Voltage-dependent ion channel; drug candidate;

XX KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;

XX KW anticonvulsant; antiarrhythmic; rat; alpha 1G subunit; ds.

XX OS Rattus norvegicus.

XX PN US2004175761-A1.

XX PD 09-SEP-2004.

XX 01-MAR-2003; 2003US-00377139.

PF 01-MAR-2003; 2003US-00377139.

XX (MACK/) MACKINNON R.

PR (MACK/) MACKINNON A L.

XX (JIAN/) JIANG Y.

XX (RUTA/) RUTA V.

PA Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;

PI WPI; 2004-642122/62.

XX REFSQ; NM\_031601.

DR Screening drug candidates that target voltage dependent ion channel

PT protein, involves contacting screening protein with chemical compound,

PT which is drug candidate and determining whether chemical compound binds

PT to screening protein.

XX Disclosure; SEQ ID NO 7; 61pp; English.

PS The invention relates to the composition of matter suitable for use in

XX identifying chemical compounds that bind to voltage-dependent ion channel

CC proteins. The composition comprises a screening protein that consists of

CC an ion channel voltage sensor domain of the ion channel protein

CC immobilised on a solid support. The invention is useful for identifying

CC chemical compounds (drug candidate) that bind to voltage-dependent ion

CC channel proteins. The drug candidate of the invention is utilised for

CC treating a condition mediated by aberrant electrical activity that

CC initiates uptake or release of neurotransmitters and contraction of

CC muscles. The drug candidate of the invention is also utilised for

CC treating epilepsy and arrhythmia. The present sequence is a voltage-

CC dependent calcium channel DNA.

XX SQ Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6942

Score: 10945.00 Matches: 2107

Percent Similarity: 93.99% Conservative: 34

Best Local Similarity: 92.49% Mismatches: 101

Query Match: 91.94% Indels: 36

DB: 13 Gaps: 6

US-09-611-257A-37 (1-2266) x ADS16295 (1-6942)

Qy 1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20

Db 114 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGACAGCCCCGTGCTTACG 173

Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40

Db 174 CAGCTCAACGACCTGTCCGGGGCGGGGGCGCGGAGGGGGCGGCGGCGGCGGCGGAC 233

Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60

Db 234 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCGCGGCTAGCCCCGGTGGT 293

Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80

Db 294 TTCTTCTACTTGAGCCAGGACAGCGCGCGCGGAGCTGGTGTCTCCGACGGTCTGTAAC 353

Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100

Db 354 CCGTGGTTCGAGCGAGTCAGTATGTTGGTCACTTCTTCTCACTGTGTGACTCTGGGTATG 413

Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120

Db 414 TTCAGGCGGTGTGAGGACATTGCTGTGACTCCCGCGCTGCCGGATCCTGCAGGCTTC 473

Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValLysMetValAlaLeuGly 140

Db 474 GATGACTTCATCTTTGCCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 533

Qy 141 IlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160

Db 534 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTC 593

Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180

Db 594 ATTGCAGGGATGCTGGAGTATTGCTGGACCTGCAGAACCTCAGCTTCTCCGAGTCAGG 653

Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200

Db 654 ACAGTCCGTGCTGCGACCGCTCAGGCCATTAAACCGGTGCCAGCATGCGCATCTC 713

Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220

Db 714 GTCACATTACTGCTGGACACCTTGCCCTATGCTGGGCAACGTCCTGCTGCTTCTTCTTC 773

Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240

Db 774 GTCTTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGCAGGACTGCTTCCGAACCGG 833

Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260

Db 834 TGCTTCTCCCGAGAACTTTCAGCCTCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 893

Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280

Db 894 ACAGAGAAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGA 953

Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300

Db 954 TCCTGCAGGAGTGTGCCACACTGCGTGGGAAGCGGTGGTGGCCACCCCTGCAGTCTG 1013

Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320

Db 1014 GACTATGAGACCTATAACAGTTCACGAACACCACCTGTGTCAACTGGAAACCACTACTAT 1073

Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340

Db 1074 ACCAACTGCTCTGCGGGCGAGACAAACCCCTTCAAAGGCGCATCAACTTTTGACAAACATT 1133

Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360

Db 1134 GGCTATGCCTGGATCGCCATCTTCCAGGTCAACACTGAGGGCTGGGTCGACATCATG 1193

Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380

Db 1194 TACTTCGTAAATGGACGCTCACTCCTTCTACAACTTTCATCTACTTCACTTCTTCTCATCATC 1253

Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400

Db 1254 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGTATGCCACGCAGTTCTCCGAG 1313

Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420

Db 1314 ACCAAACAGCGGAGAGTCAGCTGATCGGGAGCAGCGTGTACGATTCTCTGCCAATGCT 1373

Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440

Db 1374 AGCACCCCTGGCAAGCTTCTCTGAGCCAGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1433

Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460

Db 1434 GTGTACATCTCCGAAAAGCAGCCCGAAGGCTGGCCAGGCTCTAGGGCTATAGGCGTG 1493

Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480

Db 1494 CGGGCTGGGCTGCTCAGCAGCCCACTGGGCCCGTAGTGGGAGGAGCCCAAGCCAGTGGC 1553

Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500

Db 1554 AGCTGCACTCGCTCACACCGTCTGCTGTGTCCACCACCTGGTCCACCACCATCACAC 1613

Qy 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520

Db 1614 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCAGAG 1673

Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540

Db 1674 ATCCAGGACAGGATGCCAATGGGTCTCGCCGGCTCATGTACCACCACCTCTACACCC 1733

Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560

Db 1734 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1793

Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580

Db 1794 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 1853

Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600

Db 1854 GGTAGGACTGTGGGTAGTGGAAAGGTGTACCCCACTGTGCATACCAGCCCTCCACAGAG 1913

Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620

Db 1914 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACTCACC 1973

Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640

Db 1974 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 2033

Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660

Db 2034 ACGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGA 2093

Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680

Db 2094 GCCTGCGGGCCGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGCCAGAGTCC 2153

Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700

Db 2154 GCTGACCATGTATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCCACAGGACGCT 2213

Qy 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719

Db 2214 CAGCACAGTGACCTCCGGGATCCCAACAGCCCGCGGCGCAGCGGAGCCTGGGCCCAGAT 2273

Qy 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739

Db 2274 GCAGAGCCTAGTTCTGTGTGGCTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2333

Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759

Db 2334 GTAGATAGCAAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2393

Qy 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779

Db 2394 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCAACCAACGCCCTGGAAATCAGCAAC 2453

Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799

Db 2454 ATCGTCTTACCAGCCCTTTCGCTTGGAGATGCTGTGAAAACCTGTTGTCTACGGTCCC 2513

Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819

Db 2514 TTTGGCTACATTAAAGATCCCTTACAACATCTTTGATGGTGTCAATTGTTGTCATCAGTGTG 2573

Qy 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839

Db 2574 TGGGAGATTGTGGCCAGCAGGAGGAGTGGCCTGTCCGTGCTCGGACCTTCCGCCCTGATG 2633

Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859

Db 2634 CGGGTGTCTGAAGCTGGTGGCTTCTTCCGGGCCCTTGACGGCCAGCTCGTGGTGTCTCATG 2693



QY	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe	879
DB	2694	AAGACCATGGACAACTGGCCACCTTCTGTCATGCTCCTCATGCTGTTTCATCTTCATCTTC	2753
QY	880	SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899
DB	2754	AGCATCTCTGGGCATGCATCTCTTTGGTTGCAAGTTGCGATCTGAACGGGATGGGGACAG	2813
QY	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919
DB	2814	TTGCCAGACCGGAAGATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT	2873
QY	920	LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp	939
DB	2874	CTGACTCAGGAAGACTGGAATAAAGTCTCTACACGGCATGGCCTCCACATCGTCTTGG	2933
QY	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959
DB	2934	GCTGCTCTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTCTCTTTAACCTGCTG	2993
QY	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
DB	2994	GTGGCCATTCTTGTGGAGGATTCCAGGCAGAG-----	3026
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
DB	3027	-----GGAGATGCCACCAAGTCT	3044
QY	1000	GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
DB	3045	GAGTCAGAGCCTGATTTCTTTTCGCCCACTGTGGATGGTATGGGACAGAAAGAACGC	3104
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039
DB	3105	TTGGCCCTGGTGGCTTTGGGAGAACACCGCGGAACATACGAAAGAGCCTTTTGGCCACCCCTC	3164
QY	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
DB	3165	ATCATCCATACGGCTGGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGG	3224
QY	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1079
DB	3225	GAAGCACCTGGCTCTGGCTCTCGACGTACCGTAGCAGTGGGTCCGCTGAGCCTGAGCT	3284
QY	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098
DB	3285	GCCCAACCATGAGATGAATGTCCGCCAAGTCCCCCGAGCTCCCCGCACAGTCCCTGGAGT	3344
QY	1099	AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118
DB	3345	CGGGCAAGCAGCTGGACAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGC	3404
QY	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu	1138
DB	3405	CTAAAGCGGAGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAG	3464
QY	1139	SerGlnAspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis	1158
DB	3465	AGTCAGGATGAGGAGGAAGTTTCAGAAAGAGGACCGGGCCAGCCAGCAGGCAGTGACCAT	3524
QY	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178
DB	3525	CGCCACAGGGGTTCCTTGGAACTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTG	3584
QY	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198
DB	3585	CAGGTGCCGGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCCTCTGAGCACCAAGAC	3644
QY	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro	1218
DB	3645	TGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCCGACCCCTGAGGACTGATGATGATGATG	3704
QY	1219	LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238

Db	3705	CTGGATGGGGATGATGACAATGATGAGGGAATCTGAGCAAGGGGAACGCATACAAGCC	3764
Qy	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle	1258
Db	3765	TGGGTGAGATCCGGCTTCTGCCTGTTGCCGAGAGCGAGATTCTCTGGTCGGCCTATATC	3824
Qy	1259	PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278
Db	3825	TTTCTCTCAGTCAAGGTTTCGTCTCCTGTCACCGGATCATCACCCACAAGATGTTT	3884
Qy	1279	AspHisValValIleIlePheLeuAasnCysIleThrIleAlaMetGluArgPro	1298
Db	3885	GACCATGTGGTCCTCGTCATCATCTTCTCTCACTGTATCACCATCGCTATGGAGCGCCCC	3944
Qy	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	3945	AAAATTGACCCCAACAGCGCTGAGCGCATCTTCTGTGACCCCTCTCCAACTACATCTTCACG	4004
Qy	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu	1338
Db	4005	GCAGTCTTTCTAGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTCTTGGGGAG	4064
Qy	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	4065	CAGGCCTACCTGCGCAGCAGCTGGAATGTGTGGACGGCTTGTCTGGTGTCTATCTCCGTC	4124
Qy	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	4125	ATCGACATCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGG	4184
Qy	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	4185	GTGCTGCGGCTGCTGCGGACCCCTGCTCCACTCAGGGTTCATCAGCCGGGCCAGGGACTG	4244
Qy	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418
Db	4245	AAGCTGGTGGTAGAGACTCTGATGTATCCTCAAACCCATTTGGCAACATTTGGTTCATT	4304
Qy	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	4305	TGCTGTGCCCTCTTCATCATTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTC	4364
Qy	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	4365	TTCTGTGTGTCAGGTTGAGGACACCAGGAACATCACTAACAAATCCGACTCGCTGAGGCC	4424
Qy	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4425	AGTACCGATGGTCCGGCACAAGTACAACATTTGACAACCTGGGCCAGGCTCTGATGTCC	4484
Qy	1479	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4485	CTGTTTGTGCTGGCCTCCAAGGATGGTTGGGTGACATCATGTATGATGGGCTGGATGCT	4544
Qy	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
Db	4545	GTGGGTGTGGATCAGCAGCCCCATCATGAACCAACCAACCCCTGGATGCTGTATACCTTCATC	4604
Qy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	4605	TCCTTCTCTCATCGTGGCCTTCTTTGTCTGCTGAACATGTTTGTGGCGTGGTGGAG	4664
Qy	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys	1558
Db	4665	AACCTCCATAAGTGCAGACAGCACCCAGGAGGAGGAGGCGGCGCTGAGGAGAAG	4724
Qy	1559	ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln	1571
Db	4725	CGACTACGGAGGCTGGAGAAAAAGAGAGAGTAAGGAGAAGCAGATGGCCCGAAGCCAG	4784
Qy	1572	CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr	1591

Db 4785 TGCAAGCCCTACTCTCTGACTACTCGAGATTCCGGGTCCTTGTCTCCACCACCTGTGTACC 4844

QY 1592 SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla 1611

Db 4845 AGCCACTACTGGACCTCTTTCATCACTGGTGTATCGGGCTGAACGTGGTCACTATGGCC 4904

QY 1612 MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle 1631

Db 4905 ATGGAACATTACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATC 4964

QY 1632 PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651

Db 4965 TTTACCGTCACTTTTGTCTTTGAGTCAGTTTCAAACCTTGTGGCCTTTGGCTTCCGCCGT 5024

QY 1652 PhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly 1671

Db 5025 TTCTTCCAGACAGGTGGAACAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGC 5084

QY 1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691

Db 5085 ATCACACTGGAGGAGATTGAGGTCAATCTGTCTGCTGCCCATCAACCCCAACCATCCGT 5144

QY 1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMet 1711

Db 5145 ATCATGAGGGTGTCCGCATTGCTCGAGTTCTGAAGCTGTGAAGATGGTGTGGGCATG 5204

QY 1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu 1731

Db 5205 CGGGCACTGCTGCACACGGTGATGAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTC 5264

QY 1732 PheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751

Db 5265 TTCATGTTATTGTTTTTCATCTTTGAGCTCTGGCGGTGGAGCTCTTTGGAGACCTGGAG 5324

QY 1752 CysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGly 1771

Db 5325 TGTGATGAGACACACCCCTTGTGAGGGGTTGGGTGCGCATGCCACCTTTAGGAACTTGGT 5384

QY 1772 MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys 1791

Db 5385 ATGGCCCTTCTGACCCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAG 5444

QY 1792 AspThrLeuArgAspCysAspGlnGlnSerThrCysTyrAsnThrValIleSerProIle 1811

Db 5445 GACACCCCTCCGGACTGTGACCAGGAGTCCACCTGTACAACTGTCTATCTCCCTATC 5504

QY 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaVal 1831

Db 5505 TACTTTGTCTCGTCTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCAATAGCTGTG 5564

QY 1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAla 1851

Db 5565 CTGATGAAGCACTTGAAGAAGCAACAAGAGGCCAAGGAGGCGCGAGCTCGAGGCC 5624

QY 1852 GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro 1871

Db 5625 GAGCTGGAGCTGGAGATGAAGCGCTCAGCCCGCAGCCCCCACTCCCGCTGGGCAGCCCC 5684

QY 1872 PheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeu 1891

Db 5685 TTCTCTGGCCCCGGGTGGAGGCTGTCACAGCTACTGACAGCCCTAAGCCTGGGGCTCCA 5744

QY 1892 HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln 1911

Db 5745 CACACCACTGCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCAACGATGGTA 5804

QY 1912 ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer 1928

Db 5805 CCCCACCCCGAGGAGTGCCAGTCCCCCTAGGACCAGACCTGTGACTGTGAGGAAGTCT 5864

QY 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948

Db 5865 GGTGTACGCCGACGCACTCTCTGCCCAATGACAGCTACATGTGCGCAATGGGAGCACT 5924

QY 1949 AlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerVal 1968

Db 5925 GCTGAGAGATCCCTAGGACACAGGGGCTGGGGCTCCCCAAAGCCAGTCAGGTCCATC 5984

QY 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988

Db 5985 TTGTCCGTTCACTCCCAACCAGCAGACACCACTGCTATCCTACAGCTTCCCAAGATGTG 6044

QY 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2008

Db 6045 CACTATCTGCTCCAGCCTCATGGGGCTCCCACTGGGGCGCCATCCCTAAACTACCCCA 6104

QY 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp 2028

Db 6105 CCTGGCCGCTCCCTCTGGCTCAGAGGCCCTCTCAGCGGCCAGGCAATAAGGACTGAC 6164

QY 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyPro 2048

Db 6165 TCCCTGGATGTGAGGGCTGGGTAGCCGGGAAGACCTGTTGTCTCAGAGGTGAGTGGGCC 6224

QY 2049 SerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068

Db 6225 TCCTGCCCTCTGACCCGCTCCTCATCTTCTGGGGCGGTGAGCATCAGGTGCAGCAG 6284

QY 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088

Db 6285 CGTTCGGCATCCAGAGCAAAAGTCTCCAAGCACATCCGCTGCCAGCCCTTGCCAGGC 6344

QY 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuLeuAspThr 2108

Db 6345 CTGGAACCCAGCTGGGCCAAGGACCTCCAGAGACCAGAGCAGCTTAGAGCTGGACAG 6404

QY 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSer 2128

Db 6405 GAGCTGAGCTGGATTTCAGGAGACCTCCTT---CCCAGCAGCCAGGAAGAACCCCTGTTT 6461

QY 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148

Db 6462 CCACGGGACCTGAAGAAGTGTACAGTGTAGAGACCAGAGCTGCAGCGCAGGCTGGG 6521

QY 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168

Db 6522 TTCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGTCTGAGTGTCTGGACAGCGGTCC 6581

QY 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGly 2188

Db 6582 CAACCCCGCCTATGTCCAAAGCCCTCAAGCCTCGGGGGCCAACTCTTTGGGGTCTTGGG 6641

QY 2189 SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGln 2208

Db 6642 AGCCGGCCTAAGAAAAAACTCAGCCCCACCCAGTATCTCTATAGACCCCGGAGAGCCAG 6701

QY 2209 GlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAsp 2228

Db 6702 GGCTCTCGGGCCCCCATGCACTGCTGGTGTCTGCCCTCAGGAGGAGGGCGCCGCGCAGTGAC 6761

QY 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248

Db 6762 TCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCAGGCTGCCTCACCTTCCCCAAG 6821

QY 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266

Db 6822 AAAGACACGCTGAGTCTCTCTGGTTGTCTTCTGACCCCAACAGACATGGACCCC 6875

RESULT 14

AAx83486  
ID AAx83486 standard; cDNA; 6795 BP.  
XX  
AC AAx83486;  
XX  
DT 07-DEC-1999 (first entry)  
XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1b) cDNA.  
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
XX Rattus sp.  
OS  
XX WO9929847-A1.  
PN 17-JUN-1999.  
PD 30-OCT-1998; 98WO-US023161.  
XX 05-DEC-1997; 97US-00985809.  
PR (LOYO ) UNIV LOYOLA CHICAGO.  
XX Perez-Reyes E, Cribbs LL;  
PI WPI; 1999-394972/33.  
XX P-PSDB; AAY14591.  
DR New T-type voltage-gated calcium channels.  
PT Disclosure; Page 76-85; 138pp; English.  
PS This sequence represents the coding region for a rat T-type voltage-gated  
XX calcium (Ca) channel alpha-1-G designated rCav1b. Voltage gated channels  
CC are membrane bound glycosylated proteins formed of several subunits. The  
CC large alpha subunits form a pore in the membrane that is selective for a  
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III  
CC and IV) and each domain contains 6 putative transmembrane helical  
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage  
CC than L- or N-type channels. Characteristics of T-type channels include  
CC short current time, slow activation kinetics near threshold, fast  
CC inactivation kinetics and slow tail current. The sequences AAX83481-  
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans  
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region  
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type  
CC voltage-gated calcium channel proteins can be used to screen for drugs  
CC which affect calcium channels. Methods are also disclosed for treating a  
CC disease or disorder associated with a deficiency in a native T-type  
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 6795  
Score: 10939.50 Matches: 2107  
Percent Similarity: 93.53% Conservative: 34  
Best Local Similarity: 92.05% Mismatches: 101  
Query Match: 91.90% Indels: 47  
DB: 2 Gaps: 6  
  
US-09-611-257A-37 (1-2266) x AAX83486 (1-6795)  
  
QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20  
DB 1 ATGGACGAGGAGGAGATGGAGCGGGCCGAGGAGTCGGGACAGCCCCGTAGCTTCAGG 60  
  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
DB 61 CAGCTCAACGACCTGTCCGGGGCCCGGGCCCGGAGGGCCGGGTGCGACGGAAGGAC 120  
  
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
DB 121 CCGGGCAGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 180  
  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
DB 181 TTCTTCTACTTGAGCCAGGACAGCGCCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAC 240  
  
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100

DB 241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCACTTCTCAACTGTGTGACTCTGGGTATG 300  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
DB 301 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 360  
QY 121 AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly 140  
DB 361 GATGACTTCATCTTTGCCCTTCTTGTGTAATGGTGGTGAAGATGGTGGCCTTGGGC 420  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160  
DB 421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGCTTGACTTTTTCATTGTC 480  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 481 ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTTCCTCCGCAGTCAGG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGGCATCTC 600  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
DB 601 GTCACATTACTGTGGACACCTTGCCTATGCTGGGCAACGTCTGTCTGTCTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
DB 661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGAGGAGTGTTCGCAACCGG 720  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
DB 721 TGCTTCTCTCCCGAGAACTTCAGCTCCCTCCCTGAGCGTGGACCTTGAGCCTTATTACCAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
DB 781 ACAGAGAAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGGAGAAATGGCATGAGA 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
DB 841 TCCTGCAGGAGTGTGCCACACTGCGTGGGGAAGCGGTGGTGGCCACCCTGCAGTCTG 900  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
DB 901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCCAGTACTAT 960  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnPropheLysGlyAlaIleAsnPheAspAsnIle 340  
DB 961 ACCAACTGCTCTCGGGCGAGCACAACCCCTTCAAAGGGCCCATCAACTTTGACACATT 1020  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
DB 1021 GGCTATGCTGGATCGCCATCTTCCAGGTATCACACTGAGGGCTGGGTGCGACATCATG 1080  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
DB 1081 TACTTCGTAATGAGCGCTCACTCTCTTCTACAACTTCACTTCTTCTTCTCATCATC 1140  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
DB 1141 GTGGGCTCTTCTTCATGATCAACCTGTGCCTGGTGGTGAATGCCACGAGTTCCTCCGAG 1200  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
DB 1201 ACCAAACAGCGGAGAGTCAGCTGATCGGGAGCAGCGGTACGATTCTGTCCAATGCT 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440  
DB 1261 AGCACCTTGGCAAGCTTCTCTGAGCCAGGACGCTGTATGAGGAGTACTCAAGTACCTG 1320  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460

Db 1321 GTGTACATCTCCGAAAAAGCAGCCCGAAGGCTGGCCAGGTCTCTAGGCTATAGCGGTG 1380

QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480

Db 1381 CGGGCTGGGCTGCTCAGCAGCCCGAGTGGCCGCTAGTGGCAGGAGCCCGCAGTGGC 1440

QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500

Db 1441 AGCTGCACCTCGCTCACACCGTCTGTCTGTCTCCACCACTGGTCCACCACTACCCAC 1500

QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520

Db 1501 CACCATCACCACTACCACTGGGTAATGGACGCTCAGAGTTCCCCGGGGCCAGCCAGAG 1560

QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540

Db 1561 ATCCAGGACAGGATGCCAATGGGTCTCGCCGGTCTATGCTACCACTTACACCC 1620

QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560

Db 1621 ACTCCCTCTGGGGCCCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580

Db 1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCATCGGAGGCATCT 1740

QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600

Db 1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACAGAG 1800

QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620

Db 1801 ATACTGAAGGATAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACC 1860

QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640

Db 1861 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAT 1920

QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660

Db 1921 ACGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGA 1980

QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680

Db 1981 GCCTGGGGCCGGACAGTTGTCCCTACTGTGCCCGACAGGAGCAGGAGCCAGATCC 2040

QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700

Db 2041 GCTGACCATGTTCATGCTGACTCAGACAGCGAGGCTGTGTATGAGTTCCACACAGGACGCT 2100

QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719

Db 2101 CAGCACGTGACCTCCGGATCCCCACAGCCGGCGGCAGCAGCGGAGCCTGGGCCAGAT 2160

QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739

Db 2161 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCGGGAAGATC 2220

QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759

Db 2221 GTAGATAGCAAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2280

QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779

Db 2281 ATGGGCATCGAGTACCACAGCAGCCCGAGGAGTCAACCAACGCCCTGGAAATCAGCAAC 2340

QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799

Db 2341 ATCGTCTTACCAGCCCTCTCGCCTTGGAGATGCTGTGAAACTGCTGTGTCTACGGTCCC 2400

QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819

Db 2401 TTTGGCTACATTAAAGATCCCTACAACATCTTTGATGGTGTCTATTGTGGTCACTAGTGTG 2460

QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839

Db 2461 TGGGAGATTGTGGCCAGCAGGAGGTGGCTGTTCGGTGTCTGGGACCTTCCGCCTGATG 2520

QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859

Db 2521 CGGGTGTGAAGCTGGTGGCTTCTCTCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCATG 2580

QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879

Db 2581 AAGACCATGGACAACGTGGCCACCCTTTCGCATGCTCTCATGTGTTCATCTTCATCTTC 2640

QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899

Db 2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCCGCACTGACACGCGGATGGGACACG 2700

QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919

Db 2701 TTGCCAGACCCGGAAGAAATTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

QY 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939

Db 2761 CTGACTCAGGAAGACTGGAATAAAGTCTCTACAAACGGCATGGCTCCACATCGTCTTGG 2820

QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959

Db 2821 GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979

Db 2881 GTGCCATTCTTGTGGAGGATTCCAGGCAGAG----- 2913

QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999

Db 2914 -----GGAGATGCCACCAAGTCT 2931

QY 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019

Db 2932 GAGTCAGAGCCTGATTTCTTTTCGCCCAGTGTGATGGGACAGAAAGACGC 2991

QY 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu 1039

Db 2992 TTGGCCCTGGTGGCTTTGGGAGAAACACGCGGAACACTCGAAAGAGCCTTTTGCCACCCCTC 3051

QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059

Db 3052 ATCATCCATACGGCTGCGACACCAATGTACACCCCAAGAGTCCAGCACAGGTGTGGGG 3111

QY 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079

Db 3112 GAAGCACTGGGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCT 3171

QY 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098

Db 3172 GCCCACCATGAGATGAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGT 3231

QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118

Db 3232 CGGCAACGACGCTGGACCAGCAGCGGCTCCAGCAGGAACAGCTTGGCCGGGCCCCAGC 3291

QY 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlu 1138

Db 3292 CTAAGCGGAGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAG 3351

QY 1139 SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158

Db 3352 AGTCAGGATGAGGAGGAAAGTTTCAGAAAGAGGACCGGGCCAGCCAGCAGGAGTGACCAT 3411

QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178

Db 3412 CGCCACAGGGGTCTCTTGAACGTGAGGCCAAGAGTTCTTTGACCTGCCTGACACTCTG 3471





Db 5632 AACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTTGGAGCAGCC 5691

Qy 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918

Db 5692 TCGGGCTTCTCCCTTGAGACACCCACGATGGTACCCACCCGAGGAGGTGCCAGTCCCC 5751

Qy 1919 --GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937

Db 5752 CTAGGACCAGACTGTGACTGTGAGGAAGTCTGGTGTACGCCGCGACGCACTCTCTGCC 5811

Qy 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957

Db 5812 AATGACAGCTACATGTGCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGC 5871

Qy 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977

Db 5872 TGGGGGCTCCCAAGCCAGTCAGGCTCCATCTTGTTCGTTCACCTCCCAACACGAGAC 5931

Qy 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997

Db 5932 ACCAGCTGATCTCTACAGCTTCCCAAGATGTGCACTATCTGCTCCAGCCTCATGGGCT 5991

Qy 1998 ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017

Db 5992 CCCACCTGGGGCGCCATCCCTAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGG 6051

Qy 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037

Db 6052 CCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGAGGGCCTGGTAGC 6111

Qy 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057

Db 6112 CGGAAGACCTGTGTGAGAGGTGAGTGGGCCCTCCTGCCCTCTGACCCGCTCCTCATCC 6171

Qy 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077

Db 6172 TTCTGGGGGGTGGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAGTCTCC 6231

Qy 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097

Db 6232 AAGCACATCCGCGTCCAGCCCTTGCCAGGCCCTGGAAACCCAGCTGGGCCAAGACCCT 6291

Qy 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117

Db 6292 CCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGTGGATTTCAGGAGACCTC 6351

Qy 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSer 2137

Db 6352 CTT---CCAGCAGCCAGGAAGAACCCCTGTTCACCGGACCTGAAGAAGTGTACAGT 6408

Qy 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHis 2157

Db 6409 GTAGAGACCCAGAGCTGCAGGCGCAGCCTGGTTCGGCTAGATGAACAGCGGAGACAC 6468

Qy 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177

Db 6469 TCCATTGCTGTACGCTGTCTGGACAGCGGCTCCCAACCCCGCCTATGTCCAAGCCCTCA 6528

Qy 2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerPro 2197

Db 6529 AGCCTCGGGGGCCAACTCTTTGGGGTCTCTGGAGCCGGCTAAGAAAAAATCAGCCCA 6588

Qy 2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217

Db 6589 CCCAGTATCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGTCAGTCTGGT 6648

Qy 2218 IleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237

Db 6649 GTCTGCCTCAGAGGAGGGCGCGCGCAGTGACTTAAGGATCCCTCGGTCTCCAGCCCC 6708

Qy 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257

Db 6709 CTTGACAGCAGCGCTGCCTCACCCCTCCCAAGAAAGACACGCTGAGTCTCTCTGTTTG 6768

Qy 2258 SerSerAspProAlaAspLeuAspPro 2266

Db 6769 TCITCTGACCCCAACAGACATGGACCCC 6795

RESULT 15

AAX83487

ID AAX83487 standard; cDNA; 6816 BP.

XX

AC AAX83487;

XX

DT 07-DEC-1999 (first entry)

XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c) cDNA.

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO ) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR

P-PSDB; AAY14592.

XX

New T-type voltage-gated calcium channels.

PS

Disclosure; Page 85-94; 138pp; English.

This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCavT1c. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

SQ Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6816

Score: 10925.00 Matches: 2106

Percent Similarity: 93.16% Conservative: 33

Best Local Similarity: 91.72% Mismatches: 103

Query Match: 91.78% Indels: 54

DB: 2 Gaps: 6

US-09-611-257A-37 (1-2266) x AAX83487 (1-6816)

Qy 1 MetAspGluGluAspGlyAlaGluSerGlyGlnProArgSerPheMet 20

Db 1 ATGGACGAGGAGGAGGATGGAGCGGGCCGAGGAGTCGGGACAGCCCCCGTAGCTTCAGC 60

QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40  
Db 61 CAGCTCAACGACCTGTCCGGGCCCGGGCCGGCAGGGCCGGGTCCGACGGAAGGAC 120  
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
Db 121 CCGGGCAGCGCGACTCCGAGCGGAGGGGTGCCGTACCCCGCGCTAGCCCGGTGTT 180  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
Db 181 TTCTTCTACTTGACCCAGGACAGCCCGCCGGGAGCTGGTGTCTCCGACCGTCTGTAAC 240  
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 300  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 301 TTCAGGCCGTGTGAGGACATTGCCGTGTGACTCCAGCGCTCCGAGATCCTGCAGGCCCTTC 360  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly 140  
Db 361 GATGACTTCATCTTTGCCCTTCTTTGCTGTGAAATGGTGTGAAGATGGTGGCCTTGGC 420  
QY 141 IlePheGlyLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160  
Db 421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTTGACTTTTTCATTGTC 480  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 481 ATTGCAGGGATGCTGGAGTATTTCGTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATTTCTC 600  
QY 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCACATTACTGCTGGACACCTTGCTATGCTGGCAACGTCCTGCTGCTGCTGCTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGAGGACTGCTTCGCAACCGG 720  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
Db 721 TGCTTCTCTCCCGAGAACTTCAGCCTCCCTGAGCGTGGACCTGGAGCCTTATTACGAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 781 ACAGAGAAATGAGGAGGAGAGCCCTTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGA 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCCTGCAGGAGTGTGCCACACTGCGTGGGAAGCGGTGGTGGCCCACTGTCAGTCTG 900  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 901 GACTATGAGACCTTATAACAGTTCCAGCAACACCACCTGTGTCACTGGAACCACTACTAT 960  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
Db 961 ACCAACTGCTCTCGGGCGGAGCACAAACCCCTTCAAAGGGCCCACTCAACTTTGACAACTT 1020  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1021 GGCTATGCTGGATCGCCCATCTTCCAGGTTCATCACACTGGAGGCTGGGTGACATCATG 1080  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
Db 1081 TACTTCGTAATGGACGCTCACTCCTTCTTACAACCTTCATCTACTTTCATTCTTCTCATCATC 1140  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400

Db 1141 GTGGGCTCCTTCTTTCATGATCAACCTGTGCCTGGTGGTATTGCCACGCAGTTCTCCGAG 1200  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAACAGCGGAGAGTCAGCTGATGCGGGAGCAGCGGTGTACGATTCTGTCCAATGCT 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440  
Db 1261 AGTACCCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaGlyVal 460  
Db 1321 GTGTACATCCTCCGAAAGCAGCCCGAAGGCTGGCCAGGTCTCTAGGGCTATAGCGCTG 1380  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGGCTGGGCTGCTCAGCAGCCCACTGGCCCCGTAGTGGGCGAGGAGCCCCCAGGTGGC 1440  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
Db 1441 AGCTGCACCTCGCTCACACCGCTGCTGTCTGTCCACCACTGGTCCACCACTACCCAC 1500  
QY 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CACCATCACCACTACCACTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCAGAG 1560  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
Db 1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTGTACCACTACACCTCTACACCC 1620  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db 1621 ACTCCCTCTGGGGCCCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
Db 1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCACAGATGCCCATCGGAGGCATCT 1740  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
Db 1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACAGAG 1800  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
Db 1801 ATACTGAAGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCCACCCTCAC 1860  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db 1861 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGTCTCCAAGGCAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db 1981 GCCTGCGGGCCGACAGTTGTCCCTACTGTGCCCGACAGGACAGGAGCCAGAGTCC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCTGACCATGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719  
Db 2101 CAGCACAGTGACCTCCGGATCCCGGATCCCGCAGCCCGCGGACAGGAGCCTGGGCCACAGAT 2160  
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739  
Db 2161 GCAGAGCCTAGTCTGTGCTGGCTTCTGGAGGCTGATCTGTGACACATTTCCGGAAGATC 2220  
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759

Db 2221 GTAGATAGCAATACTTTGGCCGGGAATCATGATCGCCATCTCTGGTCAATACACTCAGC 2280  
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779  
Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340  
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Db 2341 ATCGTCTTCACAGCCTCTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGCTACGGTCCC 2400  
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819  
Db 2401 TTTGGCTACATTAAGAATCCCTACAAACATCTTTGATGGTGTCTATTGGTTCATCAGTGTG 2460  
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839  
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Db 2581 AAGACCATGGACAACGTGGCCACCTCTGTCATGCTCTCCATGCTGTTCATCTTCATCTTC 2640  
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QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer 979  
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QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999  
Db 2914 -----GGAGATGCCACCAAGTCT 2931  
QY 1000 GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019  
Db 2932 GAGTCAGAGCCTGATTCTTTTCGCCAGTGGATGGTATGGGACAGAAAGAGCGC 2991  
QY 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu 1039  
Db 2992 TTGGCCCTGGTGGCTTTGGGAGAACACCGCGGAACACTACGAAAGAGCTTTGCCACCCCTC 3051  
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Db 3052 ATCATCCATACGGCTGCGACACCAATGTACACCCCCAAGAGCTCCAGCACAGGTGTGGGG 3111  
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QY 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098  
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QY 1139 SerGlnAspGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158  
Db 3352 AGTCAGGATGAGGAGGAAGTTTCAGAAAGAGACCGGGCCAGCCAGCAGCAGTGACCAT 3411  
QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178  
Db 3412 CGCCACAGGGGTTCCTTGGAACGTGAGGCCAAGAGTTCTTTGACCTGCCTGACACTCTG 3471  
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198  
Db 3472 CAGGTGCCGGGCTGCACCCGACAGCCAGCGCGCGGAGCTCTGCCTCTGAGCACCAGAC 3531  
QY 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218  
Db 3532 TGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCCGACCCCTGAGACTGATGACCCCAA 3591  
QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238  
Db 3592 CTGGATGGGATGATGACAATGATGAGGAAATCTGAGCAAAAGGGAAACGCAGACAAGCC 3651  
QY 1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258  
Db 3652 TGGTTCAGATCCCGGCTCTCTGCTGTTGCGAGAGCGAGATTCTCGTGGCTATATC 3711  
QY 1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278  
Db 3712 TTTCTCTCTCAGTCAAGGTTTCGTCTCTCTGTGTCCCGATCATCACCACCAAGATGTTT 3771  
QY 1279 AspHisValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298  
Db 3772 GACCATGTGGTCTCTCGTTCATCATCTTCTCAACTGTATCACCATCGCTATGGAGCGCCC 3831  
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Db 3832 AAAATTGACCCCAACAGCGCTGAGCGCATCTTCTGACCCCTCTCCAACATCATCTTCACG 3891  
QY 1319 AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGlu 1338  
Db 3892 GCAGTCTTTCTAGCTGAAATGACAGTGAAGTGGTGGCAGCTGGGCTGGTGTCTTCCGTC 3951  
QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358  
Db 3952 CAGGCCTACCTGCGCAGCAGCTGGAATGTGCTGACCGCTTGTGTGTCTCATCTCCGTC 4011  
QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378  
Db 4012 ATCGACATCCTGGTCTCCATGCTCTCCGACAGCGGCACCAAGATCCTTTGGCATGTGAGG 4071  
QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398  
Db 4072 GTGCTGGGCTGCTGGGACCCCTGCGTCCACTCAGGTCATCAGCCGGCCAGGGACTG 4131  
QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418  
Db 4132 AAGCTGGTGTAGAGACTCTGTATGTATCCCTCAAACCCATTGGCAACATTGTGTGTCATT 4191  
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438  
Db 4192 TGCTGTGCTTCTTCATCATTTTGGAAATTTCTCGGGTGCAGCTCTTCAAAGGGAAGTTC 4251  
QY 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458  
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QY 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478  
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 QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuTyrPheIle 1518  
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 QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu 1538  
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 QY 1559 ArgLeuArgArgLeuGluLysLysArg- 1568  
 DB 4612 CGACTACGGAGGCTGGAGAAAAAGAGAGGAGTAAGGAGAGCAGATGGCCGATCTAATG 4671  
 QY 1569 -----LysAlaGlnCysLys 1573  
 DB 4672 TTGGACGATGTAATTGCTTCCGGCAGCTCAGCCAGCGCTGCGTCAGAACCCAGTGAAG 4731  
 QY 1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis 1593  
 DB 4732 CCTACTACTCTGACTACTCGAGATTCCGGCTCTTGTCCACCACCTGTGTACCAGCCAC 4791  
 QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613  
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 DB 4852 CATTACCAGCAGCCCCAGATCTCGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACC 4911  
 QY 1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe 1653  
 DB 4912 GTCATCTTTGCTTGTGAGTCAGTTCATGTTTCAAACTTGTGGCCTTTGGCTTCCGCCGTTTCTTC 4971  
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 QY 1694 ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla 1713  
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 QY 1734 LeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753  
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 QY 1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773  
 DB 5272 GAGACACACCTTGTGAGGGCTTGGGTGGCATGCCACCTTTAGGAACCTTTGGTATGGCC 5331  
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 DB 5332 TTTCTGACCCCTCTCCGAGTCTCCACTGGTGACAACTGGAATGCTATTATGAAGGACACC 5391  
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 QY 2031 AspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerPro 2050  
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 QY 2051 ProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSer 2070  
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 DB 6232 GGCATCCAGAGCAAGTCTCCAAGCACATCCGCTGCCAGGCCCTTGGCCAGGCTGGA 6291  
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Mon Apr 18 12:41:45 2005

Db 6529 CGCCTATGTCCAAGCCCCCTCAAGCCTCGGGGGCCAAACCTCTTGGGGGTCTGGAGCCGG 6588

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QY 2251 ValLeuSerLeuSerGlyLeuSerSerAspProAlaAlaSerPro 2266  
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Db 6769 ACGCTGAGTCTCTCTGGTTTGTCTTGACCCCAACACAGACATGGACCCC 6816  
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Search completed: April 16, 2005, 03:33:49  
Job time : 2872 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 02:25:35 ; Search time 726 Seconds  
(without alignments)  
5107.167 Million cell updates/sec

Title: US-09-611-257A-37  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO\_spool/US09611257/runat\_13042005\_170154\_186/app\_query.fasta\_1.2439  
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Database : Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11877.5	99.8	6822	3	US-09-426-998-3
2	11877.5	99.8	7741	3	US-09-426-998-4
3	11241	94.4	7405	4	US-09-949-016-3859
4	6315.5	53.1	3993	4	US-09-398-522-51
5	6214.5	52.2	7898	3	US-08-984-709A-49
6	5492.5	46.1	6816	3	US-09-404-650-1
7	5492.5	46.1	6816	4	US-09-935-541-1
8	5484	46.1	6855	3	US-09-404-650-3
9	5484	46.1	6855	4	US-09-935-541-3
10	5418.5	45.5	6503	3	US-09-404-650-12
11	5418.5	45.5	6503	4	US-09-935-541-12
12	2237	18.8	70308	4	US-09-949-016-15601

13	1971.5	16.6	1669	3	US-08-984-709A-51	Sequence 51, Appl
14	1786.5	15.0	7376	3	US-09-268-163-3	Sequence 3, Appli
15	1784.5	15.0	7362	1	US-08-455-543A-7	Sequence 7, Appli
16	1784.5	15.0	7362	2	US-08-193-078B-7	Sequence 7, Appli
17	1784.5	15.0	7362	2	US-08-223-305C-7	Sequence 7, Appli
18	1784.5	15.0	7362	2	US-08-149-097D-7	Sequence 7, Appli
19	1784.5	15.0	7362	3	US-08-949-386-7	Sequence 7, Appli
20	1784.5	15.0	7362	3	US-08-450-562-7	Sequence 7, Appli
21	1784.5	15.0	7362	3	US-08-984-709A-7	Sequence 7, Appli
22	1784.5	15.0	7362	3	US-08-450-272-7	Sequence 7, Appli
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24	1784	15.0	7266	3	US-08-713-118-1	Sequence 1, Appli
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26	1782.5	15.0	7364	3	US-09-268-163-5	Sequence 5, Appli
27	1778	14.9	7175	1	US-08-455-543A-8	Sequence 8, Appli
28	1778	14.9	7175	2	US-08-193-078B-8	Sequence 8, Appli
29	1778	14.9	7175	2	US-08-223-305C-8	Sequence 8, Appli
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36	1776	14.9	7177	3	US-09-268-163-7	Sequence 7, Appli
37	1728.5	14.5	7011	3	US-09-268-163-9	Sequence 9, Appli
38	1711.5	14.4	5975	1	US-08-404-354B-1	Sequence 1, Appli
39	1711.5	14.4	5975	1	US-08-314-083B-1	Sequence 1, Appli
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41	1711.5	14.4	5975	3	US-08-884-599-1	Sequence 1, Appli
42	1701.5	14.3	5975	1	US-08-336-257A-3	Sequence 3, Appli
43	1691	14.2	6112	4	US-09-495-714C-3	Sequence 3, Appli
44	1690	14.2	6114	4	US-09-495-714C-5	Sequence 5, Appli
45	1690	14.2	7089	3	US-08-949-386-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-426-998-3  
; Sequence 3, Application US/09426998  
; Patent No. 6358706  
; GENERAL INFORMATION:  
; APPLICANT: DUBIN, ADRIENNE E.  
; APPLICANT: PYATI, JAYASHREE  
; APPLICANT: ZHU, JESSICA Y  
; APPLICANT: ERLANDER, MARK G  
; APPLICANT: GALINDO, JOSE E  
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM  
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)  
; FILE REFERENCE: ORT-1057  
; CURRENT APPLICATION NUMBER: US/09/426,998  
; CURRENT FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PATENTIN VER. 2.0  
; SEQ ID NO 3  
; LENGTH: 6822  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-426-998-3

Alignment Scores:			
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Score:			Matches: 2264
Percent Similarity:	99.65%		Conservative: 1
Best Local Similarity:	99.60%		Mismatches: 1
Query Match:	99.78%		Indels: 7
DB:	3		Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-426-998-3 (1-6822)

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QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
DB	61	CGGCTCAACGACCTGTCCGGGGCCGGGGCCGGGGCCGGGGTCCAGAGAAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	121	CCGGGCAGCGGACTCCGAGCGGAGGGGTCCGTACCCCGCGCTGGCCCCGGTGGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	181	TTCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGGTGTCTCCGACGGTCTGTAA	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	241	CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTCCGGCCATCGAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCTGTCAGGCCCTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTCATCTTTGCCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal	160
DB	421	ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGAACCGGCTTGACTTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	481	ATCGCAGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTGAGCTTCTCAGCTGTGAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
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DB	601	GTCACGTTGCTGTGGATACGCTGCCATGCTGGGCAACGTCTCTGCTGTCTGCTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	661	GTCTTTCTTCATCTTCGGCATCGTCCGGCTCCAGCTGTGGGCGAGGGCTGCTTCGGAACCGA	720
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QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	781	ACAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACGCGCATGCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
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QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
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DB	1021	GGCTATGCTGGATCGCCATCTTCCAGGTTCATCACGCTGGAGGGCTGGGTCCGACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
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QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
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QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1201	ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCTCTCTCCAAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
DB	1261	AGCACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1321	GTGTACATCCTTCCGTAAGGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
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QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
DB	1561	ATCCAGGACAGGATGCCAATGGGTCCCGCAGGCTCATGCTGCCACCACTTCGACGCCT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
DB	1621	GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGTTCTACCATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
DB	1681	TGCCACTTAGAGCAGTCCGCTGCCAGGGCCCCCTCCCAGGTCCCCATCTGAGGCATCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
DB	1741	GGCAGGACTGTGGGACGCGGAAGGTGTATCCACCGTGCACACCAGCCCTCCACCGGAG	1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
DB	1801	ACGCTGAAGGAGAGGCACTAGTAGAGTGGTGGTCCAGCTCTGGGCCCCCAACCTCACC	1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
DB	1861	AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAAGTGTCTGGAGACACAGAT	1920
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
DB	1921	ACAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA	1980
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
DB	1981	GCCTGTGTTCCAGACAGTGCCTTACTGTGCCCCGGSCGGGCGAGGAGGTGGAGCTC	2040
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
DB	2041	GCCGACCGTGAAATGCCTGACTCAGACAGCGAGGCACTTATGAGTTTACACAGGATGCC	2100
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
DB	2101	CAGCACAGCGACCTCCGGGACCCCCACAGCCCGGGCAACGAGCCTGGGGCCAGATGCA	2160
QY	721	GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal	740
DB	2161	GAGCCACAGCTCTGTGCTGGCTTCTGGAGGCTAATCTGTGCACACCTTCCGAAAGATTGTG	2220
QY	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760



Db 2221 ||||| GACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAACACACTCAGCATG 2280  
QY 761 ||||| GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Db 2281 ||||| GGCATCGAATACCAGAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340  
QY 781 ||||| ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800  
Db 2341 ||||| GTCTTCAACGAGCTCTTTGCCCTGGAGATGCTGTGAAGCTGCTGTGTATGGTCCCTTT 2400  
QY 801 ||||| GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820  
Db 2401 ||||| GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTCAATTGTGGTTCATCAGCGTGTGG 2460  
QY 821 ||||| GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
Db 2461 ||||| GAGATCGTGGCCAGCAGGGGGCGGCTGTGCGTGTGCGGACCTTCGCGCTGATCGGT 2520  
QY 841 ||||| ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
Db 2521 ||||| GTGCTGAAGCTGGTGGCTTCTCTGCCGGCGTGCAGGGGAGTGGTGTGCTCATGAAG 2580  
QY 861 ||||| ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
Db 2581 ||||| ACCATGGACAACTGGCCACCTTCTGCAATGCTGCTTATGCTCTTCATCTTTCAGC 2640  
QY 881 ||||| IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
Db 2641 ||||| ATCCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCTCTGAGCGGGATGGGACACCTG 2700  
QY 901 ||||| ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
Db 2701 ||||| CCAGACCGGAAGAATTTTGACTCTCTGCTGGGCCATCGTCACTGTCTTTCAGATCCTG 2760  
QY 921 ||||| ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940  
Db 2761 ||||| ACCCAGGAGGACTGGAACAAAGTCTCTACAATGGTATGGCTCCACGTCTCTCTGGCG 2820  
QY 941 ||||| AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
Db 2821 ||||| GCCCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTCTCTTCAATTTGCTGGTC 2880  
QY 961 ||||| AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
Db 2881 ||||| GCCATTTCTGTTGAGGGCTTCCAGGCGAGGAAATCAGAAACGGGAAGATCGGAGTGA 2940  
QY 981 ||||| GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
Db 2941 ||||| CAGTTAAGCTGTATTGAGTGCCTGTGACTCCAGGGGGAGATGCCAACAAAGTCCGAA 3000  
QY 1001 ||||| SerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020  
Db 3001 ||||| TCAGAGCCCCGATTCTTCTCACCCAGCTGGATGGTGTGGGACAGGAAGTCTTG 3060  
QY 1021 ||||| AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040  
Db 3061 ||||| GCCTTGGTGTCCCTGGGAGAGCACCCGAGCTGCGGAAGAGCTGTGCCCTCTCATC 3120  
QY 1041 ||||| IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
Db 3121 ||||| ATCCACACGGCGCCACACCCATGTGCTGCCAAGAGCACAGCACGGGCTGGGCGAG 3180  
QY 1061 ||||| AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
Db 3181 ||||| GCGCTGGGCCCTGCGTGGCGCGCACCCAGCAGCGGGTGGCAGAGCCTGGGGCGGCC 3240  
QY 1081 ||||| HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
Db 3241 ||||| CACGAGATGAAGTACCGCCCGCGCAGCTCTCCGACAGCCCCCTGGAGCGCTGCA 3300  
QY 1101 ||||| SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120

Db 3301 ||||| AGCAGCTGGACCAGCAGGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3360  
QY 1121 ||||| ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140  
Db 3361 ||||| CGGAGAAGCCCAAGTGGAGAGCGGCGTCCCTGTTGTTCGGAGAAGGCCAGGAGCCAG 3420  
QY 1141 ||||| AspGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
Db 3421 ||||| GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCCAGCCCTGCGGCGAGTACCATCGCCAC 3480  
QY 1161 ||||| ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
Db 3481 ||||| AGGGGTCCCTGGAGCGGAGGCCAAGAGTTCCTTTGACCTGCCAGACACACTGCGGTG 3540  
QY 1181 ||||| ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
Db 3541 ||||| CCAGGGCTGCATCGCACTGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACGAGACTGCAAT 3600  
QY 1201 ||||| GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
Db 3601 ||||| GGCAAGTCGGCTTCAGGGCGCTTGGCCCGGCCCTGCGGCTGATGACCCCCACTGGAT 3660  
QY 1221 ||||| GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
Db 3661 ||||| GGGGATGACCGCATGACGAGGGCAACCTGAGCAAAGGGGACGGGTCCGCGCTGGATC 3720  
QY 1241 ||||| ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
Db 3721 ||||| CGAGCCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCT 3780  
QY 1261 ||||| ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
Db 3781 ||||| CCTCAGTCCAGGTTCCGCCCTCCTGTGTCAACCGGATCATACCCACAAGATGTTTCGACCAC 3840  
QY 1281 ||||| ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
Db 3841 ||||| GTGGTCTTGTTCATCATCTTCTTAACTGATCACCATCGCATCGGATGGAGCGCCCCAAAT 3900  
QY 1301 ||||| AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
Db 3901 ||||| GACCCCCACAGCGCTGAACGCATCTTCTTGACCCCTCTCCAAATACATCTTCAACCGCAGTC 3960  
QY 1321 ||||| PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340  
Db 3961 ||||| TTTTCTGGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTGTCTCGGGAGCAGCGC 4020  
QY 1341 ||||| TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
Db 4021 ||||| TACCTGCGGAGCAGTTGGAACGTGTGGACGGGCTGTTGGTGTCTCATCTCCGTATCGAC 4080  
QY 1361 ||||| IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380  
Db 4081 ||||| ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTG 4140  
QY 1381 ||||| ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
Db 4141 ||||| CGGCTGTGCGGACCTTGGCCCGCTCAGGGTGTATCAGCCGGCGCAGGGGCTGAAGCTG 4200  
QY 1401 ||||| ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420  
Db 4201 ||||| GTGGTGGAGACGCTGATGTCTCTACTGAACCCCATCGGCAACATTTGTAGTCTGTGTG 4260  
QY 1421 ||||| AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
Db 4261 ||||| GCCTTCTTCATCATTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4320  
QY 1441 ||||| CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
Db 4321 ||||| TGCCAGGCGAGGATACCAGGAACATCACCAATAATCGGACTGTGCCGAGGCCAGTTAC 4380  
QY 1461 ||||| ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
Db 4381 ||||| CGGTGGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCAGGCCCTGTATGTCCCTGTT 4440

QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
Db 4441 GTTTTGGCTCCAAGGATGGTGGTGGACATCATGTACGATGGCTGGATGCTGTGGGC 4500  
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520  
Db 4501 GTGGACACAGCCCATCATGAACACACACACCCCTGGATGCTGTGTACTTCATCTCGTTC 4560  
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540  
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QY 1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu 1560  
Db 4621 CACAAGTGTGGCAGCACCCAGGAGGAGGAGGCGCGCGGGAGGAGGAGGAGGAGGAGG 4680  
QY 1561 ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys 1573  
Db 4681 CGAAGACTGGAGAAAGAGAGAGGAGTAAGGAGAGCAGATGGCTGAAGCCAGTGCAAA 4740  
QY 1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis 1593  
Db 4741 CCTTACTACTCCGACTACTCCCGCTTCGGCTCCTCGTCCACCACTTGTGCACAGCCAC 4800  
QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613  
Db 4801 TACCTGGACCTCTTCAATCACAGGTGTATCGGCTGAACGTGGTCAACCATGGCCATGGAG 4860  
QY 1614 HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr 1633  
Db 4861 CACTACACAGCAGCCCGAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT 4920  
QY 1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe 1653  
Db 4921 GTCATCTTTGTCTTGGAGTCAGTTTTTCAAACTTGTGGCCCTTTGGTTCCGTCGGTCTTC 4980  
QY 1654 GlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673  
Db 4981 CAGGACAGGTGGAAACAGCTGGACCTGGCCATGTGTCTGTCTCCATCATGGGCATCACG 5040  
QY 1674 LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693  
Db 5041 CTGGAGGAAATCGAGGTCAACGCCTCGTGCCCATCAACCCCATCATCCGCATCATG 5100  
QY 1694 ArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAla 1713  
Db 5101 AGGGTGTGCGCATTTGCCCGAGTGTGAAGCTGTGAAGATGGCTGTGGCATGCGGGCG 5160  
QY 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733  
Db 5161 CTGCTGGACACGGTGATGCAGGCCCTGCCCGAGTGGGGAACCTGGGACTTCTCTTCATG 5220  
QY 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753  
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QY 1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773  
Db 5281 GAGACACACCCCTGTGAGGCGCTGGGCCGTGCATGCCACCTTTCGGAACCTTGGCATGGCC 5340  
QY 1774 PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr 1793  
Db 5341 TTCCTAACCCCTCTTCGAGTCTCCACAGGTGACAAATGGAAATGGCATTAATGAAGACACC 5400  
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QY 1834 LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaLysGluAlaGluLeuAlaGluLeu 1853  
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QY 1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873  
Db 5581 GAGTGGAGATGAAGACCTCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCC 5640  
QY 1874 TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro 1893  
Db 5641 TGGCCCTGGGTCGAGGGCCCGCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAG 5700  
QY 1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913  
Db 5701 GCGGCCACCGGAGATCAGCCTTCCACTTTTCTCTGGAGCACCCACGATGCAGCCCCAC 5760  
QY 1914 ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr 1933  
Db 5761 CCCACGGAGCTGCCAGGACCACTTACTGACTGTGGGAAAGTCTGGGGTGCAGCCGAACG 5820  
QY 1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu 1953  
Db 5821 CACTCTCTGCCCAATGACAGCTACATGTGTGGCATGGAGCACTGCCGAGGGGCCCTCG 5880  
QY 1954 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973  
Db 5881 GGACACAGGGGCTGGGGCTCCCCAAAGCTCAGTCAGGCTCCGCTTGTTCGCTCACTCC 5940  
QY 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993  
Db 5941 CAGCCAGCAGATACCACTACATCTCTGAGCTTCCCAAGATGCACCTCATCTGCTCCAG 6000  
QY 1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProProGlyArgSerPro 2013  
Db 6001 CCCACAGCGCCCAACCTGGGGCACTATCCCCAACTGCCCCCAGGAGCGCTCCCT 6060  
QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033  
Db 6061 TTGGCTCAGAGGCCACTCAGGCGCCAGGAGCAATAGGACTGACTCTCTTGGACGTTCCAG 6120  
QY 2034 GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla 2053  
Db 6121 GGTCTGGGCGAGCCGGGAAGACCTGTGTGGCAGAGGTGAGTGGGCCCTCCCCCGCCCTGGCC 6180  
QY 2054 ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073  
Db 6181 CGGGCTACTCTTTCTGGGGCAGTCAAGTACCCAGGACAGCAGCACTCCCGCAGCCAC 6240  
QY 2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp 2093  
Db 6241 AGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGGCCAGCCCTTGGCCAGCCCACTGG 6300  
QY 2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113  
Db 6301 GGCAAGGCCCTCCAGAGACCAAGAGCAGCTTAGAGTTGGACACGGAGCTGAGCTGGATT 6360  
QY 2114 SerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLys 2133  
Db 6361 TCAGGAGACCTCTGCCCCCTGGCGCCAGGAGGAGGCCCTCATCCCCACGGACCTGAAG 6420  
QY 2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153  
Db 6421 AAGTGCTACAGCGTGGAGGCCCGCAGAGTGCAGCGCCGCGCTACGTCTCGCTGGATGAG 6480  
QY 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173  
Db 6481 CAGAGGAGACACTCTATCGCGCTCAGTGCCTGGACAGCGGCTCCCAACCCACCTGGGC 6540  
QY 2174 ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2193  
Db 6541 ACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTGGGGGGCCGGGAGCCGGCCCAAGAAA 6600  
QY 2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213

Db 6601 AAACACAGCCCGCTAGTATCACCATAGACCCCGAGAGCCAAAGGTCTCTGGACCCCG 6660  
Qy 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233  
Db 6661 CCCAGCCCTGGTATCTGCTCCGAGGAGGGCTCCGTCCAGCGACTCCAAGGATCCCTTG 6720  
Qy 2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer 2253  
Db 6721 GCCTCTGGCCCGCTGACAGCATGGCTGCGCTCCCGCTCCCGCAAGAAAGATGTGCTGAGT 6780  
Qy 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 6781 CTCTCCGGTTTATCCTCTGACCCAGCAGACCTGGACCCC 6819

RESULT 2  
US-09-426-998-4  
; Sequence 4, Application US/09426998  
; Patent No. 6358706  
; GENERAL INFORMATION:  
; APPLICANT: DUBIN, ADRIENNE E.  
; APPLICANT: PYATI, JAYASHREE  
; APPLICANT: ZHU, JESSICA Y  
; APPLICANT: ERLANDER, MARK G  
; APPLICANT: GALINDO, JOSE E  
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM  
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)  
; FILE REFERENCE: ORT-1057  
; CURRENT APPLICATION NUMBER: US/09/426,998  
; CURRENT FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PATENTIN VER. 2.0  
; SEQ ID NO 4  
; LENGTH: 7741  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-426-998-4

Alignment Scores:  
Pred. No.: 0 Length: 7741  
Score: 11877.50 Matches: 2264  
Percent Similarity: 99.65% Conservative: 1  
Best Local Similarity: 99.60% Mismatches: 1  
Query Match: 99.78% Indels: 7  
DB: 3 Gaps: 1  
US-09-611-257A-37 (1-2266) x US-09-426-998-4 (1-7741)  
Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20  
Db 523 ATGGACGAGGAGGATGGAGCGGGCGCGAGGAGTCGGGACAGCCCCCGAGCTTCATG 582  
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40  
Db 583 CGGCTCAACGACCTGTCCGGGGCCGGGGCCGGCGGGGTCAGCAGAAAGGAC 642  
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
Db 643 CCGGGCAGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTT 702  
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
Db 703 TTCTTCTACTTGAGCCAGGACAGCCCGCGGGAGCTGGTGTCTCCGACGGTCTGTAAC 762  
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 763 CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGGCATG 822  
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 823 TTCCGGCCATCGGAGGACATCGCCTGTGACTCCAGCGCTCCAGCGCTGCGGATCCTGCAGGCCTT 882  
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

Db 883 GATGACTTCATCTTTTGCCTTCTTTTGCCTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC 942  
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160  
Db 943 ATCTTTGGGAAAAAGTGTATTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 1002  
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 1003 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTCAGCTGTCAAG 1062  
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 1063 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATCCTT 1122  
Qy 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 1123 GTCACGTTGCTGTGATACGCTGCCATGCTGGGCAACGTCCTGCTGCTGCTTCTTC 1182  
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 1183 GTCTTCTTCATCTTCGGCATCGTCGGCTCCAGCTGTGGGAGGGCTGCTTCGGAACCGA 1242  
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Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
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Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 1363 TCCTGCAGAAAGCTGCCACCGCTGCGGGGGACCGGGGGGCTGGGCCACCTTGGCGTCTG 1422  
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
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Db 1483 ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGGCATCAACTTTTGACAACATT 1542  
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1543 GGCTATGCTGGATCGCCATCTTCCAGGTTCATCACGCTGAGGGCTGGGTGACATCATG 1602  
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
Db 1603 TACTTTGTGATGGATGCTCATCTCTTCTACAATTTTCATCTACTTCTCCTCCTCATCATC 1662  
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
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Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1723 ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTTCTGTGCCAACGCC 1782  
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440  
Db 1783 AGCACCTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1842  
Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1843 GTGTACATCCTTCGTAAGGCAGCCCGCAGGCTGGCTCAGTCTCTCGGGCAGCAGGTGTG 1902  
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1903 CGGGTTGGGCTGCTCAGCAGCCCGCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC 1962  
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500

Db 1963 AGCTGCTCTCGCTCCACCGCGCCTATCCGTCCACCACTGGTGCACCAACCACCCAC 2022

QY 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520

Db 2023 CATCACCACTACTACCTGGGCAATGGACGCTCAGGCCCCCGCGGCGAGCCCGGAG 2082

QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540

Db 2083 ATCCAGGACAGGGATGCCAATGGGTCCCGCAGGCTCATGTGCCACCACTCGACGCCT 2142

QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560

Db 2143 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2202

QY 561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580

Db 2203 TGCCACTTAGACCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCCATCTGAGGCATCC 2262

QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600

Db 2263 GGCAGGACTGTGGGCAGCGGGAAGGTGTATCCACCGTGACACCAAGCCCTCCACCGGAG 2322

QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620

Db 2323 ACGCTGAAGGAGAAGGCCTAGTAGAGGTGGTGCACGCTCTGGGCCCCCAACCTCACC 2382

QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640

Db 2383 AGCCTCAACATCCACCCGGGCCCCCTACAGCTCCATGTCACAAGCTGCTGGAGACACAGT 2442

QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660

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Db 2563 GCCGACCGTGAATGCCTGACTCAGACAGCAGGCGAGTTTATGAGTTTACACAGGATGCC 2622

QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720

Db 2623 CAGCACAGCAGACCTCCGGGACCCCCACACCGCGGCGCAACGAGCCTGGGCCCCAGATGCA 2682

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QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920

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QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940

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Db 3403 GCCATTCTGGTGGAGGCTTCCAGCGGAGGAAATCAGCAACCGGAAGATGCGAGTGA 3462

QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000

Db 3463 CAGTTAAGCTGTATTACGTGCCTGTCGACTCCAGGGGGAGATGCCAACCAAGTCCGAA 3522

QY 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020

Db 3523 TCAGAGCCCGATTTCTTCTCACCCAGCCTGGATGGTATGGGACAGGAAGTGTCTG 3582

QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040

Db 3583 GCCTTGGTGTCCCTGGGAGAGCACCCGGAGTGGGAAAGAGCCTGTCGCCCTCTCATC 3642

QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060

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Db 3943 GATGAAGAGGAGAGCTCAGAGAGGAGCGGGCCAGCCCTGCGGGCAGTGAACCATGCCAC 4002

QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180

Db 4003 AGGGGTCCCTGGAGCGGAGGCAAGAGTTCTTTTACCTGCCAGACACTGCAGGTG 4062

QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200

Db 4063 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAAGGACTGCAAT 4122

QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220

Db 4123 GGCAAGTCGGCTTCAGGGCGCCTGCGCGGCCCTGCGGCTGTATGACCCCACTGGAT 4182





; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3859

Alignment Scores:
Pred. No.: 0 Length: 7405
Score: 11241.00 Matches: 2162
Percent Similarity: 95.12% Conservative: 1
Best Local Similarity: 95.07% Mismatches: 1
Query Match: 94.43% Indels: 110
DB: 4 Gaps: 4
US-09-611-257A-37 (1-2266) x US-09-949-016-3859 (1-7405)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGACGAGGAGGAGGATGGAGCGGGCGCGGAGGTCCGGACACGCGGAGCTTCATG 432
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACGACCTGTCCGGGGCCGGGGCGCGGCGCGGGGTCCAGAGAAAGGAC 492
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 493 CCGGCGAGCGCGGACTCCGAGGGCGGAGGGGTGCGGTACCCCGCGGTGGCCCGGTGGTT 552
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 553 TTCCTCTACTTGAGCCAGGACAGCCCGCGCGAGGTGGTGTCTCCGACGGTCTGTAAAC 612
QY 81 Pro---TrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGly 99
Db 613 CCTACTGGTTTGAGCGCATCAGCATGTTGGTTCATCTCTCAACTGCGTGACCTGGGC 672
QY 100 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 119
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QY 140 GlyIlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIle 159
Db 793 GGCATCTTTGGGAAAAAGTTACTTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATC 852
QY 160 ValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaVal 179
Db 853 GTCATCGCAGGATGCTGGAGTACTCGTGGACCTGCAGAACCTGCAGCTTCAGCTGTC 912
QY 180 ArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIle 199
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QY 220 PheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsn 239

6343 CACTCTCTGCCCAATGACAGCTACATGTGTCCGATGGAGCACTCCGAGGGGCCCTG 6402
QY 1954 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973
Db 6403 GGACACAGGGGCTGGGGCTCCCAAGCTCAGTACGGCTCCGTCTTGTCCGTCACTCC 6462
QY 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993
Db 6463 CAGCCAGCAGATACAGCTACATCTCTGCAGCTTCCCAAGATGCACCTCATCTGCTCCAG 6522
QY 1994 ProHisSerAlaProThrTyrGlyThrIleProLysLeuProProProGlyArgSerPro 2013
Db 6523 CCCACAGCGCCCAACCTGGGGCACCATCCCCAACTGCCCCACCCAGGACGCTCCCT 6582
QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033
Db 6583 TTGGCTCAGAGGCCACTCAGCGCCAGGCAGCAATAAGGACTGACTCCTTGGAGCTTCAG 6642
QY 2034 GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla 2053
Db 6643 GGTCTGGGAGCGGGAGACCTGTGGCAGAGGTGAGTGGGCCCTCCCGCCCTGGCC 6702
QY 2054 ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
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QY 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
Db 7003 CAGAGGAGACACTCTATCGCGTCACTGCTGGACAGCGGCTCCCAACCCACCTGGGC 7062
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Db 7063 ACAGACCCCTTAACCTTGGGGCCAGCCTCTTGGGGGCGCGGAGCGCGCCCAAGAAA 7122
QY 2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213
Db 7123 AAACCTAGCCCGCTAGTATACCATAGACCCCCCGAGAGCCCAAGGTCTCTCGACCCCG 7182
QY 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
Db 7183 CCCAGCCCTGGTATCTGCTCCGAGGAGGGCTCCGTCCAGCGACTCCAAGGATCCCTTG 7242
QY 2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer 2253
Db 7243 GCCTCTGGCCCCCTTGACAGATGGTGGCTCGCTCCCTCCCAAGAAAGATGTGTGAGT 7302
QY 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7303 CTCTCCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 7341

RESULT 3
US-09-949-016-3859
; Sequence 3859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

Db 1033 T T C G T C T T C A T C T T C G G C A T C G T C G G C T C C A G C T G T G G C A G G G C T G C T T C G G A A C 1092  
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Db 1093 C G A T G C T T C C T A C C T G A G A A T T T C A G C C T C C C C C T G A G C G T G G A C C T G A T T A C 1152  
QY GlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMet 279  
Db 1153 C A G A C A G A A C A G G A T G A G A G C C C C T T C A T C T G C T C C C A G C A C G C G A G A A C G G C A T G 1212  
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Db 1213 C G G T C C T G C A G A G C G T G C C A C G C T G C G C G G G A C G G G C G C G T G G C C C A C C T T G C G G T 1272  
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Db 1273 C T G G A C T A T G A G C C T A C A A C A G C T C C A C A C C A C C C T G T C A A C T G T G A A C C A G T A C 1332  
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QY IleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIle 359  
Db 1393 A T T G G C T A T G C C T G G A T C G C C A T C T T C C A G G T C A T C A C G T G G A G G C T G G T C G A C A T C 1452  
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QY IleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSer 399  
Db 1513 A T C G T G G G C T C T T T C A T G A T C A A C T G T G C C T G T G T G A T G C C A C G C A G T T C T C A 1572  
QY GluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsn 419  
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Db 1633 G C C A G C A C C C T G G C T A G C T T C T C T G A G C C C G C A G C T G C T A T G A G A G C T G C T C A A G T A C 1692  
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Db 1873 C A C C A T C A C C A C C A C T A C C A C C T G G C A A T G G G A C G C T C A G G C C C C C C C G G C C A G C C G 1932  
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Db 2833 T G G A G A T C G T G G G C C A G C A G G G G G C G C C T G T C G G T G C T G C G A C C T T C C G C C T G A T G 2892  
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Db 2893 C G T G T G C T G A A G C T G G T G C G C T T C C T G C G G C G C T G C A G C G C A G C T G G T G G T C A T G 2952  
QY LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879  
Db 2953 A A G A C C A T G A C A A C G T G G C C A C C T T C T G C A T G C T G C T T A T G C T C T T C A T C T T C A T C T T C 3012  
QY SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899  
Db 3013 A G C A T C C T G G G C A T G C A T C T C T T C G G C T G C A A G T T T G C C T C T G A G C G G G A T G G G G A C A C C 3072  
QY LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919  
Db 3073 C T G C C A G A C C G G A A G A A T T T T G A C T C C T T G C T C T G G G C C A T C G T C A C T G T C T T T C A G A T C 3132  
QY LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939  
Db 3133 C T G A C C C A G G A G A C T G G A A C A A A G T C C T C T A C A A T G G T A T G G C C T C C A C G T C G T C C T G G 3192  
QY AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959  
Db 3193 G C G G C C C T T A T T T C A T T G C C C C T C A T G A C C T T C G G C A A C T A C G T G C T C T T C A A T T G C T G 3252

QY	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
DB	3253	GTGGCCATTCTGGTGGAGGGCTTCCAGGGGAG-----	3285
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
DB	3286	-----GGAGATGCCAACCAAGTCC	3303
QY	1000	GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
DB	3304	GAATCAGAGCCCGATTCTTCTCACCCAGCTGGATGGTATGGGACAGGAAGATGC	3363
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039
DB	3364	TTGGCCTTGGTGTCCCTGGGAGAGCACCCGAGCTGCGAAGAGCGCTGCTGCCGCCTCTC	3423
QY	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
DB	3424	ATCATCCACACGGCCGCCACACCCATGTGCTGTGCCAACAGAGCACACGCGGCCTGGGC	3483
QY	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1079
DB	3484	GAGGCGTGGCCCTGCGTCCGCGCCGACCCAGCAGCAGCGGGTTCGGCAGAGCCTGGGGCG	3543
QY	1080	AlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAla	1099
DB	3544	GCCACAGATGAAGTACCGCCCGCAGCGCCGCGAGCTCTCCGCACAGCCCTGGAGCGCT	3603
QY	1100	AlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeu	1119
DB	3604	GCAAGCAGCTGGACCAAGAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTG	3663
QY	1120	LysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSer	1139
DB	3664	AACGGAGAACCCCAAGTGGAGAGCGCGGTCCCTGTGTCTCGGAGAGGCGCAGGAGAGC	3723
QY	1140	GlnAspGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArg	1159
DB	3724	CAGGATGAAGAGGAGAGCTCAGAAAGAGGAGCGGGCCAGCCCTCGGGCAGTGACCATCGC	3783
QY	1160	HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGln	1179
DB	3784	CACAGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAG	3843
QY	1180	ValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCys	1199
DB	3844	GTGCCAGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAAGACTGC	3903
QY	1200	AsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeu	1219
DB	3904	AATGGCAAGTCGGCTTCAGGGCGCTTGGCCCGGCGCTGCGGCCTGATGACCCCCACTG	3963
QY	1220	AspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrp	1239
DB	3964	GATGGGATGACCCCGATGACGAGGCAACCTGAGCAAAAGGGGAACGGGTCCGGCGGTGG	4023
QY	1240	IleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhe	1259
DB	4024	ATCCGAGCCCGACTCCCTGCCTGTGCTCGAGCGAGACTCCTGGTTCAGCCTACATCTTC	4083
QY	1260	ProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAsp	1279
DB	4084	CCTCCTCAGTCCAGGTTCCGCTCCTGTGTGTACCCGGATCATCACCACCAAGATGTTCCAC	4143
QY	1280	HisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLys	1299
DB	4144	CACGTGTCCTGTGTATCATCTTCTTAACTGCATCACCATCGCATGGAGCGCCCCCAA	4203
QY	1300	IleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAla	1319
DB	4204	ATTGACCCCCACAGCGCTGAACGCATCTTCTGTGACCCCTCTCCAAATTACATTTTCCACGCA	4263

QY	1320	ValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGln	1339
Db	4264	GTCCTTCTGGCTGAAATGACAGTGAAGGTGGTGACCTGGCTGGTGGTTCGCGGAGCAG	4323
QY	1340	AlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuValLeuIleSerValIle	1359
Db	4324	CGGTACTCGGAGCAGTTGGAACGTGCTGGACCGGGCTGTTGGTGCTCATCTCCGTCATC	4383
QY	1360	AspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal	1379
Db	4384	GACATTCTGGTGTCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTG	4443
QY	1380	LeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLys	1399
Db	4444	CTGCGGCTGCTGCGGACCCCTGCGCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAG	4503
QY	1400	LeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCys	1419
Db	4504	CTGGTGGTGAGACGCTGATGTCCTCACTGAAACCCATCGGCAACATTGTAGTCATCTGC	4563
QY	1420	CysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePhe	1439
Db	4564	TGTGCCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTTTTC	4623
QY	1440	ValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSer	1459
Db	4624	GTGTGCCAGGCGAGGATACCCAGGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGT	4683
QY	1460	TyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeu	1479
Db	4684	TACCGTGGGTTCGGCACAAAGTACAACTTTGACAACTTGGCCAGGCCCTTGATGTCCCTG	4743
QY	1480	PheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaVal	1499
Db	4744	TTCTGTTTTGGCCTCCAAAGGATGGTTGGTGGACATCATGTACGATGGGCTGGATGCTGTG	4803
QY	1500	GlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSer	1519
Db	4804	GGCGTGGACCCAGCAGCCCATCATGAAACCACCAACCCCTGGATGCTGTGTACTTTCATCTCG	4863
QY	1520	PheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsn	1539
Db	4864	TTCTGCTCATTTGGCTCTCTTTGTCTCTGAACATGTTTGTGGGTGTTGGTGGAGAAC	4923
QY	1540	PheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArg	1559
Db	4924	TTCCACAAGTGTCCGCAGCACCCAGGAGGAGAGGCCGCCGCGGCGGAGAGAGAGCGC	4983
QY	1560	LeuArgArgLeuGluLysLysArgArg-----LysAlaGlnCys	1572
Db	4984	CTACGAAGACTGGAGAAAAGAGAGAGGAGTAAGAGAGAGCAGATGGCTGAAGCCAGTGTC	5043
QY	1573	LysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSer	1592
Db	5044	AAACCTTACTACTCCGACTACTCCCGCTTCCGGCTCTCCGCTCCCTCGTCCACCACCTTGTGCACCAGC	5103
QY	1593	HisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMet	1612
Db	5104	CACTACCTGGACCTCTTCATCACAGGTGTCTATCGGGCTGAACGTGGTCAACATGGCCATG	5163
QY	1613	GluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePhe	1632
Db	5164	GAGCACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTTC	5223
QY	1633	ThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhe	1652
Db	5224	ACTGTTCATCTTTGCTTTGGAGTCAGTTTTCAAACTTGTGGCCCTTTGGTTTCCGTCGGTTC	5283
QY	1653	PheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIle	1672
Db	5284	TTCCAGGACAGGTGGAAACCAGTGGACCTGGCCATTGTGCTGTGCTGTCCATCATGGGCATC	5343
QY	1673	ThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIle	1692



||||| 5344 ACCTGGAGGAATCGAGGTCAACGCCCTCGCTGCCCATCAACCCACCATCATCCGCATC 5403  
QY ||||| 1693 MetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArg 1712  
Db ||||| 5404 ATGAGGGTGTGGCATGCCCCGAGTGTGAAGCTGTGAAGATGGCTGTGGGCATCGCG 5463  
QY ||||| 1713 AlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPhe 1732  
Db ||||| 5464 GCGTGTGGACACGGTGATGCAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTCTTC 5523  
QY ||||| 1733 MetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlyCys 1752  
Db ||||| 5524 ATGTTGTTGTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGT 5583  
QY ||||| 1753 AspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMet 1772  
Db ||||| 5584 GACGAGACACACCCCTGTGAGGCCCTGGGCCGTATGCCACCTTTCGGAACCTTTGGCATG 5643  
QY ||||| 1773 AlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAsp 1792  
Db ||||| 5644 GCCTTCCCTAACCTCTTCCGAGTCTCCACAGGTGACAATTGGAATGGCATTATGAGGAC 5703  
QY ||||| 1793 ThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyr 1812  
Db ||||| 5704 ACCCTCCGGGACTGTGACCAGGAGTCCACCTGTCTACAACACGGTCATCTCGCCTATCTAC 5763  
QY ||||| 1813 PheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeu 1832  
Db ||||| 5764 TTTGTGTCTTCTGCTGACGGCCCACTGCTGTAGTCAACGTGGTGATCGCCGTGTG 5823  
QY ||||| 1833 MetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGlu 1852  
Db ||||| 5824 ATGAAGCACCTTGAGGAGAGCAACAAGGAGGCCAAGGAGGCCGAGCTAGAGGCTGAG 5883  
QY ||||| 1853 LeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPhe 1872  
Db ||||| 5884 CTGGAGCTGGAGATGAAGACCTCAGCCCCCAGCCCCACTCGCCACTGGGCAGCCCCCTTC 5943  
QY ||||| 1873 LeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHis 1892  
Db ||||| 5944 CTCTGGCCTGGGTGAGGGCCCCGACAGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCAC 6003  
QY ||||| 1893 ProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnPro 1912  
Db ||||| 6004 CCAGCGGCCACGCGAGATCAGCCTCCACTTTTCCCTGGAGCACCACCGATGCAGCCC 6063  
QY ||||| 1913 HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArg 1932  
Db ||||| 6064 CACCCACGGAGTCCAGGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCCAGCGA 6123  
QY ||||| 1933 ThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyPro 1952  
Db ||||| 6124 ACGCACTCTTGCCCCAATGACAGCTACATGTGTGGCATGGGAGCACTGCCGAGGGGCC 6183  
QY ||||| 1953 LeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis 1972  
Db ||||| 6184 CTGGGACACAGGGCTGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCTTGTCCGTTCAC 6243  
QY ||||| 1973 SerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeu 1992  
Db ||||| 6244 TCCCAGCCAGCAGATACCAGCTACATCTGTCAGCTTCCCCAAAGATGCACCTCATCTGCTC 6303  
QY ||||| 1993 GlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSer 2012  
Db ||||| 6304 CAGCCCCACAGCCCCCAACCTGGGGCACCATCCCCAAACTGCCCCACCCAGGACGCTCC 6363  
QY ||||| 2013 ProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspVal 2032  
Db ||||| 6364 CCTTTGGCTCAGAGGCCACTCAGGGCGCAGGCAGCAATAGGACTGACTCTCTTGACGTT 6423  
QY ||||| 2033 GlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProLeu 2052

Db 6424 CAGGGTCTGGCAGCCCGGAAGACCTGTGGCAGAG----- 6459  
QY 2053 AlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSer 2072  
Db 6459 ----- 6459  
QY 2073 HisSerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsn 2092  
Db 6459 ----- 6459  
QY 2093 TrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrp 2112  
Db 6459 ----- 6459  
QY 2113 IleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeu 2132  
Db 6460 -----GAGGAGCCCCCATCCCCACGGGACCTG 6486  
QY 2133 LysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAsp 2152  
Db 6487 AAGAAGTGCTACAGCGTGGAGGCCAGAGCTGCCAGCGCGGCCACGTCCTGGCTGGAT 6546  
QY 2153 GluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeu 2172  
Db 6547 GAGCAGAGGAGACACTCTATCGCCGTCAGCTGCTTGGACAGCGGCTCCCAACCCACCTG 6606  
QY 2173 GlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLys 2192  
Db 6607 GGCACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTGGGGGGCCTGGGAGCCGGCCCAAG 6666  
QY 2193 LysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThr 2212  
Db 6667 AAAAAACTCAGCCCGCTAGTATACCATAGACCCCCCGAGAGCCAAAGGTCTCTCGGACC 6726  
QY 2213 ProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspPro 2232  
Db 6727 CCGCCACGCCCTGGTATCTGCCTCGGAGGAGGGCTCCGTCAGCGACTCCAAGGATCCC 6786  
QY 2233 LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysAspValLeu 2252  
Db 6787 TTGGCCTCTGGCCCCCTTGACAGCATGGCTGCCTCGCCCTCCCCAAAGAAAGATGTGCTG 6846  
QY 2253 SerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 6847 AGTCTCTCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 6888

RESULT 4

US-09-398-522-51  
; Sequence 51, Application US/09398522  
; Patent No. 6783933  
; GENERAL INFORMATION:  
; APPLICANT: Issa, Jean-Pierre  
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: JHUI590  
; CURRENT APPLICATION NUMBER: US/09/398,522  
; CURRENT FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 3993  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel  
; NAME/KEY: CDS  
; LOCATION: (373)...(3993)  
US-09-398-522-51

Alignment Scores:  
Pred. No.: 0 Length: 3993  
Score: 6315.50 Matches: 1207

Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	0
Query Match:	53.05%	Indels:	23
DB:	4	Gaps:	1

US-09-611-257A-37 (1-2266) x US-09-398-522-51 (1-3993)

QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20
DB	373	ATGACGAGAGGAGGATGGAGCGGGCCGAGGAGTCGGGACAGCCCGAGCTTCATG	432
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
DB	433	CGGCTCAACGACCTGTGGGGCCGGGGCCGGCCGGGGTCCAGCAGAAAGGAC	492
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	493	CCGGGCAGCGGGAATCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCGGTGTT	552
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	553	TTCTTCTACTTGAGCGAGACATCGCTGTGACTCCAGCGCTGCCGGATCCTGCAAC	612
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	613	CCCTGGTTTGAGCGCATCAGCATGTTGGTCACTCTCTCAACTGCGTGACCCCTGGGCATG	672
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	673	TTCCGGCCATCGAGGACATCGCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCCTTT	732
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	733	GATGACTTCATCTTTGCCCTTCTTTGCCGTGGAGATGGTGAAGATGGTGGCCTTTGGGC	792
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal	160
DB	793	ATCTTTGGGAAAAGTGTTACTTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC	852
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	853	ATCGCAGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTGAGCTTCTCAGCTGTCAAG	912
QY	181	ThrValArgValLeuArgProIleArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	913	ACAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCATCCTT	972
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	973	GTCACGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCTGTGCTCTGCTTCTTC	1032
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	1033	GTCTTCTTCACTTCGGCATCGTCGGCGTCCAGCTGTGGGAGGGCTGCTTCGGAACCGA	1092
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	1093	TGCTTCTTACCTTGAGAAATTCAGCCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAG	1152
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	1153	ACAGAGAACGAGGATGAGAGCCCTTCACTGCTCCAGCCACGCGAGAACGGCATGCGG	1212
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
DB	1213	TCTTGAGAAGCGTGCCACGCTGCGCGGGACGGGGCGGTGGCCCACTTGGGCTCTG	1272
QY	301	AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
DB	1273	GACTATGAGGCCTACACAGCTCCAGCAACACCACTGTGTCACTGGAAACCACTACTAC	1332
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340







Db 2051 CCTCAGGCTGGCCACAGGGCTGGGCACCATGAACATACCCACAGATCCTGCCCTCAGGGGT 2110  
 QY 594 -----HisThrSerPro-----ProPr 599  
 Db 2111 GGGCAGCGCAAGGACAGCACCGCCCGGACCCCAAGGGGAAGTGGCGCGGTGGACCGCC 2170  
 QY 599 oGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLe 619  
 Db 2171 AGGCACC-----GGGGGGCACGGCCCGTTGAGCTT 2200  
 QY 619 uThrSerLeuAsnIleProProGlyProTyrrSerSerMetHisLysLeuLeuGluThrG1 639  
 Db 2201 GAACAGC-----CCTGATCCCTACGAGAAGATCCCGCATGTGTCGGGGAGCA 2248  
 QY 639 nSerThrGlyAlaCysGlnSer-----SerCysLysIleSerSe 652  
 Db 2249 TGGACTGGGCCAGGCCCTGGCCATCTGTGGGCCCTAGTGTGCCCTTGCCCCAG 2308  
 QY 652 rProCysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrrCysAlaAr 672  
 Db 2309 CCCC-----CCAGCGGGCACACTGACCTGTGAGCTGAAGAGCTGCCCGTACTGCACCCG 2362  
 QY 672 gAla---GlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerG1 691  
 Db 2363 TGCCCTGGAGACCGGAGGTGAGCTCAGCGGCTCGGAAAGTGGAGACTCAGATGGCCG 2422  
 QY 691 uAlaValTyrrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro----- 708  
 Db 2423 TGGCGTCTATGAATTACGCAGGACGTCCGGCACGGTGACCGTGGGACCCACCGGACC 2482  
 QY 709 -----HisSerArgArgGlnArgSe 715  
 Db 2483 ACCCGTGGACGGACACACAGGCCCGAGGCCAGGCCCGCCAGCGGGGGCACAGCA 2542  
 QY 715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspTh 735  
 Db 2543 GAGGGCAGCCCGGGCGAGCCAGGCTGGATGGCGCCCTCTGGGTACCTTCAGCGGCAA 2602  
 QY 735 rPheArgLysIleValAspSerLysTyrrPheGlyArgGlyIleMetIleAlaIleLeuVa 755  
 Db 2603 GCTCGCGCGCATCGTGACAGCAAGTACTTCAGCCGTGGCATCATGATGGCCATCCTTGT 2662  
 QY 755 lAsnThrLeuSerMetGlyIleGluTyrrHisGluGlnProGluGluLeuThrAsnAlaLe 775  
 Db 2663 CAACACGCTGAGCATGGCGGTGGAGTACCATGAGCAGCCCGAGGAGCTGACTAATGCTCT 2722  
 QY 775 uGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLe 795  
 Db 2723 GGAGATCAGCAACATCGTGTTCACACGATGTTTGCCCTGGAGATGCTGTGAAGCTGCT 2782  
 QY 795 uValTyrrGlyPropheGlyTyrrIleLysAsnProTyrrAsnIlePheAspGlyValIleVa 815  
 Db 2783 GGCCTGCGGCCCTCTGGGCTACATCCGGAACCCGTTACAACATCTTCGACGGCATCATCGT 2842  
 QY 815 lValIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgTh 835  
 Db 2843 GGTCAATCAGCTCTGGGAGATCGTGGGGCAGGGCGGACCGTGGCTTGTCTGTGCTGGCAC 2902  
 QY 835 rPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLe 855  
 Db 2903 CTTCCGGCTGTGCGTGTGCTGAAGCTGGTGCCTTTCTGCCAGCCCTGCGGGCGCAGCT 2962  
 QY 855 uValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPh 875  
 Db 2963 CGTGGTGTGGTGAAGACCATGGACAACGTGGTACCTTCTGCACGCTGCTCATGCTCTT 3022  
 QY 875 eIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluAr 895  
 Db 3023 CATTTTCATCTTCAGCATCTGGGCATGCACCTTTTCGGCTGCAAGTTTCAGCCTGAAGAC 3082  
 QY 895 gAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleVa 914  
 Db 3083 AGACACCGGAGACACCGTGCCTTGACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGT 3142

QY 914 lThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrrAsnGlyMetAl 934  
 Db 3143 CACCGTGTTCAGATCCTGACCCAGGAGGACTGGAACGTGTCTGTACACGGCATGGC 3202  
 QY 934 aSerThrSerSerTrpAlaAlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrVa 954  
 Db 3203 CTCCACCTCCTCTGGCGCGCCCTCTACTTCGTGGCCCTCATGACCTTCGGCAACTATGT 3262  
 QY 954 lLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLy 974  
 Db 3263 GCTCTTCAACCTGTGTGGCCATCCTCGTGAGGGCTTCAGGGCGGAG----- 3311  
 QY 974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyG1 994  
 Db 3312 -----GG 3313  
 QY 994 yAspAlaAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAsp-- 1013  
 Db 3314 CGATGCCAACAGATCCGACACGACGAGGACAAGACGTTCGGTCCACTTCGAGGAGGACTT 3373  
 QY 1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerLe 1025  
 Db 3374 CCACAAGCTCAGAGAACTCCAGACCACAGAGCTGAAGATGTGTTCCTGGCCGTGACCCC 3433  
 QY 1025 uGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAl 1045  
 Db 3434 CAACGGGCACCTGGAGGGACGAGGACGCTGTCCCTCCTCCCTCATGTGCACAGCTGC 3493  
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 Db 3494 CACGCCCATGCCCTACCCCAAGAGCTCACCATTTCCTGGATGCAGCCCCCAGCCTCCCGA 3553  
 QY 1065 aSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSe 1085  
 Db 3554 CTCTCGCGCTGGCAGCAGCAGCTCCGGGGACCCGCCA-----CTGGAGACCAGAACCC 3607  
 QY 1085 rProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105  
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 QY 1125 rGlyGluArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSe 1145  
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 QY 1145 rSerGluGluGluArgAlaSerProAla-----GlySerAspHisArgHisArgGlySe 1163  
 Db 3783 -GCTGAGACGGCAGGGCCGCGCGGCCCGCTGCCACCCCACTGCGCGGGCGCGAGTC 3841  
 QY 1163 rLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu----- 1178  
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 QY 1179 -----GlnValProGlyLeuHis-----ArgThrAlaSerGlyArgGlySe 1192  
 Db 3902 CGGGCAGTGGTGGCCCTGCCAGCGACTTCTTCTGCGCATCGACAGCCACCGTGAGGA 3961  
 QY 1192 rAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLe 1212  
 Db 3962 TGCAGCCGAGCTTGACGACGACTCGGAGGACAGCTGCTGCTCCGCTGCATAAAGTGCT 4021  
 QY 1212 uArgProAspAspProProLeuAspGlyAspAlaAspGluGlyAsnLeuSerLy 1232  
 Db 4022 GGAGCCCTACAAGCCC----- 4037  
 QY 1232 sGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrrLeuGluArgAs 1252  
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Qy 1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAs 1987

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Qy 1987 pAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuPr 2007

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Qy 2007 oProProGly-----ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAl 2025

Db 6245 CCCTCGGGGCACAGCCCGCTCCCGCCAGTCTCAGCCGGCTGTCTGCAGACAGGAGGTGT 6304

Qy 2025 eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeu-----Al 2043

Db 6305 GCACACCGATTCTTGAAGGAAG---ATTGACAGCCCTAGGGACACCCCTGGATCCTGC 6361

Qy 2043 aGluValSerGlyProSerPro-----ProLeuAlaArgAlaTyrSerPheTrpGly-- 2060

Db 6362 AGAGCCTGTGTGAGAAAAACCCCGGTGAGGCCCGGTGACCCAGGGGGCTCCCTGCAGTCCCC 6421

Qy 2061 ----GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHi 2079

Db 6422 ACCACGCTCCCGCCAGCGCCCGCCAGCGTCCGCACTCGTAAGTATACC---TTCCGGACAGCA 6478

Qy 2079 sMetThrProProAlaPro---CysProGlyProGluProAsnTrpGlyLysGlyProPr 2098

Db 6479 CTGCGTCTCCAGCGCGCGCGCGCGCGCGCGCGGAG----- 6515

Qy 2098 oGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLe 2118

Db 6516 -GAGGCCGAGGCTCGGACCCAGCCAGGAGGAGGTGAGCCACATCACCAGTCCCGCTG 6574

Qy 2118 upro-----ProGlyGlyGlnGluGluProPro-----SerPr 2129

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Qy 2231 ----AspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLy 2249

Db 6971 GGGGACCCCTGCAGCCCAAGGGGAGCGCTGGGGCCAGGCC-----TCCTGCCCGGC 7021

Qy 2249 sAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeu----- 2264

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Qy 2265 -AspPro 2266

Db 7082 AGACCCCT 7088

RESULT 6

US-09-404-650-1

; Sequence 1, Application US/09404650

; Patent No. 6309858

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGiven, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/404,650

; CURRENT FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 6816

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (192)..(6716)

US-09-404-650-1

Alignment Scores:

Pred. No.: 0 Length: 6816

Score: 5492.50 Matches: 1236

Percent Similarity: 60.30% Conservative: 213

Best Local Similarity: 51.44% Mismatches: 506

Query Match: 46.14% Indels: 449

DB: 3 Gaps: 55

US-09-611-257A-37 (1-2266) x US-09-404-650-1 (1-6816)

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Qy 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66

Db 324 GCTGATCCTCATGTCCACACCCAGACCTGGCGCCTATTGCTTCTTCTGCCTCGGACAG 383

Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86

Db 384 ACCACCAACCCCGGAACTGGTGCATCAAGATGGTGTGCAACCCCGTGGTTGAATGTGTC 443

Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106

Db 444 AGCATGTGTGTGATCCTGTGTAACCTGCGTGACACTTGGCATGTACCAGCCGTGCGACGAC 503

Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126

Db 504 ATGGACTGCTGTCCGACCCGCTGCAAGATCCTGCAGGTCTTGTGATGACTTTCATCTTATC 563

Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146

Db 564 TTCCTTGGCATGGAGATGGTGTCTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAAGTGC 623

Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166

Db 624 TACCTCGGGGACACATGGAAACCCGCTGGATTTCCTTCATCGTCATGGCAGGGATGGTCGAG 683

Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186

Db 684 TACTCCCTGGACCTTCAGAAACATCAACCTGTTCAGCCATCCGACCCGTGCGCGTCTTGAGG 743

Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206

Db 744 CCCCTCAAAGCCCATCAACCCGCTGCCAGTATCGGATCTGGGTGAACCTGCTCCTGGAC 803

Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226

Db 804 ACACCTGCCCATGCTGGGGAATGTCCTGTCTGCTCTGCTCTTCTTCTTCTTCTTCTTGGC 863







1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640  
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1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660  
1688 TGTGCTGAAGCTGTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACAGCT 4747  
1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluLeuValas 1680  
1748 GGACCTGGCCATTGCTACTGTGCTCAGTCACTGGGCATCACCTGGAGGATCGAGATCAA 4807  
1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700  
1808 TGGCGCCCTGCCCATCAATCCCATCATCCGATCATGAGGTTCTGCGCATTTGCCCG 4867  
1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720  
1868 AGTGCTGAAGCTGTTGAAGATGGCCACAGGAATGCGGGCCCTGCTGGACACGGTGTGCA 4927  
1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl 1740  
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1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760  
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1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780  
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1837 uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMe 1857  
5288 CGACAGCAACAAGAGCGCGCAGGACGCGGATGATGATGATGATGATGATGATGATGATGAT 5347  
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1876 yValGluGlyProAspSerProAsp----- 1884  
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1885 -----SerProLysProGlyAlaLeu----- 1891  
5462 CTGCTACTCGCCCTGCCAGGACTCCTTGGAGGGGAGCTGACCATCATCGACAACCTGTC 5521  
1892 -----HisProAlaAlaHisAla----- 1897  
5522 GGGCTCCATCTTCCACCACTACTCCTCGCCTGCCGGTGCACGAAGTGTACACACGACAA 5581  
1898 ----- 1901  
5582 GCAAGAGGTGACGTGGTGTGAGACGGAGGCTTCTCCCTGAACTCAGACAGGTCTCTGTC 5641  
1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912  
5642 CATCCTGCTGGTGACGACCTGAGTCTCGAGGACCCACAGCCTGCCACCTGGCGCAAA 5701

1913 ---HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929  
5702 GGACAGCAAGGTGAGCTGACCCACCTGAGCCCATCGGTGTGGAGACCTGGCGGAATG 5761  
1930 -----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHi 1945  
5762 CTTCTTCCCTTGTCTCTACGGCGCTCTCGCGGATCCAGAGAACTTCTGTGTGAGAT 5821  
1945 sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe 1965  
5822 GGAGGAGATCCCATTAACCTGTC-----CGTCTCTGG-----CTGAACATGACAG 5869  
1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr 1985  
5870 CAGTCAACACCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCTCTGCCCATGCC 5929  
1985 oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999  
5930 AGCCGAGTTCTTCCACCTGCACTGTCTGCCAGCAGAAAGGCCAGAAAGGGCAGCTGG 5989  
1999 rTrpGlyThrIleProLysLeuProProGly-----ArgSerProLe 2014  
5990 CACTGGAACCTCTCCCAAGATTGGCTGCAGGGCTCTCTGGCATCTCTCGGTCAACAAG 6049  
2014 uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGl 2034  
6050 GGTCAACTGTACCTCTCTCCGGCAGGCCACCCGGGAGCGACACGTCTGCTGGAC----- 6101  
2034 yLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAlaAr 2054  
6102 -----GCCAGCCAGCAGCTCCGCGGCGAG 6127  
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6128 CCTGCAGACCACTCGAGGACAGCCTGACCTGAGCGCAGCAGCCCCCGGCGTGC----- 6182  
2074 rLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGl 2094  
6183 -----CTGGGGCGCGCGCGCTCTCCAGGACCCCGGCGCGCTGTC 6226  
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6275 CCTGCGGGGCTGCGGCG-----CATCA 6298  
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2174 rAspProSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgPr 2191  
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6468 -----CCGCGCGCAGCCCCCGCTCACGCGCGCGCGCGCGCGCGCGCGCGCGAG 6517  
2228 pSer-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSe 2244  
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RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1
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Alignment Scores:

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Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 4 Gaps: 55
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US-09-611-257A-37 (1-2266) x US-09-935-541-1 (1-6816)

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QY 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTGCCACACCCAGACCTCGCGCCTATTGCCTTCTTCTGCCTGCGACAG 383
QY 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgile 86
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QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
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QY 107 IleAlaCysAspSerGlnArgCysArgileLeuGlnAlaPheAspAspPheIlePheAla 126
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QY 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
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QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys 438
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Db 1554 GGCCTCTACCAGGCCCTGCAGAGCGCGCGCCAGGCCCTGGGC----- 1595
QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHis 498
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QY 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
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Qy 1885 -----SerProLysProGlyAlaLeu----- 1891  
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Qy 1892 -----HisProAlaAlaHisAla----- 1897  
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1898 QY -----ArgSerAlaSe 1901  
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5642 Db CATCCTGCTGGGTGACGACCTGAGTCTCGAGGACCCACAGCCTGCCACCTGGCGGCAA 5701  
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5930 Db AGCGGAGTTCTTCCACCTGTCAGTGTCTGCGAGGCTCTGCGGATCTCTGCGGTACCAAG 5989  
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2244 QY rProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264  
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; Sequence 3, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 6855  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (192)..(6755)  
US-09-404-650-3  
Alignment Scores:  
Pred. No.: 0 Length: 6855  
Score: 5484.00 Matches: 1237  
Percent Similarity: 59.93% Conservative: 211  
Best Local Similarity: 51.20% Mismatches: 507  
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QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86  
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QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106  
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QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126  
Db 504 ATGGACTGCTGCTCCGACCGCTGCAAGATCTGCAGGTCTTGTGATGACTTCTTCTTATC 563  
QY 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys 146  
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QY 1882 -----SerPro----- 1883

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QY 1893 -----ProAlaAla----- 1895  
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QY 1896 -----HisAlaArgSerAlaSer-----HisPh 1903  
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QY 1903 eSerLeuGluHisProThrMetGlnPro-----HisProThrGluLeuPr 1918  
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QY 1991 -----LeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLe 2006  
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QY 2041 uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTyrGlyGl 2061  
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QY 2081 rProProAlaProCysProGlyProGluProAsnTyrGlyLysGlyProProGluThrAr 2101  
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QY 2101 gSerSerLeuGluLeuAspThrGluLeuSerTyrIleSerGlyAspLeuLeuProProGl 2121  
Db 6278 CCGCCGCTGAGCCTG----- 6293  
QY 2121 yGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGl 2141  
Db 6294 -----CGCGCGCGGGCCTCTTTCAGCCTCGGGGGGTGCGGGCG-- 6332  
QY 2141 nSerCysGlnArgArgProThrSerTyrLeuAspGluGlnArgHisSerIleAlaVa 2161  
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Qy 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744  
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Db 2190 AACCCCTACAACTCTTCGACAGCATCATTTGTCATCATCAGCATCTGGGAGATCGTGGG 2249

Qy 825 GlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844  
Db 2250 CAGGCGGACGGTGGGTGTCCGGTGTGCGGACCTTCCGGGTGTGCGGTGTGAACATG 2309  
Qy 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864  
Db 2310 GTGCGCTTCATGCTCCCTGCGGCGCCAGCTCGTGGTGTCTATGAAGACCATGGACAAC 2369  
Qy 865 ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMet 884  
Db 2370 GTGGCCACCTTCTGCATGCTGCTCATGCTCTTTCATCTTTCATCTTTCAGCATCTTGGGATG 2429  
Qy 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903  
Db 2430 CATATTTTGGTGCAGTTTCAGCTCCGACCGGACACTGGAGACACGGTGGCCGACAGG 2489  
Qy 904 LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu 923  
Db 2490 AAGAACTTCGACTCCCTGCTGTGGGCCATCGTCACTGTGTCCAGATCTCACCACGAG 2549  
Qy 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr 943  
Db 2550 GACTGGAACGTCTTCTTACAATGGCATGGCTCCACTTCTCCCTGGGCCTCCCTCTAC 2609  
Qy 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963  
Db 2610 TTTGTGCGCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTGTGTGGCCATCCTG 2669  
Qy 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983  
Db 2670 GTGGAGGCTTCCAGCGGAG----- 2690  
Qy 984 CysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPro 1003  
Db 2691 -----GGTGACGCCAATCGTCTCTACTCGGACGAG 2720  
Qy 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013  
Db 2721 GACCAGAGCTCATCCAACATAGAGAGTTTGATAAGTCCAGGAAGGCTTGACAGCAGC 2780  
Qy 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033  
Db 2781 GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGCAC----- 2825  
Qy 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053  
Db 2826 -----CTGGACCCC-----AGTCTCCCACTGGGT 2849  
Qy 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069  
Db 2850 GGGCACCTAGGTCTCTGTGGGGTGGGGACCTGCCCCCGACTCTCACTGCAGCCCGGAC 2909  
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080  
Db 2910 CCCATGTGTGGTGGCCCTGGGCTCCGAAAGAGCAGTGTCTCTAGGAGGATGAGC 2969  
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
Db 2970 TATGACCAGCGCTCCCTGTCCAGCTCCGGAGTCTCTACTACGGGCCATGGGGCCGAGC 3029  
Qy 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
Db 3030 GCGGCTTGGCCAGCGCTGCTGCCAGTCCAGCTGGAAC-----AGCCTCAAG 3071  
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139  
Db 3072 CACAAGCCCGCTCGCGGAGCATGAGTCCCTGCTCTCTCGGAGCGCGCGCGCGGCC 3131  
Qy 1140 GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157  
Db 3132 CGGGTCTCGAGGTTGCCCGGACGAGGGGGCGCGCGCGGCGCGCACCCCTGCACACCCCA 3191

QY	1158	His	-----ArgHisArgGly	1162
Db	3192		CACGCCCACCATTCATCAGGGCCCATCTGGCGCACCGSCACCGCCCGCG	3251
QY	1163		serLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly	1182
Db	3252		ACGCTGTCCCTCGACAAACAGGACTCGGTGGACCTGGCCGAGCTGGTCCCGCGGTGGC	3311
QY	1183		LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3312		GCCACCCCGCGCGCCTGGAGGGCGGAGCCCGCCCGCGGCATGAGGACTGCAAT	3371
QY	1201		GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As	1220
Db	3372		GGCAGGAT-GCCAGCATCGC--CAAGACGCTCTTACCAAGATGGCGACCCGCGGGA	3427
QY	1220		pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTprIl	1240
Db	3428		TCGCGGGGAGGATGAGGAGGAATCGACTACACCCCTGTGCTTCGCGTCCGCAAGATGAT	3487
QY	1240		eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr	1260
Db	3488		CGACGCTCTATAAGCCCGACTGGTGGAGGTCGCGGAAGACTGGTGTGTCTACCTCTTCTC	3547
QY	1260		oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi	1280
Db	3548		TCCCGAGAACAGGTTCCGGGTCTGTGTCTGTCAGACCATATTGCCCCACAAACTCTTCGACTA	3607
QY	1280		sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI	1300
Db	3608		CGTGTCTTGGCCTTCATCTTCTCAACTGCATCACCATCGCCCTGGAGCGGCCTCAGAT	3667
QY	1300		eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa	1320
Db	3668		CGAGCGCGGAGCACCAGACGATCTTTCTCACCGTGTCCAACACTACATCTTTCACGGCCAT	3727
QY	1320		lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAl	1340
Db	3728		CTTCGTGGCGGAGATGACATGAAGGTAGTCTCGCTGGCCCTGTACTTCGCGGAGCAGGC	3787
QY	1340		aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs	1360
Db	3788		GTACCTACGACGACGCTGGAACTGCTGGATGGCTTCTTGTCTTCGTGTCCATCATCGA	3847
QY	1360		pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe	1380
Db	3848		CATCGTGTGTCCCTGGCCTCAGCCGGGGAGGCCAAGATCTTGGGGTCCCTCCGAGTCTT	3907
QY	1380		uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe	1400
Db	3908		GCGGCTCTCTGGCACCCCTACGCCCTCGCTGCTCATCAGCCGGGGCGCGGGCTGAAGCT	3967
QY	1400		uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy	1420
Db	3968		GGTGTGGAGACACTCATCTCCTCCCTCAAGCCCATCGGCCAACATCGTGCTCATCTGCTG	4027
QY	1420		sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa	1440
Db	4028		TGCCTTCTTCATCATCTTTGGCATCCTGGGAGTGCAGCTCTTCAAGGGCAAGTCTTACCA	4087
QY	1440		lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy	1460
Db	4088		CTGTCTGGGCGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCAACTA	4147
QY	1460		rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh	1480
Db	4148		CCGCTGGGTCCATCAAAATACAACTTCGACAACTGGGCCAGGCTCTGATGTCCCTCTT	4207
QY	1480		eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGl	1500
Db	4208		TGTCTGGCATCCAAAGGATGGTTGGTGGAGACATCATGTACATGGAGCTGGATGCTGTGC	4267
QY	1500		yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh	1520

4268 TGTGGACGAGCAGCCTGTGACCAACCAACCCCTGGATGCTGTACTTTCATCTCCTT 4327

1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540

4328 CCTGCTCATCGTCAGCTTCTTTGTGCTCAACATGTTTGTGGGTGTCGTGGTGGAGAACTT 4387

1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLe 1560

4388 CCACAAGTCCGGCAGCACACGAGAGGCTGAAGAGGCACGGCGGCTGAGGAGAAGCGGCT 4447

1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580

4448 GCGGGCCTGGAGAGAAGCGCGGAAGGCCAGGCCGCTGCCCTACTATGCCACCTATTG 4507

1580 rArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600

4508 TCACACCCGGGTGCTCATCCACTCCATGTGCACCGCACTACCTGGACATCTTCATCAC 4567

1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI 1620

4568 CTTTCATCATCTGCCTCAACGTGGTCACCATGTCCCTGGAGCACTACAATCAGCCACGTC 4627

1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640

4628 CCTGGAGACAGCCCTCAAGTACTGCAACTATATGTTACCACCTGTCTTTGTGCTGGAGGC 4687

1640 rValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTyrAsnGlnLe 1660

4688 TGTGCTGAAGCTGGTGGCATTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACCACT 4747

1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680

4748 GGACCTGGCCATTGTGCTACTGTCTAGTCATGGGCATCACCCCTGGAGGAGATCGAGATCAA 4807

1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700

4808 TGCGGCCCTGCCCATCAATCCCACCATCATCCGCATCATGAGGGTTCTGCGCATTTGCCG 4867

1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720

4868 AGTGCTGAAGCTGTTGAAGATGGCCACAGGAATGCGGGCCCTGCTGGACACCGTGGTGCA 4927

1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740

4928 AGCTTTGCCCCAGGTGGGCAACCTTGGGAGCTGCTGCAACGACGAGAACCCCGTCCGAGG 4987

1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760

4988 TGCTCTCGGGTGGAGCTTTTGGGAAGCTGCTGCAACGACGAGAACCCCGTCCGAGG 5047

1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780

5048 CATGAGCCGGCATGCCACCTTCGAGAACCTTCGGCATGGCCCTTCTTCACACCTCTTCCAGGT 5107

1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspGl 1799

5108 CTCCACGGGTGACAACTGGAAACGGGATCATGAAGGACACGCTGCGGACTGCACCCACGA 5167

1799 nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa 1817

5168 CGAGCGCAGCTGCCTGAGCAGCCCTGCAGTTTGTGTCGCGCTGTACTTCGTGAGCTTCGT 5227

1817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGl 1837

5228 GCTCACCCGCGCAGTTTCGTGCTCATCAACGTGGTGGTGGCTGTGCTCATGAAGCACCTTGA 5287

1837 uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMe 1857

5288 CGACAGCAACAAGGAGCGCAGAGGACGCCCGAGATGGATGCCGAGCTCGAGCTGGAGAT 5347

1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGl 1876



Db 5348 GGCCCATGGCCTGGGCCCTGGCCCGAGGCTGCTACCGGCTCCCGGGCGCC---CCTGG 5404  
Qy 1876 yValGluGlyProAsp----- 1881  
Db 5405 C---CGAGGGCCGGAGGGGGCGGGCGGGGGCGACACCGAGGGCGGCTTGTCGGCGG 5461  
Qy 1882 -----SerPro----- 1883  
Db 5462 CTGCTACTGCGCTGCCAGGAGAACCTTGCGTGGTGACAGCGTCTCTTTAATCATCAAGGA 5521  
Qy 1884 -----AspSerProLysProGlyAlaLeuHis----- 1892  
Db 5522 CTCCTTGGAGGGGAGCTGACCATCATCGACAACCTGTGGGGCTCCATCTTCCACCACTA 5581  
Qy 1893 -----ProAlaAla----- 1895  
Db 5582 CTCCTCGCCTGCGGCTGCAAGAGTGTCAACACGACGAGGTGCAGCTGGGTGA 5641  
Qy 1896 -----HisAlaArgSerAlaSer-----HisPh 1903  
Db 5642 GACGGAGGCTTCTCCTCGAAGTGTCAACACGACGAGGTCTCGTCCATCTGCTGGGTGACGACCT 5701  
Qy 1903 eserLeuGluHisProThrMetGlnPro-----HisProThrGluLeuPr 1918  
Db 5702 GAGTCTCGAGGACCCACAGCCTGCCACCTGGCCGCAAGACAGCAAGGTGAGTGA 5761  
Qy 1918 oGlyProAspLeuLeuThrValArgLysSerGly-----ValSerArgTh 1933  
Db 5762 CCCACCTGAGCCCATGCGTGTGGGAGACCTGGGGAATGCTTCTTCCCTTGTCTCTAC 5821  
Qy 1933 rHisSerLeuProAsn---AspSerTyrMetCysArgHisGlySerThrAlaGluGlyPr 1952  
Db 5822 GGCCGTCTCGCGGATCCAGAGAACTTCTGTGTGAGATGGAGGAGATCCCATTCACCC 5881  
Qy 1952 oLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi 1972  
Db 5882 TGTC-----CGTCTGG-----CTGAACATGACAGCACTCAAGCACCCCAAGTCC 5929  
Qy 1972 sSerGlnProAlaAspThrSertyrIleLeuGlnLeuProLysAspAlaProHis----- 1990  
Db 5930 CTTCTCCCGGATGCTCCAGCCCTCTCTGCCATGCCAGCGAGTCTTCCACCCCTGC 5989  
Qy 1991 -----LeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLe 2006  
Db 5990 AGTGCTGCCAGCCAGAAAGGCCCAAGAGGCACTGGCACTGGAAACCTCCCAAGAT 6049  
Qy 2006 uProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr 2021  
Db 6050 TGGCTGAGGGCTCTGCGCATCTTGGGTACCAAGGGTCAACTGTACCTCTCTCCG 6109  
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041  
Db 6110 GCAGGCCACCGGAGCGACACGTGCTGGAC----- 6140  
Qy 2041 uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTyrGlyGl 2061  
Db 6141 -----GCCAGCCCCAGCAGCTCCGCGGCGAGCTCGCAGACCACTCGAGGA 6187  
Qy 2061 nSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetTh 2081  
Db 6188 CAGCCTGACCTGAGCGACAGCCCCCGCGTGCC-----CTGGG 6226  
Qy 2081 rProProAlaProCysProGlyProGluProAsnTyrGlyLysGlyProProGluThrAr 2101  
Db 6227 GCCGCCCGCGCTGCTCCAGGACCCCGCGCGCTGTCC-----CCCGCGCTCG 6277  
Qy 2101 gSerSerLeuGluLeuAspThrGluLeuSerTyrPileSerGlyAspLeuLeuProGlu 2121  
Db 6278 CCGCCGCTGAGCTG----- 6293  
Qy 2121 yGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGl 2141  
Db 6294 -----CGCGGCCGGGCTCTTTCAGCCTGCGGGGCTGCGGGCG-- 6332

Qy 2141 nSerCysGlnArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVa 2161  
Db 6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358  
Qy 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178  
Db 6359 CTCC---ACCAGCCCGGCTGCACCCACACGACTCCATGGACCCCTCGGACGAGGAGG 6415  
Qy 2179 -LeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProPr 2198  
Db 6416 CCGCGGTGGCGGGCGGGCGGGCGGCGGAGCACTCGGAGACCTCAGCAGCCT 6475  
Qy 2198 oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSe 2215  
Db 6476 CTCGCTCACCTCCTTCTTCTGCCCCCGCCC-----CCGCCGCCAGC 6517  
Qy 2215 rProGlyIleCysLeuArgArgAlaProSerSerAspSer-----LysAs 2231  
Db 6518 CCCCCGCTCAGCCCCCGCAGGAAGTTCAGCAGCACCCAGCAGCTGGCCGCCGCGG 6577  
Qy 2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa 2251  
Db 6578 CCCCCAGCCGCCCTTGGCCCACTGGCCCTGGCCCGGAGCCCTCGTGGCGCGGAC-- 6635  
Qy 2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 6636 -----CGCAGCAAGGACCCCCCGCGCGGACCG 6665

RESULT 10

US-09-404-650-12  
; Sequence 12, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-404-650-12

Alignment Scores:

Pred. No.:	0	Length:	6503
Score:	5418.50	Matches:	1212
Percent Similarity:	60.47%	Conservative:	209
Best Local Similarity:	51.57%	Mismatches:	446
Query Match:	45.52%	Indels:	484
DB:	3	Gaps:	53

US-09-611-257A-37 (1-2266) x US-09-404-650-12 (1-6503)

Qy 27 GlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46  
Db 320 GGAATCACTGAGCAGCGGGCGCGGAGTCCCTCCATCCCTCCAGGCTGGAGGAG 379  
Qy 47 GluAlaGluGly-----LeuProTyrProAlaLeuAlaProValValPhephe 62  
Db 380 CCATTGGAAGGAACCAACCTGAGTCCCATCCAGACCTGGCTCTGTGCTTCTTC 439  
Qy 63 TyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyr 82  
Db 440 TGCCTGCCAGACCAACGAGCCCACTGGTGCATCAAGATGTTTGTAAACCCGTGG 499  
Qy 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102

Db 500 TTCGAGTGTGTGAGCATGCTGGTTATTCTGCTGAACCTGTGTGACCCCTGGGCATGTACCAG 559  
QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122  
Db 560 CCATGTGATGACATGGAGTGGCTGTGCGACCGTTGCAAGATCCTGCAGGCTTCGATGAC 619  
QY 123 PheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGlyIlePhe 142  
Db 620 TTCATCTTCATCTTCTTGGCCATGGAGATGGTGTAAAGATGGTGGCCCTGGGCATTTTT 679  
QY 143 GlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAla 162  
Db 680 GGCAAGAGTGTACTACCTCGGAGACACATGGAACCGCTGGATTCTTTCATTTGTCATGGCA 739  
QY 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182  
Db 740 GGGATGGTTGAGTACTCTCTGGACCTACAGAACATCAACCTGTGAGCCATCGGCACTGTG 799  
QY 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202  
Db 800 CGTGTCTGAGCCCTCTCAAAGCCATCAACCGTGTACCCAGCATGCGGATCCTGGTGAAC 859  
QY 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhe 222  
Db 860 CTGCTGCTCGACACGCTGCCATGTGGGAACGTTGCTCTGCTCTGTTTCTTCGCTCTTC 919  
QY 223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe 242  
Db 920 TTCATCTTCGGCATCATTTGGCGTGCAGCTCTGGGAGGCGCTGTACGGAACCGCTGCTTC 979  
QY 243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGlnThrGlu 262  
Db 980 CTGGAAGAGAACTTCACCATACAAGGGGATGTGGCCCTGGCCCTTATTACCAACCCAGAG 1039  
QY 263 AsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282  
Db 1040 GAGGATGACGAGATGCCCTTTATCTGCTCCCTGACTGGGACAATGGCATCATGGGCTGC 1099  
QY 283 ArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300  
Db 1100 CACGAGATCCCCCACTGAAGGAGCAG-----GGCCGGGAATGCTGCCTGTCCAAA 1150  
QY 301 -----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysVal 314  
Db 1151 GATGATGTGTATGACTTCGGGGCGGGCGCAGGACCTCAACGCCAGCGGTCTGTGCGTC 1210  
QY 315 AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAla 334  
Db 1211 AACTGGAACCGCTACTACAACGCTCTGCCGACGGCAACGCCAACCCCTCACAAGGGCGCC 1270  
QY 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354  
Db 1271 ATCAACTTTGACAACATGGCTATGCCGGGATGTGATTTTCCAGGTGATCACTCTGGAA 1330  
QY 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374  
Db 1331 GGCTGGGTGGAGATCATGTACTATGTATGGACGCACATTTCTTCTACAACTTCATCTAC 1390  
QY 375 PheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValIle 394  
Db 1391 TTCATCTGCTCATCATAGTGGGCTCCTTCTTCATGATCAACTTGTGCTCGTTGTCTATA 1450  
QY 395 AlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414  
Db 1451 GCAACCCAGTTCCTGTAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAACGCCAG 1510  
QY 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434  
Db 1511 CGCTACTGTCC--TCCAGCACGGTGGCCAGTTACGCTGAGCCCGGTGATTGCTATGAG 1567  
QY 435 GluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnVal 454  
Db 1568 GAGATCTTCCAATATGTCTGTGCATCTCTTCGCAAGCCCAAGCGCCGCTAGGCCTC 1627

QY 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474  
Db 1628 TACCAGGCCCTGCAGAACCGG----- 1648  
QY 475 GluThrGlnProSerSerCysSerArgSerHisArgArgLeuSerValHisLeu 494  
Db 1648 ----- 1648  
QY 495 ValHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAla 514  
Db 1648 ----- 1648  
QY 515 ProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu 534  
Db 1649 -----CGCCAGGCCCATGGGC----- 1663  
QY 535 ProProProSerThrProAlaLeuSerGlyAlaProProGlyAlaGluSerValHis 554  
Db 1664 -----CCGGGGACACCAGCC-----CCTGCCAAGCCTGGGCC----- 1696  
QY 555 SerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArg 574  
Db 1697 -----CATGCCAAG-----GAGCCACGCCACTGCAAGCTGTGCCACGACAC 1738  
QY 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594  
Db 1739 AGCCCCCTGGAC----- 1762  
QY 595 ThrSerProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSer 614  
Db 1763 ACACCTGGTGACGCC----- 1777  
QY 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634  
Db 1777 ----- 1777  
QY 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys 654  
Db 1778 -----ATCTCTGCCATT 1789  
QY 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672  
Db 1790 CTGGCCTCTGAC-----CCAGCAGCTGCCCTCACTGCCAGCAGCAGGCA 1834  
QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSer 688  
Db 1835 GGCAGCGGCCCTCTGGCCTGGGCGAGCAGCTGAC---TCAGGCCAGGAAGGCTCAGGTTCT 1891  
QY 689 AspSerGluAlaValTyrGluPheThrGlnAspAla---GlnHisSerAsp-LeuArgAs 707  
Db 1892 GGTGGCTCTGAGAGGCCCGAAGCAATGGGGATGGACTCCAGAGCAGTGAGGATGGGTC 1951  
QY 707 pProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe 724  
Db 1952 TCCTCGACCTGGGAAGGAGGAGGAACAGGAGGACGGG-----CAGCCCGACTG 2002  
QY 724 rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTy 744  
Db 2003 TGTGGG-GATGTGTGGCGCGGAGACACGAAAAAGCTGCGGGGCATCGTGGACAGCAAGTA 2061  
QY 744 rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTy 764  
Db 2062 CTTCAACAGAGGTATCATGATGCTATCCTGTTGAACACAGTCAGCATGGGCGATCGAGCA 2121  
QY 764 rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe 784  
Db 2122 CCACGAACAGCCCGAGGAGCTGACCAACATCCTGGAGATCTGCAATGTGTTCTTACCAG 2181  
QY 784 rLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLy 804  
Db 2182 TATGTTTGCCTGGAGATGATCCTGAAACTGGCCGCTTTGGGCTCTTCGACTACCTGCG 2241



Db 4237 CCTGGCCAGGCATGATGTCCTCTTTGTCTTGGCCCTCCAAAGGACGGCTGGGTGAACAT 4296  
QY 1491 eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr 1511  
Db 4297 CATGTATAATGATTAGATGCTGTTGCTGTGGACAGCAGCCAGTGACGAACCAACCC 4356  
QY 1511 oTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe 1531  
Db 4357 CTGGATGCTACTGTACTTCTTCATTCTGCTCTCATCTGTCAGCTTCTTGTGCTCAACAT 4416  
QY 1531 tPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG1 1551  
Db 4417 GTTTGTGGCGTGGTCTGGAGAACTTCCAAAGTGCCGGCAGCACCCAGGAGCTGAGGA 4476  
QY 1551 uAlaArgArgArgGluGluLysArgLeuArgArgLeuLysLysLysArgLysAlaG1 1571  
Db 4477 GGCGCGGAGCGCTGAGGAGAAACGGCTGCGGCGCTGGAAAGAACGCCCTAAGGCTCA 4536  
QY 1571 nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysTh 1591  
Db 4537 GAGGCTGCCCTACTATGCTACCTACTGTCCCAAGGCTGCTCATCCACTCCATGTGCAC 4596  
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Db 4597 CAGCCACTACCTGGACATCTTCACTACCTTCATCATCTGCTCAATGTTGTACCATGTC 4656  
QY 1611 aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl 1631  
Db 4657 CTTGGAGCACTACAACACGAGCTACATCCCTAGAGACAGCCCTTAAGTACTGCAACTACAT 4716  
QY 1631 ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr 1651  
Db 4717 GTTCACCACCTGCTTGTGCTGGAGGCTGTGCTGAAGCTGTGTCGATTTGGCCTGAGGCG 4776  
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Db 5377 GATGATGCTGAGATCGAGTGGAGATGGCCCATGGCTCGGCCCTCGCCCT----- 5428  
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QY 1887 sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi 1907  
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QY 1907 sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal--- 1925  
Db 5444 -CCCTGCCCTGCCCTGCCCTGCCCTGTGTGCTGGCCGAGGCTGCCCTAGTTTCAACC 5502  
QY 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941  
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QY 1941 rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuPr 1961  
Db 5560 CCTGTGCCG----- 5569  
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QY 2001 yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021  
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QY 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041  
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QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer 2077  
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Db 5809 AAGGAGAGCAAG-----GGTGAACATA 5829  
QY 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyr--- 2136  
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QY 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170  
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QY	2171	-----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGl	2188
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Dd	6046	GTTCTTCCACCTGTGTGTCTGCCAGCCAGAAGGGGCAGGAACCGGCATGAGTCAGG	6105
QY	2188	ySerArgProLysLysLeuSerProProSerIleThrIleAspProProGluSerGl	2208
		:::	
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QY	2208	nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs	2228
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Dd	6139	GGCATCGCTGAGGTACCGAGTGTCAACTGCACCCCTTTGCGCCAGGCTACTGTGAGTGA	6198
QY	2228	pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy	2248
		:::     ::::         :::	
Dd	6199	CACGTCC-----TTGGATGCCAGTCTTAGCAGCTCAGCGGGCAGCCTACAGACCACACT	6252
QY	2248	sLysAspValLeuSerLeuSer	2255
		:::         ::	
Dd	6253	GGAAGACAGTCTGACTCTGAGT	6274

## RESULT 11

US-09-935-541-12

Sequence 12. Application US/09935541

; Patent No. 6589787

**GENERAL INFORMATION:**

APPLICANT: Dietrich, Paul S.

APPLICANT: McGivern, Joseph G.

**; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;**

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

;  
; CURRENT FILING DATE: 2001-08-23

09/404,650

;  
; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12  
CONTINUED Below is a list of

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12

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; SEQ ID NO 12
: LENGTH: 6

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; LENGTH: 6503
; TYPE: DNA

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TYPE: DNA  
ORGANISM:

ORGANISM: KALCUB sp.  
US-09-935-541-12

2T-T4C-CCC-EN-EN

Alignment Scores:

Alignment Score:	0	Length:	6503
Pred. No.:	5418.50	Matches:	1212
Score:	60.47%	Conservative:	209
Percent Similarity:	51.57%	Mismatches:	446
Best Local Similarity:	45.52%	Indels:	484
Query Match:	4	Gaps:	53
DB:			

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Qy	47	GluAlaGluGly-----LeuProTyrProAlaLeuAlaProValValPhePhe	62
Dd	380	CCATTGGAAAGGAACCAACCCTGACGTCCACATCCAGACCTGGCTCCTGTTGCTTTCTTC	439
Qy	63	TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp	82
Dd	440	TGCCTGCGCCAGAC'CACGAGCCACGGAACTGGTGTCATCAAGATGGTTTGTAAACCCGTGG	499
Qy	83	PheGluArgIleSerMetLeuValIleLeuAsnCysValThrLeuGlyMetPheArg	102
Dd	500	TTCGAGTGTGTGAGCATGCTGGTTATTCTGCTGAAC'TGTGTGACCCCTGGGCATGTACCCAG	559
Qy	103	ProCysGluaspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp	122
Dd	560	CCATGTGATGACATGGAGTGCCTGT'CGGACCGTTGCCAAGATCCTGCAGGTC'TTCGATGAC	619
Qy	123	PheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePhe	142



QY 1159 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAs 1173  
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QY 1173 pLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG1 1191  
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QY 1191 ySerAlaSerGluHisGlnAspCysAenGlyLysSerAlaSerGlyArgLeuAlaArgAl 1211  
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DB 4537 GAGGCTGCCCTACTATGTACTACTGTCCCACAAGGCTGCTCATCTCCACTCCATGTGCAC 4596  
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RESULT 12

US-09-949-016-15601  
; Sequence 15601, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15601  
; LENGTH: 70308  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15601

Alignment Scores:

Pred. No.: 2.33e-127 Length: 70308  
Score: 2237.00 Matches: 730  
Percent Similarity: 21.93% Conservative: 25  
Best Local Similarity: 21.20% Mismatches: 64  
Query Match: 18.79% Indels: 2626  
DB: 4 Gaps: 19

US-09-611-257A-37 (1-2266) x US-09-949-016-15601 (1-70308)

QY 2 AspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArg----- 17  
Db 9554 GATGAGGAA-----GCTGGGTCCAGAGAGTGAGATGACCAAGTGGGACTCCCT 9604  
QY 18 SerPheMetArgLeuAsnAspLeuSerGlyAlaGlyGlyArg-----ProGlyProGly 35  
Db 9605 TCTCTGATGAGGAGTCTGGGGCTG---GGGGCTGCTCGTGTATGTACAGGGCCCTGGC 9661  
QY 36 SerAla-----GluLysAspProGly----- 42  
Db 9662 ACCACACCTGCTTAGCCTCAGATGGAGCCAGGAGGTAAACGAGGAGGTGTAGGGCG 9721  
QY 43 SerAlaAspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProValValPhePhe 62  
Db 9722 GGGTCGGGGGGCGGCGCTCAGCTCCAGCCTTGGCCAGCTGTTTC----- 9766  
QY 63 TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82  
Db 9767 -----TTGACTGCCAGTACCTGG 9784  
QY 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102  
Db 9785 TTTGAGCGCATCAGCATGTTGGTCACTCTTCTCAACTGCGTGACCCCTGGGCATGTTCCGG 9844  
QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeu----- 117



Db 9845 ||||| CCATCGAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCTGCAGGTGAGTGTGT 9904  
QY 117 ----- 117  
Db 9905 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGGGTTGGGCCCTCTTAATCTTAATAC 9964  
QY 117 ----- 117  
Db 9965 CCTTACTCCTCTGCAAGAGGCCCTGACCCAACTGGTGGGACTAGGGTGGACTAGAGG 10024  
QY 118 -----GlnAlaPheAsp 121  
Db 10025 GTATTCCCTCACCCACGTCTCAGTTTCAGCCACCTCTTGTGCCACATCAGGCCCTTGAT 10084  
QY 122 AspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIle 141  
Db 10085 GACTTCATCTTTGCCCTCTTTGCCGTGGAGATGGTGTGAAGATGGTGGCCTTGGGCATC 10144  
QY 142 PheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIle 161  
Db 10145 TTTGGGAAAAAGTTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCATC 10204  
QY 161 ----- 161  
Db 10205 GCAGGTGAGGACCTGGGCTGGGGTGGGAGAGCAATGGATCAGATCGGTCCCTTCCCGG 10264  
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Db 10265 GGCCAGGGTTCTGGGCCCTGTGACCTCTCAGCTCCAGCCCAGTTACAGCACCACCTTTCTCC 10324  
QY 161 ----- 161  
Db 10325 CTGGCTATCTCTGAGGGTCTGAGGCTGCCCTGCCTCTAGCACTGTAGCCTATATTTCTAA 10384  
QY 161 ----- 161  
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QY 161 ----- 161  
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QY 162 -----AlaGlyMetLeu 165  
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QY 186 ArgProLeuArgAlaIleAsnArgValProSer----- 196  
Db 10684 CGACCGCTCAGGGCCATTAAACCGGTGCCAGTGAGTGACCCCTCAGCCCTCAGCCCTG 10743  
QY 196 ----- 196  
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QY 196 ----- 196  
Db 11104 GCTGGTGACACACGCTGGCCACGCTGAACGTGACTTCTCTCAAGACAAGGCCACTCCATG 11163  
QY 196 ----- 196  
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QY 196 ----- 196  
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Db 11464 CGCTCTGT 11523  
QY 196 ----- 196  
Db 11524 GCTGCTGCCCTGGGAGGGCAGAGCTGTGAATGTGTCTCTGGGGCTCGGGGTGTGTG 11583  
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Db 11584 GTGTTAACAGGAGCTCCAGAAGAGGGGCATGCCCTCGCTCTCTCCGCCCCAGGTGATG 11643  
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Db 11824 GAGGGTTAATTAGCTGTGTCTTAGCAGCTTTTGGCCCTGGAGGGGCCAGGGGCCATAGAT 11883  
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QY 196 ----- 196  
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QY 196 ----- 196  
Db 12004 GGAAGTAACCCCTAACAGGGCTTTTGAGGAGGGGTTTTCAGTGGCTTTCCCTATGGAGGGG 12063



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Db	14343	ATACCACCTCTCCAGAGGGCATTTGGAAATGGGAAAGGTGATCTGGTTTGTGATTTT	14402	
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Db	14643	CTCTTATTCCTGCCAGTTCAGAAATTCAGACACTTTAAGAGGCAGAGACGGAGGCAAA	14702	
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QY	380	-----	-----	380
Db	14763	ACTTTGAGCTAATATTTATTGAGCACTTACTATGCGCCAGCCCTGATCTAAGCACTTTC	14822	
QY	380	-----	-----	380
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Db	15063	CCCAGAGGTGGGTCACTGGGCCAAGATCACACAGAAAGTAAGCGGCTGGGGCTGAGAA	15122	
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Db	15183	GACAGAGCCAGACAGAGGGACAGACATTGAGAGAAAGAGATTAAAGATCTA	15242	
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Db	15243	CTCAGGACCTAGACTAGCTCCAGAGAGAGATGAAGACAAAATAAGGCAGCTCCTTGTGA	15302	
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Db	15303	GAGACAGAGGGTAGGCCCTGAGAAAGAGCAAGTCCCCAAGSCACCTCATTTCTGCCTGCG	15362	
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Db	15363	TAACTTCCCTGGTGGGAAGAGTGGCAGGCTTGGGGCGAAGCCTGACTGGAGGCCTGT	15422	
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Db	15483	TCACCATGTGCCCCCCCCACCCCACTCCCTTTCCCTCCTGGGCTTGGGAGAGGGGAAG	15542	
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Db	15543	GAAGCAGACAGGGAGATAAGGGGCTAGTTTCCACCTCCACACACCCCTGAAAAATC	15602	
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Db	15663	GATCTAGAAAAAAAATCTGCTTTGTCCACCATAAATATTCATTTCTCTTCAATTTGGGATT	15722	
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Db	15783	GGGTAGTGTGAGCAAGTCAGGTGGCAGCCTGACTAGTCTGTAGGGTCAAGGGTTCAGCC	15842	
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Db	15963	GCTAGAAATGGGGCTAGAAGCAGGAGTCTTGTAATGATGTTTTTGTCAAGATCTCAAGG	16022	
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Db	16023	CTCAATATAATTTGAAAAACCCCATGTCCCTAATATTGCGTTCATTTCCACAGCATTCGCT	16082	
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Db	16143	AGGGAATTTGAGAGATTGCAGGATAACACCATGTTCAATAGCAATATCTTGGAATTTTCAT	16202	
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Db	16203	AGAGCTTGGTTCAGTCTTAGCCCTTGCTCTGAAATTAGCTGAGTGATCTTTGGGCAATGTT	16262	
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Db	16263	TGACCTCTGTGGACCTGAGTTTCTTACCTGTCTGTATGGAGATTACAATAGCATCACCTC	16322	
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Db	16323	CTGAGGCTGCTTTAAAAATAAAATAGATAAATGCTTTGGAAAAATAACTGAGCGTGGCGCTT	16382	
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Db	16383	GGCTCATAGGAATGCCCTCCGTATGTGGTGGCTGGCATTTGTGATTCACTTTCTTCAGGAC	16442	

QY	381	-----ValGlySerPhePheMetIleAsnLeuCysL	391	QY	641	-----	641
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QY	391	euValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgG	411	QY	641	-----	641
Db	16503	TGGTGGTGATGCCACGCAGTTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGATGCGGG	16562	Db	17583	TGGATCCTCTCTACCCATTAAAGTAGAGCTTTCTTAGCATCCCCATTGTGTGGATGAGA	17642
QY	411	luGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlyS	431	QY	641	-----	641
Db	16563	AGCAGCGTGTGCGGTTCTGTCTCAACGCCAGCACCCCTGGGTAGCTTCTCTGAGCCCGGCA	16622	Db	17643	ACCAGGAGGCTTGAGGGGATGCATGACTTGCCCAAGGCTTTGCTATTGGTGAGGGCGG	17702
QY	431	erCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgL	451	QY	641	-----	641
Db	16623	GCTGCTATGAGAGCTGCTCAAGTACCTGGTGATCATCTTCGTAAGGCAGCCCGCAGGC	16682	Db	17703	ACTCGGGGCCCGCACTCGGGACTCCTTGTGTGAGGCTCAGAGAGGAAATGGTGTGTGAC	17762
QY	451	euAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProL	471	QY	641	-----	641
Db	16683	TGGCTCAGGTCTCTCGGGCAGCAGGTGTGCGGTTGGGTGTGCTCAGCAGCCCAAGCACCCC	16742	Db	17763	TGTGCCCCAGCTTCATGCCCCACTGGCTAAACCTGAGTCTCATTTGCCTCCGCACAGGGAGA	17822
QY	471	euGlyGlyGlnGluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerV	491	QY	641	-----	641
Db	16743	TCGGGGGCCAGAGACCCAGCCAGCAGCAGCTGCTCTCGTCTCCACCGCCGCTATCCG	16802	Db	17823	CCCAGTTCAGGGAGCTTGTGTCTGATGGGTGACACTCCCAGTGTCTGTGGGGGCAGTGAG	17882
QY	491	alHisHisLeuValHisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyT	511	QY	641	-----	641
Db	16803	TCCACCACCTGGTGCACCAACCACCACTACCACTACCACTACCACTGGGCAATGGGA	16862	Db	17883	ACACATAGGGACGTGCGGCTCTCCCCAGCAGACAGGTTCACTGTAGCTGCAGCCCCACGGC	17942
QY	511	hrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgA	531	QY	641	-----	641
Db	16863	CGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGATGCCAATGGGTCCCGCC	16922	Db	17943	CTGTGTTCAGGAAGATGTGGCACGTGGGGAGCAGCGGGATATTCTGTGGGATGTTACG	18002
QY	531	rgLeuMetLeuProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaG	551	QY	641	-----	641
Db	16923	GGCTCATGTGCCACACCCCTCGACGCTGCCCTCTCCGGGCCCCCCTTGGTGGCGCAG	16982	Db	18003	TGGGAATGTGGCTGGGACCAGAAAGGTGCTATCACAGAAACCAGAGCGAAAGGTTTCTAT	18062
QY	551	luSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaP	571	QY	641	-----	641
Db	16983	AGTCTGTGCACAGCTTCTACCATGCCACTGCCACTTAGAGCAGTCCGCTGCCAGGCGC	17042	Db	18063	GCCAGTCTCTCCACTACCTGCCACGGGACGTGGGCCAGTCACATGCACCCACAGTTTATA	18122
QY	571	roProProArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrP	591	QY	641	-----	641
Db	17043	CCCCCTCCAGGTCCCCTCTGAGGCATCCGGCAGGACTGTGGCAGCGGGAAGGTGTATC	17102	Db	18123	TTTTCTCTGTGTAAAGGCAAGGCTGGGCCCAATAATTACTCTCAGTGGGTGCTTACTGA	18182
QY	591	roThrValHisThrSerProProGluThrLeuLysGluLysAlaLeuValGluValA	611	QY	641	-----	641
Db	17103	CCACCGTGCAACCAGCCCTCCACCCGGAGACGCTGAAGGAGAGGCACCTAGTAGAGTGG	17162	Db	18183	CTCCCTCTCTGTGTGCAGATGCAGTCAAGGGAGAAATGTCGCTGAGAGCCCCACCTGGGGCC	18242
QY	611	laAlaSerSerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerS	631	QY	641	-----	641
Db	17163	CTGCCAGCTCTGGGCCCCCAACCCCTCACAGCCTCAACATCCACCCGGGCCCTACAGCT	17222	Db	18243	AGGCCCTGAGCGGGGGCTTCCACATCCATGCTTTACCTGGTACTCTCTGAGGTTCTCAT	18302
QY	631	erMetHisLysLeuLeuGluThrGlnSerThr-----	641	QY	641	-----	641
Db	17223	CCATGCACAAGCTGTGGAGACACAGATACAGGTGAGAACTCTGGGTGGAGGCATGTGG	17282	Db	18303	ATTCTGTGATCAAAGCTGGATTAAAGGGACATTGATGTCTTGGGTAGGTCCCTGAGTG	18362
QY	641	-----	641	QY	641	-----	641
Db	17283	GTGCCCTCGTCTGGGGACTGGGTGGGTGCCAGAGGGGACTAGGGGGTCTGGAGTCAGAG	17342	Db	18363	TGTGGCACGAGTGCACTCTAGTATGCGTGTATGCGTCTATGTCCATGAAGGGTCCAGTG	18422
QY	641	-----	641	QY	641	-----	641
Db	17343	GGACCAGGGCTTATATTCTCATGTCTGCCTCTCATGGCTTAGGCACCTTCAACCAGTCACA	17402	Db	18423	TGTGTGTGCGTGTGTGCATGCACGTGTCTGTGGTTCATATGCATATGTGTGCACATGT	18482
QY	641	-----	641	QY	641	-----	641
Db	17403	TCCCTGCTATGAGCTCGAATTTTCTCATCTGCTAAAGTGAACCTCATATAATTCCTACATTG	17462	Db	18483	GCTTGATGTGTGTAGGTGCATGTGCGATGTGAAGCTCTTTCCTTGGTGTGTGTGCATGTG	18542
QY	641	-----	641	QY	641	-----	641
Db	17463	TAATAGCAGTAACATATCATGTAATAAGCACCTGCTTCGTGTGTTTGCAATGATGTCTAG	17522	Db	18543	TGCATATGTCTGGCATATGTGCCGTGTGTGAATGTGTGTGTGTGCACACATGTGTGGTATG	18602
				QY	641	-----	641



Db 18603 TGCATGTATGTGTGCCCATATGGTGTGTCTCCAAATAGTATACATGTGTACACGAGTGTGC 18662  
QY 641 ----- 641  
Db 18663 GCATCTGGAGCAGCTGTGCAGGTGCACGTGTCTGGTGTGGTGTGTGTGCAAGTGCACGT 18722  
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Db 18843 AGCTGTCCAGGACCTCAGAGGACATCCAGGCCACCTCTCTGAGCCCCCAGGACACTCAGCA 18902  
QY 641 ----- 641  
Db 18903 GTGACTGTCAATGAAGTGCTATTGACATTAGGGCATCTTGTGGGTCAAGACTGCCACCT 18962  
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Db 18963 TGCCTGACATTGAGCACCCCTGGCCCACTAAGTGCCTAGCACCCCATCACTGTAAACAAC 19022  
QY 641 ----- 641  
Db 19023 CCAGACTCCCTGACTCATTTTACACATACTCACAGGGCAGGTAGCCCCAGGTACGAGAC 19082  
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Db 19083 TCTGGAGCCTCTCACCTCTACTCTCTCTGTTCAGGTGCCTGCCAAAGCTCTTGCAAGATC 19142  
QY 651 SerSerProCysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCys 670  
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Db 19203 GCCCGGCGGGCAGGGAGGTGGAGTGCCTGCCAGCCAGCTCTGTGTGGCTTCTGGAGG 19262  
QY 691 GluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSer 710  
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QY 751 IleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGlu 770  
Db 19443 ATCGCCATCCTGGTCAACACACTCAGCATGGGCATCGAATACCAGAGCAGGTAGGAGAG 19502  
QY 771 LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet 790  
Db 19503 TGGGCAGAGGCA-----GGGCTCCTGCCAGCTGCTTTT 19535  
QY 791 LeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe 810  
Db 19536 CGCCTGGGGCTG-----GGGCTTCTACCTCCCGCACCCCTCCTCCTGAGTGC 19586  
QY 811 AspGlyValIleValValIleSer-ValTTPGluIleValGlyGlnGlnGlyGlyGlyLe 830  
Db 19587 AGCTTCCTCTCCATGCTGTAGCCCACTGGCAGGTAGGAGGGGAGGTGGGTGATGGA-- 19644  
QY 830 uSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe----- 847

Db 19645 ----GCAATGCATGGGATTCTCTAGAGGGAGTGTCTTAAAGTCTCTGAGTATGGAGGTCG 19700  
QY 848 -----LeuPro-----AlaLeuGlnArgGlnLeuValVa 857  
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QY 857 1 857  
Db 19761 G 19761  
RESULT 13  
US-08-984-709A-51  
; Sequence 51, Application US/08984709A  
; Patent No. 6320032  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Mark E.  
; APPLICANT: Stauderman, Kenneth A.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McAuliffe  
; STREET: 4250 Executive Square, Suite 700  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/984,709A  
; FILING DATE: 02-DEC-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 450-8400  
; TELEFAX: (619) 587-5360  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1669 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
US-08-984-709A-51  
Alignment Scores:  
Pred. No.: 3.36e-113 Length: 1669  
Score: 1971.50 Matches: 423  
Percent Similarity: 57.77% Conservative: 38  
Best Local Similarity: 53.01% Mismatches: 83  
Query Match: 16.56% Indels: 255  
DB: 3 Gaps: 8  
US-09-611-257A-37 (1-2366) x US-08-984-709A-51 (1-1669)  
QY 109 CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePhe 128  
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QY 129 AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeu 148

Db 62 GCGGTGGAGATGGTTCATCAAGATGGTGGCCTTGGGGCTGTTCCGGGCAGAGTGTACCTG 121

Qy 149 GlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer 168

Db 122 GGTGACACGTGGAAACAGGTGGATTCTTCATCGTGGTGGCGGCATGATGGAGTACTCG 181

Qy 169 LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 188

Db 182 TTGGACGGACACAACGTGAGCCTCTCGGCTATCAGACCGTGGGTGCTGGGCCCTC 241

Qy 189 ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu 208

Db 242 CGCGCCATCAACCGGTGCTAGCATCGGATCCCTGGTCACTCTGCTGTGGATACGCTG 301

Qy 209 ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal 228

Db 302 CCCATGCTCGGAACGTCTTCTGTGTGCTTCTTCGTCTTCTTCATTTTCGGCATCGTT 361

Qy 229 GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer 248

Db 362 GCGGTCCAGCTCTGGGCTGGCCTCCCTGCGGAACCGCTGTCTTCTGGACAGTGCTTGTG 421

Qy 249 LeuProLeuSerValAsp---LeuGluArgTyrTyrGlnThrGluAsnGluAspGluSer 267

Db 422 AGGAACAACAACCTGACCTTCTTGGCGCGTACTACACGAGGAGGGCGGAGAGAAC 481

Qy 268 PropheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro--- 286

Db 482 CCGTTTCATCTGCTCTCACCGGACGAGACACGGCATGCAAGTGTCTGCACATCCCCGGC 541

Qy 287 -----ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeuAspTyrGluAla 304

Db 542 CGCGCGAGCTGCGC-----ATGCCCTGCACCCCTGGGCTGGGAGGCC 583

Qy 305 TyrAsn-----SerSerSerAsnThrThrCysValAsnTrpAsn 317

Db 584 TACACGACGCGCAGCGCGAGGGGTGGCGCTGCACGCAACGCTGCATCAACTGGAAC 643

Qy 318 GlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPh 337

Db 644 CAGTACTACAACGTGTGCGCTCGGTGACTCCAAACCCCAACACGGTGCATCAACTTC 703

Qy 338 AspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpVal 357

Db 704 GACACATCGGTACGCTGGATTGCCATCTCCAGGTGATCAGCTGGAAGGCTGGTG 763

Qy 358 AspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeu 377

Db 764 GACATCATGTACTACGTATGACGCGCCACTCATTTACAACCTCATCTATTTCATCTG 823

Qy 378 LeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGln 397

Db 824 CTCATCATCTGGGCTCCTTCTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAG 883

Qy 398 PheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeu 417

Db 884 TTCTCGGAGACGAAGCAGCGGAGAGTCAGCTGATGCGGGAGCAGCGGCGCACGCCCTG 943

Qy 418 SerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeu 437

Db 944 TCCAACGACAGCAGCTGGCCAGCTTCTCCGAGCTGGCAGCTGCTACGAAGAGCTG--- 1000

Qy 438 LysTyrLeuValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAla 457

Db 1000 ----- 1000

Qy 458 AlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGln 477

Db 1000 ----- 1000

Qy 478 ProSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis 497

Db 1000 ----- 1000

Qy 498 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAla 517

Db 1000 ----- 1000

Qy 518 SerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProPro 537

Db 1000 ----- 1000

Qy 538 SerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyr 557

Db 1000 ----- 1000

Qy 558 HisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSer 577

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Qy 578 GluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerPro 597

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Qy 598 ProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProPro 617

Db 1012 ----- 1012

Qy 618 ThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGlu 637

Db 1012 ----- 1012

Qy 638 ThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys-LeuLysAl 657

Db 1013 -----CCGTGCCCTGGAGGA 1027

Qy 657 aaspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGl 677

Db 1028 CCGGAGGGT----- 1037

Qy 677 uValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheTh 697

Db 1038 ----GAGCTCAGCGGCTCGGAAAGTGGAGACTCAGATGGCCGTGGCTCTATGAATTCAC 1093

Qy 697 rGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGl 717

Db 1094 GCAGGACGTCCGGCACGGTACCGCTGGGACCCC-----ACGCGACC 1135

Qy 717 yProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheAr 737

Db 1136 ACCCGG-GGCGAGCCAGGTGGATGGCCGCTCTGGGTACCTTCAGCGGCAAGCTGCG 1194

Qy 737 gLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnTh 757

Db 1195 CCGCATCGTGGACAGCAAGTACTTCAGCCGTGGCATCATGATGGCCATCCTTGTCAACAC 1254

Qy 757 rLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIle 777

Db 1255 GCTGAGCATGGCGTGGAGTACCATGAGCAGCCCGAGGAGCTGACTAATGCTCTGGAGAT 1314

Qy 777 eSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTy 797

Db 1315 CAGCAACATCGTGTTCACCAGCATGTTGCCCTGGAGATGCTGCTGAAGCTCTGGCCTG 1374

Qy 797 rGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIle 817

Db 1375 CGGCCCTCTGGGCTACATCCCGGAACCCGTACAACATCTTCGACGGCATCATCGTGTGTCAT 1434

Qy 817 eSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheAr 837

Db 1435 CAGCGTCTGGAGATCGTGGGGCAGCGGACCGGTGGTGTGTCTGTGCTGGCACCTTCCG 1494

Qy 837 gLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValVa 857

Db 1495 GCTGCTGCGTGTGCTGAAGCTGGTGGCTTTTCTGCCAGCCCTTCCGGCCGAGCTCGTGGT 1554

QY 857 lLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePh 877  
Db 1555 GCTGGTGAAGACCATGGACAACGTGGTACCTTCTGCACGCTGCTCATGCTCTTCATTT 1614  
QY 877 eilePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGlu 894  
Db 1615 CATCTTCAGCATCTCTGGGCATGCACCTTTTCGGCTGGCAAGTTCAGCCTGAA 1666

RESULT 14

US-09-268-163-3  
; Sequence 3, Application US/09268163B  
; Patent No. 6353091  
; GENERAL INFORMATION:  
; APPLICANT: Lipscombe, Diane  
; APPLICANT: Schorge, Stephanie  
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF  
; FILE REFERENCE: B1055/7000  
; CURRENT APPLICATION NUMBER: US/09/268,163B  
; CURRENT FILING DATE: 1999-03-12  
; EARLIER APPLICATION NUMBER: US 60/077,901  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 7376  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 146..7174  
US-09-268-163-3

Alignment Scores:

Pred. No.: 8.8e-101 Length: 7376  
Score: 1786.50 Matches: 635  
Percent Similarity: 38.95% Conservative: 371  
Best Local Similarity: 24.58% Mismatches: 838  
Query Match: 15.01% Indels: 741  
DB: 3 Gaps: 77

US-09-611-257A-37 (1-2266) x US-09-268-163-3 (1-7376)

QY 27 GlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46  
Db 218 GGGGCGGGGGGGGGGGGGGGGGGGTCCGGGGGGGCTGCAGCGCGGCCAGCGGGTCTC 277  
QY 47 GluAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhe----- 61  
Db 278 TACAAGCAATCGATCGCGCAGCGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTC 337  
QY 62 -----PheTyrLeuSerGlnAspSerArgPro 70  
Db 338 AAGCAGAACTGCTTACCGCTCAACCGCTCGCTCTTCGTTCTTCAGCGAGGACAACGTCGTC 397  
QY 71 ArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuVal 90  
Db 398 CGCAATACCGGAAGCGCATCACCGAGTGGCTCCATTCCGAGTATATGATCCTGGCCACC 457  
QY 91 IleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAsp 110  
Db 458 ATCATCGCCAACTGCATCGTGTGGCCCTG-----GAGCAGCACCTCCCTGAT 505  
QY 111 SerGlnArgCysArgIleLeuGlnAlaPheAspAsp-----PheIlePheAlaPhe 127  
Db 506 GGGGACAAAACGCCCATGTCCGAGCGGCTGGACGACACGGAGCCCTATTTCATCGGGATC 565  
QY 128 PheAlaValGluMetValValLysMetValAlaLeuGly---IlePheGlyLysLysCys 146  
Db 566 TTTTGCTTCGAGGCGGAGATCAAAATCATCGCTCTGGGCTTGTCTTCCCAAGGGCTCT 625  
QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGlu 166  
Db 626 TACCTGCGGAACGGCTGGAACGTCATGGACTTCGTGGTCTCGTCTCACAGGGATCCTTCC 685

QY 167 TyrSer-----LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArg 183  
Db 686 ACGGCTGGAAGTACTTCCACCTCGCA-----ACACTGAGGGCTGTGCGT 730  
QY 184 ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 203  
Db 731 GTGCTGAGGCCCTGAAGCTGGTGTGGGATTCCAAAGTTTGAGAGTGTGTCAAGTCC 790  
QY 204 LeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePhe 223  
Db 791 ATCATGAAGGCCCATGGTTCACCTCTGCAGATTGGGCTGCTTCTTCTTGGCATCCTC 850  
QY 224 IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu 243  
Db 851 ATGTTTGCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCCACAAGGCTGTTC--- 907  
QY 244 ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsn 263  
Db 908 -----CCCAACAGCACAGATGCGGAG----- 928  
QY 264 GluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg 283  
Db 928 ----- 928  
QY 284 SerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeuAspTyrGlu 303  
Db 929 -----CCCGTG-----GGTGACTTCCCTGTGGCAAGGAGGCCCA 964  
QY 304 AlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys 323  
Db 965 GCCCGGCTGTGGAGGGCGACACTGAGTGC-----CGGAGTACTGGCCA----- 1009  
QY 324 SerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAla 343  
Db 1010 -----GGACCCAACTTGGCATCACCAACTTGACAATATCCTGTTTGGC 1054  
QY 344 TrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVal 363  
Db 1055 ATCTTGACGGTGTTCAGTGCATCACCATGGAGGGCTGGACTGACATCCTCTATAATACA 1114  
QY 364 MetAsp---AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGly 382  
Db 1115 AACGATGCGCGCGGCAACACCTTGAAGTGGCTCTACTTCTATCCCTCTCATCATCGGC 1174  
QY 383 SerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLys 402  
Db 1175 TCCTTCTTCATGCTCAACCTGTGTGGCGTGTCTCGGGGAGTTTGCAAGGAGCGA 1234  
QY 403 GlnArgGluSer-----GlnLeuMetArgGluGlnArgValArgPhe 416  
Db 1235 GAGAGGGTGGAGAACCGCGCGCTTCTTGAAGCTGCGCGGCGAGCAGATCGAG--- 1291  
QY 417 LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 436  
Db 1292 -----CGAGAGCTC 1300  
QY 437 LeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArg 456  
Db 1301 AACGGGTACCTGGAGTGGATCTTCAAGGCGGAGGAAGTATGTCGCGGAGGAGGACAGG 1360  
QY 457 AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThr 476  
Db 1361 AATGCA-----GAGGAGAAG 1375  
QY 477 GlnProSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHis 496  
Db 1376 TCCCTTTGGACGTGCTGAAGAGAGCGGCCCAACCAAGAGAGAGAAATGACCTGATCCAC 1435  
QY 497 HisHisHisHisHisHisTyrHisHisLeuGlyAsnGlyThrLeuArgAlaProArg 516  
Db 1435 ----- 1435

QY 517 AlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPro 536  
Db 1436 ---GCAGAGGAGGAGGAGGACCGTTTGCAGAT----- 1465  
QY 537 ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe 556  
Db 1465 ----- 1465  
QY 557 TyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerPro 576  
Db 1465 ----- 1465  
QY 577 SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer 596  
Db 1465 ----- 1465  
QY 597 ProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyPro 616  
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QY 617 ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeu 636  
Db 1465 ----- 1465  
QY 637 GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLys 656  
Db 1466 -----CTCTGTGCTGTGTGGATCCCCCTTCGCCCGC 1495  
QY 657 AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly 676  
Db 1496 GCCAGCCTCAAGAGCGGGAAGACAGAGAGCTCGTCATACTTCCGGAGG----- 1543  
QY 677 GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe 696  
Db 1544 -----AAGGAGAAGATGTTCCGGTTT 1564  
QY 697 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu 716  
Db 1564 ----- 1564  
QY 717 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736  
Db 1565 -----TTTATC 1570  
QY 737 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 756  
Db 1571 CGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGTGTCTGTCTGTGTGGTGGCCCTGAAC 1630  
QY 757 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 776  
Db 1631 ACACGTGTGTGGCCATGGTGCATTACACACGCGCGCGGCTTACCACGACCCCTGTAT 1690  
QY 777 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuVal 796  
Db 1691 TTTCAGAGTTTGTGTTCTCTGGTCTCTTCTCAGAGATGTCCCTGAAGATGTATGGC 1750  
QY 797 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 816  
Db 1751 CTGGGGCCCCAGAGCTACTTCCGGTCTCTCTCACTGCTTCACTTGGGTTCATCGTG 1810  
QY 817 IleSerValTrpGluIleValGlyGln-----GlnGlyGlyGlyLeuSer 831  
Db 1811 GGGAGCGTCTTTGAAGTGGTCTGGGGCGCCATCAAGCCGGGAAGCTCTTTGGGATCAGT 1870  
QY 832 ValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeu 851  
Db 1871 GTGTCGGGGCCCTCCGCTGTCTGAGGATCTTCAAAGTCAAGAGTACTGGAGCTCCCTG 1930  
QY 852 GlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu 871  
Db 1931 CGGAACCTGGTGTGCTGCTGAACCTCCATGAAGTCCATCATCATGAGCCTGCTCTTCTTG 1990  
QY 872 LeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPhe 891

Db 1991 CTCTTCCTGTTTCATTTGGTCTTCGCCCTGTGGGATGCAGCTGTTTGGGGACAGTTC 2050  
QY 892 AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp 911  
Db 2051 AACTTCCAGGATGAGACTCCACAC-----ACCAACTTCGACACCTTCCCTGCC 2098  
QY 912 AlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsn 931  
Db 2099 GCCATCCTCACTGTCTTCCAGATCCTGACGGGAGAGGACTGGAATGCAGTGTATC 2158  
QY 932 GlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAla 946  
Db 2159 GGGATCGAATCGCAAGCGCGCTCAGCAAGGCATGTTCTCTGCTCTTTTACTTTCATTTGC 2218  
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Db 2219 CTGACACTGTTTCGAAACTACACTCTGCTGAATGTCTTCTGGCCATCGCTGTGGACAAC 2278  
QY 967 Phe---GlnAlaGluGluIleSerLys-----ArgGluAspAlaSerGlyGln 981  
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QY 982 -----LeuSerCysIleGln 986  
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QY 1027 Glu-----HisProGluLeuArgLys 1033  
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QY 1034 SerLeuLeuProProLeuIleIleHisThr-AlaAlaThrProMetSerLeuPro---- 1051  
Db 2579 CACCTGGACCGCGCTGTGTGTGGAGCTGGCGCGCGACGGCGCGGGGGCCCGTGGGA 2638  
QY 1052 -----LysSerThrSe 1055  
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Db 2699 CACCGCACCGCGACAAGGACAAGACCCCGCGCGGGGAGCCAGGACCGAGCAGAGGCC 2758  
QY 1072 -----SerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProPr 1087  
Db 2759 CCGAAGCGGAGAGCGGGGAGCCCGGTGCGCGGAGGAGCGCGCGCGCGCAGCAGC 2818  
QY 1087 oSerAlaArg-----SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105  
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QY 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProse 1125  
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QY 1125 rGlyGlu----- 1127  
Db 2933 CGGAGCGCCCGACGCCACCGCGCGCACCGGCGGCGGCGGCGGCGGCGGCGGCGG 2992  
QY 1127 ----- 1127  
Db 2993 GCCAAGGCGAGCGCGCGCGCGCGCACCGCGGCGGCGGCGGCGGCGGCGGCGG 3052  
QY 1128 -----ArgArgSerLeuLeuSe 1133  
|||||



Db 3053 GAGAGCGGGAGAGCCGGCGCGGGCCGCGGCACCGGGCCGCGCAACAAGCGCAGCCTGCTCAC 3112  
Qy 1133 r-GlyGluGlyGln-GluSerGlnAspGluGluSerSerGluGluGluArgAlaSer 1152  
Db 3113 GAGGCTGTGGAGAAGAGACCACCGAGAAGGAGGCCACGGAGAAGGAGGCTGAGATAGTG 3172  
Qy 1153 ProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPhe 1172  
Db 3173 GAAGCCGACAAAGGAAAGGAGCTCCGGAAACCACCAGCCCCGGGAGCCACACTGTGACCTG 3232  
Qy 1173 AspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySer 1192  
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Db 3809 CTGGACTTCATTGTGGTCAGTGGCGCCTGGTGGCGTTTGTCTTCTCGAGCTTCCGTGGGA 3868  
Qy 1368 AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1387  
Db 3869 GGATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCTTCTGTCCTGCGG 3928  
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Qy 1408 SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly 1427  
Db 3989 TCCCTGAAGAATGTCTCAACATCTTGATGTCTACATGCTCTTCAATGTTTCAATTGCCC 4048  
Qy 1428 IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlu----- 1444  
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Qy 1460 TyrArg---TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478  
Db 4169 CCCAGGCACTGGAAAGAAATACGACTTTCACGTACGACAATGTGCTCTGGGCTCTGCTGACG 4228  
Qy 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498  
Db 4229 CTGTTTCACAGTGTCCACGGGAGAGGCTGGCCCATGTTGCTGAAACACTCCGTGGATGCC 4288  
Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518  
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Qy 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538  
Db 4349 GTCTACTTGTGGTCTTTCCCTTCTTCTCGTCAACATCTTGTGGCTTGTATCATCATC 4408  
Qy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys 1558  
Db 4409 ACCTTC-----CAGGAGCAGGGGACAAGGTGATGCTGAA----- 4444  
Qy 1559 ArgLeuArgArgLeuGluLysLysArgArgLysAla-----GlnCysLys 1573  
Db 4445 -----TGCAGCCTGGAGAAGAACGAGAGGGCTTGCATTGACTTCGCCATCAGCGCCAAA 4498  
Qy 1574 ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisLeu 1589  
Db 4499 CCCCTGACACGGTACATGCCCAAAACCGGCAGTCTGTTCCAGTATAAGACGTGGACATTT 4558  
Qy 1590 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609  
Db 4559 GTGGTCTCCCGCCCTTTGAAATCTTTCATCATGCCCCATGATAGCCCTCAACACTGTGTG 4618  
Qy 1610 MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629  
Db 4619 CTGATGATGAAGTTCTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCCGTGAAC 4678  
Qy 1630 TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe 1649  
Db 4679 ATCGTGTTCACATCCATGTTCTCCATGGAATGCGTGTGAAGATCATCGCCTTTGGGGTG 4738  
Qy 1650 ArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuSerIle 1669  
Db 4739 CTGAACATATTTCAGAGATGCTGGAATGTCTTTGACTTTGTCTGTGTGGGAAGTATT 4798  
Qy 1670 MetGlyIleThrLeuGluGluIle---GluValAsnAlaSerLeuProIleAsnProThr 1688  
Db 4799 ACTGATATTTAGTAACAGAGATTGCGGAACGAAC-----AATTTTCATC 4843  
Qy 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708  
Db 4844 AACCTCAGCTTCCTCCGCCTCTTTCGAGCTCGCGGGTGTATCAAGTGTCTCCGCCAGGGC 4903  
Qy 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728  
Db 4904 TACACCATCCGCATCCTGCTGTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTACGTG 4963  
Qy 1729 GlyLeuLeuPheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGly 1748  
Db 4964 TGTCTGCTCATTTGCCATGCTGTCTTCTCATCTACGCCCATCATCGGCATGCAAGTGTGGG 5023  
Qy 1749 AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg 1768  
Db 5024 AATATTGCCCTGGATGATGAC-----ACCAGCATCAACCCGCCACAACACTTCCGG 5074  
Qy 1769 AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGly 1788  
Db 5075 ACCTTTTTCGAAGCCCTGATGCTGTCTTCAGGAGCGCCACGGGGAGGCCCTGGCAGCAG 5134  
Qy 1789 IleMetLysAspThrLeuArgAsp-----CysAspGlnGlu-----SerThrCysTyr 1804  
Db 5135 ATCATGTGCTCCTGCCTGAGCAACCAAGGCGCTGTGATGAGCAGGGCCAATGCCACCGAGTGT 5194

QY	1805	AsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeu	1824
Db	5195	GGAAGTGACTTTGGCTACTTCTACTTCGTCTCTTTCATCTCTCCTGTGCTCTTCTGTATG	5254
QY	1825	ValAsnValValIleAlaValLeuMet	1833
Db	5255	TTGAACCTCTTTGTGGCTGTGATCATGGACAATTTTGAGTACCTCACGGGGACTCTTCC	5314
QY	1834	-----LysHisLeuGluGlu-SerAsnLysGluAlaLysGluAlaGluLe	1849
Db	5315	ATCCTAGGTCCTCACCACTTGGATGAGTTTCATCCGGGTCTGGGCTGATACACACCCCGCT	5374
QY	1849	uGluAlaGluLeuGluMetLysThrLeu-SerProGlnProHisSerProLeuG	1869
Db	5375	GCGTGTGGCGCATCAGTTACAATGACATGTTTGAGATGCTGAAACACATGTTCCTCCGCT	5434
QY	1869	lySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProG	1889
Db	5435	CTGGG-----GCTGGGGAAGAAATGCCCTGCTCGAGTTGCTTACAAGCGCCTG	5482
QY	1889	lyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProT	1909
Db	5483	GTTTCG---CATGAACATGCCCATCTCCAACGAGGACATGACTGTTCACTTCACGTCCACG	5539
QY	1909	hrMetGlnProHisProThr-----GluLeuProGlyPro-----	1920
Db	5540	CTGATGGCCCTCATCCGAGCGCACTGGAGATCAAGCTGGCCCCAGCTGGGACAAAGCAG	5599
QY	1921	-----AspLeuLeuThrValArgLysSerGly-----	1929
Db	5600	CATCAGTGTGACGGGAGTTGAGGAAGGAGATTTCCGTTGTGTGGGCCAATCTGCCCCAG	5659
QY	1929	-----	1929
Db	5660	AAGACTTTGGACTTGCTGTGTPACCACCCCATAGCCTGATGAGATGACAGTGGGAAGGTT	5719
QY	1930	-----ValSerArgThrHisSerLeuProAsnA	1939
Db	5720	TATGCAGCTCTGATGATATTGACTTCTACAAGCAGACAACAAACCACCAGAGACCCAGATG	5779
QY	1939	spSerTyrMetCysArg-----HisGlySerThrAlaGluGlyPro-----LeuG	1954
Db	5780	CAGCAGGCTCCTGGAGGCCCTCTCCAGATGGGTCTGTGTCCCTGTTCCACCCCTTGAAG	5839
QY	1954	lyHis-----ArgGlyTrpGlyLeuPro-LysAla	1963
Db	5840	GCCACCCCTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGCCCGGTTTTCCTTCGACAG	5899
QY	1964	GlnSerGlySerValLeuSer-----ValHisSerGlnProAla-----	1976
Db	5900	AAGAGTTCACCTCCCTCAGCAATGGCGGGCCATACAAAACCAAGAGAGTGGCATCAAA	5959
QY	1977	---AspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro---	1994
Db	5960	GAGTCTGTCTCCTGGGGCACTCAAAGGACCCAGGATGCACCCCATGAGGCCAGGCCACCC	6019
QY	1995	-----HisSerAlaProThrTrpGlyThrIleProLysLeuProProGly	2010
Db	6020	CTGGAGCGTGGCCACTCCACAGAGATC-----CCTGTGGGG	6055
QY	2011	ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArg-----	2026
Db	6056	CGGTGAGGAGCACTGGCTGTGACGTTTCAGATGCAGAGCATAAACCGGAGGGGCCCTGAT	6115
QY	2027	-----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAla	2043
Db	6116	GGGAGCCCCAGCCTGGGCTGGAGAGCCAGGGTCGAGCGGCGCTCCATGCCCCGCTTGGC	6175
QY	2044	GluValSerGlyPro-----SerProProLeuAlaArgAlaTyrSerPheTrpGly	2060
Db	6176	GCCGAGACTCAGCCCGTCAACAGATGCCAGCCCCCATGAAGCGGTCCATC-----	6223
QY	2061	GlnSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMet	2080

Db	6224	-----TCCACGCTGGCCACGGG-----CCCGTGGGAC-TCATCTTTGCAGCACCA	CCCC	6273	-----TTCACGCTGGCCACGGG-----CCCGTGGGAC-TCATCTTTGCAGCACCA	CCCC	6274
QY	2081	ThrProProAlaProCysProGly-----ProGluProAsnTrpGlyLysGlyPro	2097	2081	ThrProProAlaProCysProGly-----ProGluProAsnTrpGlyLysGlyPro	2097	2081
Db	6274	GGACCGCCACCCCTAGCCAGGCGTCGTGCACCA	6318	6274	GGACCGCCACCCCTAGCCAGGCGTCGTGCACCA	6318	6274
QY	2098	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117	2098	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117	2098
Db	6319	CCG-----	6324	6319	CCG-----	6324	6319
QY	2118	LeuProProGlyGlyGlnGlu--GluProProSerProArgAspLeuLysLysCysTyr	2136	2118	LeuProProGlyGlyGlnGlu--GluProProSerProArgAspLeuLysLysCysTyr	2136	2118
Db	6325	CCACCGCGGACAGGACAGGAAGCAGAGGTCCCTGGAGAGGGGCCAGCCTGTCTGC---	6381	6325	CCACCGCGGACAGGACAGGAAGCAGAGGTCCCTGGAGAGGGGCCAGCCTGTCTGC---	6381	6325
QY	2137	SerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArg	2156	2137	SerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArg	2156	2137
Db	6382	-----CGATATGGATGGCGCACCAAGCAG-----	6405	6382	-----CGATATGGATGGCGCACCAAGCAG-----	6405	6382
QY	2157	HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPro	2176	2157	HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPro	2176	2157
Db	6406	-----TGCTGTGGGGCGGGGCTGCCCGGGAGAGGGGCCTA-CAG	6446	6406	-----TGCTGTGGGGCGGGGCTGCCCGGGAGAGGGGCCTA-CAG	6446	6406
QY	2177	SerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSer	2196	2177	SerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSer	2196	2177
Db	6447	GCTGCCGGCGGAACGAGAGCGCCGCGAGGAGCGGGCGGTCCCAGGAGCGGAGGCAGC	6506	6447	GCTGCCGGCGGAACGAGAGCGCCGCGAGGAGCGGGCGGTCCCAGGAGCGGAGGCAGC	6506	6447
QY	2197	ProProSerIleThrIleAspProProGluSerGln-----	2208	2197	ProProSerIleThrIleAspProProGluSerGln-----	2208	2197
Db	6507	CCT-----CATCCTCCTCCTCGGAGAGCAGCGCTTCTACTCTCTCGGACC	6551	6507	CCT-----CATCCTCCTCCTCGGAGAGCAGCGCTTCTACTCTCTCGGACC	6551	6507
QY	2209	-----GlyProArgThrProProSerProGlyIleCysLeuArgArgArg	2233	2209	-----GlyProArgThrProProSerProGlyIleCysLeuArgArgArg	2233	2209
Db	6552	GCTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCCCTCAGCAGCCACCAACGTGCG	6611	6552	GCTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCCCTCAGCAGCCACCAACGTGCG	6611	6552
QY	2224	AlaProSerSerAspSerLysAspPro-----	2232	2224	AlaProSerSerAspSerLysAspPro-----	2232	2224
Db	6612	CAACAGCTGGCCAGGAGCCGGACCCCAACCCAGGGCAGTGGTTCCGTGAATGGGAGCC	6671	6612	CAACAGCTGGCCAGGAGCCGGACCCCAACCCAGGGCAGTGGTTCCGTGAATGGGAGCC	6671	6612
QY	2233	-----LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerPro	2247	2233	-----LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerPro	2247	2233
Db	6672	CCTTGCTGTCAACATCTGGTGCTAGCACCCCGCGCGGTGGGGGAGGAGCAGCTCCCC	6731	6672	CCTTGCTGTCAACATCTGGTGCTAGCACCCCGCGCGGTGGGGGAGGAGCAGCTCCCC	6731	6672
QY	2248	LysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266	2248	LysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266	2248
Db	6732	AGACGCGCCCTGACTC-----CCCGCCCCCAGCATCACT	6764	6732	AGACGCGCCCTGACTC-----CCCGCCCCCAGCATCACT	6764	6732

## RESULT 15

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US-08-455-543A-7
; Sequence 7, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

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QY 417 LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 436  
 Db 1290 -----CGAGAGCTC 1298  
 QY 437 LeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArg 456  
 Db 1299 AACGGGTACTGGAGTGGATCTTCAAGCGGAGGAAGTCATGCTGGCCGAGGAGACAGG 1358  
 QY 457 AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThr 476  
 Db 1359 AATGCA-----GAGGAGAAG 1373  
 QY 477 GlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHis 496  
 Db 1374 TCCCTTTGGACGTGCTGAAGAGAGCGGCCACCACGAAGACAGCAGAAATGACCTGATCCAC 1433  
 QY 497 HisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArg 516  
 Db 1433 -----TTTATC 1568  
 QY 517 AlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPro 536  
 Db 1434 --GCAGAGGAGGAGGAGGACCGGTTTGAGAT----- 1463  
 QY 537 ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe 556  
 Db 1463 ----- 1463  
 QY 557 TyrHisAlaaspCysHisLeuGluProValArgCysGlnAlaProProArgSerPro 576  
 Db 1463 ----- 1463  
 QY 577 SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer 596  
 Db 1463 ----- 1463  
 QY 597 ProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyPro 616  
 Db 1463 ----- 1463  
 QY 617 ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeu 636  
 Db 1463 ----- 1463  
 QY 637 GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLys 656  
 Db 1464 -----CTCTGTGCTGTGGATCCCCCTTCGCCCGC 1493  
 QY 657 AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly 676  
 Db 1494 GCCAGCCTCAAGAGCGGGAAGACAGAGCTCGTCATCTCCGGAGG----- 1541  
 QY 677 GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe 696  
 Db 1542 -----AAGGAGAAGATGTTCCGGTTT 1562  
 QY 697 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu 716  
 Db 1562 ----- 1562  
 QY 717 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736  
 Db 1563 -----TTTATC 1568  
 QY 737 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 756  
 Db 1569 CGGCGCATGGTGAAGCTCAGAGCTTCTACTGGGTGGTGTGCTGTGCTGGTGGTGGCCCTGAAC 1628  
 QY 757 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 776  
 Db 1629 ACACGTGTGTGGCCATGGTGCATTACAACACGCGCGGGCGGCTTACCACGACCCCTGTAT 1688  
 QY 777 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuVal 796

Db 1689 TTTGCAGAGTTTGTCTTCTGGGTCTCTTCTCACAGAGATGTCCTCAAGATGTATGGC 1748  
 QY 797 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 816  
 Db 1749 CTGGGGCCCAAGAAGCTACTTCCGGTCTCTCTCAACTGCTTCGACTTTGGGTTCATCGTG 1808  
 QY 817 IleSerValTrpGluIleValGlyGln-----GlnGlyGlyGlyLeuSer 831  
 Db 1809 GGGAGCGTCTTTGAAGTGGTCTGGCGCGCCCAAGCCCGGAAGCTCTTTGGGATCAGT 1868  
 QY 832 ValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeu 851  
 Db 1869 GTGCTGCGGGCCCTCCGCTGCTGAGGATCTTCAAAGTCAAGAACTACTGGAGCTCCCTG 1928  
 QY 852 GlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu 871  
 Db 1929 CGGAACCTGGTGGTGTCCCTGCTGAACCTCCATGAAGTCCATCATCAGCCTGCTCTTTG 1988  
 QY 872 LeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPhe 891  
 Db 1989 CTCTCTCTGTTTCATTTGTGTCTTCGCCCTGCTGGGATGCAGCTGTTTTGGGGACAGTTC 2048  
 QY 892 AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp 911  
 Db 2049 AACTTCCAGGATGAGACTCCACA-----ACCAACTTCGACACCTTCCCTGCC 2096  
 QY 912 AlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsn 931  
 Db 2097 GCCATCTCACTGTCTTCCAGATCCTGACGGGAGAGGACTGGAATGCAGTGATGATCAC 2156  
 QY 932 GlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAla 946  
 Db 2157 GGGATCGAATCGCAAGCGGCGCTCAGCAAAGGCATGTTCTCGTCTCTTTTACTTTCATTGTC 2216  
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 Db 2217 CTGACACTGTTTCGAAACTACACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGACAAC 2276  
 QY 967 Phe---GlnAlaGluGluIleSerLys-----ArgGluAspAlaSerGlyGln 981  
 Db 2277 CTGGCCAAACGCCCAAGAGCTGACCAAGGATGAAGAGAGAGATGGAAGAGCAGCAATCAG 2336  
 QY 982 -----LeuSerCysIleGln 986  
 Db 2337 AAGCTTGCTCTGCAAAAGGCCAAAGAGTGGCTGAAAGTCAGCCCCATGTCGCCGGAAC 2396  
 QY 987 LeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhePhe 1006  
 Db 2397 ATCTCATCGCGCCAGGACAGCAAGTCTCGGCCAAGCGCGCTCGGTGTGGGAGCAGCGG 2456  
 QY 1007 SerProSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGly 1026  
 Db 2457 GCCAGCAGCTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGGCGCTGTACAGCGAGATG 2516  
 QY 1027 Glu-----HisProGluLeuArgLys 1033  
 Db 2517 GACCCCGAGGAGCGGTGCGCTTCGCCACTACGCCCCACCTGCGGCCGACATGAAGACG 2576  
 QY 1034 SerLeuLeuProProLeuIleIleHisThr-AlaAlaThrProMetSerLeuPro----- 1051  
 Db 2577 CACCTGGACCGCGCGCTGGTGGAGCTGGGCCCGGACGCGCGCGCGCGCGCGTGGGA 2636  
 QY 1052 -----LysSerThrSe 1055  
 Db 2637 GGCAAGCCCGACCTGAGGCTGCGGAGGCCCGCCGAGGCGCTCGACCTCCGCGCAGGCAC 2696  
 QY 1055 rThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSer----- 1071  
 Db 2697 CACCGGACCGCGACAAGGACAAGACCCCGCGCGCGGGGACCCAGGACCGGACGAGGCC 2756  
 QY 1072 -----SerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProPr 1087



Db 2757 CCGAAGCGGAGAGCGGGAGCCCGGTGCCCCGGGAGGAGCGCGCGCGCCGACCGCAGC 2816  
Qy 1087 oSerAlaArg-----SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105  
Db 2817 CACAGCAAGGAGCGCGCGGGGCCCCCGGAGCGCGGAGCGAGCGCGCGCCGAGCCAGGC 2876  
Qy 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1125  
Db 2877 CCGAGGGCGCGCGCGGCACCCAGCGCGCGCTCCC-----CGGAGGAGCGCGCGCAG 2930  
Qy 1125 rGlyGlu----- 1127  
Db 2931 CGGAGCCCCAGCCACCGCGGCACCGGCACCGGACCGAGATCCGAGCAAGGAGTGCGCGCGC 2990  
Qy 1127 ----- 1127  
Db 2991 GCCAAGGGCGAGCGCGCGCGCGGCACCGCGCGCGCCCCCGAGCGGGGCCCGGAGGCG 3050  
Qy 1128 -----ArgArgSerLeuLeuSe 1133  
Db 3051 GAGAGCGGGAGGAGCGCGCGCGCGGCACCGGCCCCCGGCACCAAGCGCGAGCCTGTCTCAC 3110  
Qy 1133 r-GlyGluGlyGln-GluSerGlnAspGluGluGluSerSerGluGluGluArgAlaSer 1152  
Db 3111 GAGGCTGTGGAGAGGAGAGACCACCGAGAGGAGGCCACCGGAGAGGAGGCTGAGATAGTG 3170  
Qy 1153 ProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPhe 1172  
Db 3171 GAAGCCGACAAAGGAGAGCTCCGGAAACCACCGCCCCCGGAGCCACACTGTGACCTG 3230  
Qy 1173 AspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySer 1192  
Db 3231 GAGACCAGTGGACTGTGACTGTGGGTCCCATGCACACACTGCCAGCACCTGTCTCCAG 3290  
Qy 1193 AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeu 1212  
Db 3291 AAGGTGGAGGAACAGCCAGAGGATGCAGACAATCAGCGGAACGTCACCTCGCATGGCGAGT 3350  
Qy 1213 ArgProAspAspPro-----ProLeuAsp 1220  
Db 3351 CAGCCCCCAGACCCGAACACTATTGTACATATCCAGTGATGTGACGGGCCCTCTTGGG 3410  
Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeu-----SerLysGlyGluArg 1235  
Db 3411 GAAGCCACGGTCTGTTCCAGTGGTAACGTGGACCTGGAAAGCAAGCAGAGGGGAAGAAG 3470  
Qy 1236 -----ValArgAlaTrpIleArgAlaArgLeuProAlaCysTyr 1248  
Db 3471 GAGGTGGAAGCGGATGACGTGATGAGAGCGGCCCCCGGCTATCGTCCCATACAGC--- 3527  
Qy 1249 LeuGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeu 1268  
Db 3528 -----TCCATGTTCTGTGTTAAGCCCCCAACCACTGTCTCCGCGCTTC 3569  
Qy 1269 CysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeu 1288  
Db 3570 TGCCACTACATCGTGACCATGAGTACTTCGAGGTGGTCAITTCGTGGTCAATCGCCTTG 3629  
Qy 1289 AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1308  
Db 3630 AGCAGCATCGCCCTGGCTGCTGAGGACCCA---GTGCGCACAGACTCGCCCCAGGAACAAC 3686  
Qy 1309 PheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLys 1328  
Db 3687 GCTCTGAATACCTGGATTACATTTTCACTGGTGTCTTTACCTTTGAGATGGTGATAAAG 3746  
Qy 1329 ValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnVal 1348  
Db 3747 ATGATCGACTTGGGACTGTGCTTCCACCTGGAGCCTATTTCGGGACTTGTGGAAACATT 3806  
Qy 1349 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetVal---Ser 1367  
Db 3807 CTGGAC-----TTCAATTGTGTGTCAGTGGCGGCCCTGTGGCGTTTGTCTTCTCA 3854

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Db 3855 GGATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCCTTCGTGTCTGCGG 3914  
Qy 1388 ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1407  
Db 3915 CCCCTCAAGACCATCAAAACGGCTGCCAAGCTCAAGGCTGTGTGTTGACTGTGTGTGAAC 3974  
Qy 1408 SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly 1427  
Db 3975 TCCCTGAAGAATGCTCTCAACATCTTGATTGTCTACATGCTCTCTCATATTTCATATTGCC 4034  
Qy 1428 IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlu----- 1444  
Db 4035 GTCATTGCGGTGCAGCTCTTCAAAGGGAAGTTTTTCTACTGCACAGATGAATCCAAAGGAG 4094  
Qy 1445 -----AspThrArgAsn-----IleThrAsnLysSerAspCysAlaGluAlaSer 1459  
Db 4095 CTGGAGAGGACTGCAGGGGTCACTATTGTTGATTATGAGAAGGAGGAAGTGAAGCTCAG 4154  
Qy 1460 TyrArg---TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478  
Db 4155 CCCAGGCACTGGAAGAATACGACTTTCACACGACAATGTCTCTGGGCTCTGCTGACG 4214  
Qy 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498  
Db 4215 CTGTTACAGTGTCCACGGGAGAGGCTGGCCCATGGTGCTGCTGAAACACATCCGTGGATGCC 4274  
Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518  
Db 4275 ACCTATGAGGAGCAGGGTCCCAAGCCCTGGGTACCCGCATGGAGCTGTCCATCTTCTACGTG 4334  
Qy 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu 1538  
Db 4335 GTCTACTTTGTGGTCTTTCCCTTCTTCTTCTCGTCAACATCTTTGTGGCTTTGATCATCATC 4394  
Qy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys 1558  
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Qy 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAla 1708  
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QY 1805 AsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeu 1824  
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QY 1921 -----AspLeuLeuThrValArgLysSerGly---- 1929  
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QY 1929 ----- 1929  
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QY 1939 spSerTyrMetCysArg-----HisGlySerThrAlaGluGlyPro-----LeuG 1954  
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QY 1954 lYHis-----ArgGlyTrpGlyLeuPro-LysAla 1963  
Db 5826 GCCACCTGGAGCAGACACAGCGGCTGTGTCTCCGAGGAGCCCGGTTTCTCTTCGACAG 5885  
QY 1964 GlnSerGlySerValLeuSer-----ValHisSerGlnProAla----- 1976  
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QY 1977 ---AspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro--- 1994

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QY 1995 -----HisSerAlaProThrTrpGlyThrIleProLysLeuProProProGly 2010  
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Db 6042 CGGTACGAGACACTGGCTGTGACGTTTCAGATGCAGAGCATAAACCCGAGGGSCCTGTAT 6101  
QY 2027 -----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAla 2043  
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Db 6493 CCT-----CATCCTCTCTCTCGGAGAAGCAGCGCTTCTACTCTCTCGGACC 6537  
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QY 2224 AlaProSerSerAspSerLysAspPro----- 2232  
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Job time : 1364 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 09:17:46 ; Search time 2503 Seconds  
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Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11815.5	99.3	7648	18	US-10-377-139-10	Sequence 10, Appl
2	11815.5	99.3	7648	18	US-10-757-262-15	Sequence 15, Appl
3	11353	95.4	8116	17	US-10-062-674-2011	Sequence 2011, Ap
4	11111	93.3	7129	10	US-09-383-894-1	Sequence 1, Appli
5	11111	93.3	7285	10	US-09-383-894-3	Sequence 3, Appli
6	10945	91.9	6942	18	US-10-377-139-7	Sequence 7, Appli
7	6315.5	53.1	3993	19	US-10-930-301-51	Sequence 51, Appl
8	5496.5	46.2	6990	18	US-10-377-139-8	Sequence 8, Appli
9	5492.5	46.1	6816	9	US-09-935-541-1	Sequence 1, Appli
10	5492.5	46.1	6816	16	US-10-425-800-1	Sequence 1, Appli
11	5484	46.1	6855	9	US-09-935-541-3	Sequence 3, Appli
12	5484	46.1	6855	16	US-10-425-800-3	Sequence 3, Appli
13	5418.5	45.5	6503	9	US-09-935-541-12	Sequence 12, Appl
14	5418.5	45.5	6503	16	US-10-425-800-12	Sequence 12, Appl
15	3959.5	33.3	5562	9	US-09-030-482B-18	Sequence 18, Appl
16	3867	32.5	6073	18	US-10-377-139-11	Sequence 11, Appl
17	1786.5	15.0	7376	13	US-10-033-026-3	Sequence 3, Appli
18	1784.5	15.0	7362	17	US-10-375-253-11	Sequence 11, Appl
19	1782.5	15.0	7364	9	US-09-954-456-1179	Sequence 1179, Ap
20	1782.5	15.0	7364	13	US-10-033-026-5	Sequence 5, Appli
21	1782.5	15.0	7364	18	US-10-736-883-31	Sequence 31, Appl
22	1782.5	15.0	7364	19	US-10-843-641A-4206	Sequence 4206, Ap
23	1778	14.9	7175	17	US-10-375-253-13	Sequence 13, Appl
24	1776	14.9	7177	13	US-10-033-026-7	Sequence 7, Appli
25	1776	14.9	7177	18	US-10-736-883-33	Sequence 33, Appl
26	1773.5	14.9	6792	17	US-10-627-370-1	Sequence 1, Appli
27	1757.5	14.8	7121	18	US-10-736-883-43	Sequence 43, Appl
28	1755.5	14.7	6984	18	US-10-736-883-37	Sequence 37, Appl
29	1752	14.7	7185	18	US-10-736-883-39	Sequence 39, Appl
30	1751.5	14.7	7173	18	US-10-736-883-41	Sequence 41, Appl
31	1751.5	14.7	9695	18	US-10-736-883-27	Sequence 27, Appl
32	1751.5	14.7	9695	19	US-10-486-706-207	Sequence 207, App
33	1738.5	14.6	7363	18	US-10-723-860-5192	Sequence 5192, Ap
34	1728.5	14.5	7011	13	US-10-033-026-9	Sequence 9, Appli
35	1728.5	14.5	7011	18	US-10-736-883-29	Sequence 29, Appl
36	1725.5	14.5	6503	18	US-10-377-139-16	Sequence 16, Appl
37	1717	14.4	6083	13	US-10-029-413A-21	Sequence 21, Appl
38	1708	14.3	7477	18	US-10-322-696-177	Sequence 177, App
39	1704	14.3	8490	15	US-10-101-510-617	Sequence 617, App
40	1693.5	14.2	7348	18	US-10-322-696-175	Sequence 175, App
41	1693	14.2	7089	17	US-10-375-253-39	Sequence 39, Appl
42	1693	14.2	7291	18	US-10-322-696-83	Sequence 83, Appl
43	1692.5	14.2	8491	17	US-10-333-191-1	Sequence 1, Appli
44	1692	14.2	9704	18	US-10-322-696-80	Sequence 80, Appl
45	1690.5	14.2	8491	17	US-10-333-191-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-10-377-139-10  
; Sequence 10, Application US/10377139  
; Publication No. US20040175761A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKinnon, Roderick  
; APPLICANT: Jiang, Youxing  
; APPLICANT: Lee MacKinnon, Alice  
; APPLICANT: Ruta, Vanessa  
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins  
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9  
; CURRENT APPLICATION NUMBER: US/10/377,139  
; CURRENT FILING DATE: 2003-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 7648  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-377-139-10

Alignment Scores:  
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 Percent Similarity: 95.29% Conservative: 1  
 Best Local Similarity: 95.25% Mismatches: 1  
 Query Match: 99.26% Indels: 111  
 DB: 18 Gaps: 2

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Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920

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Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940

Db 2761 ACCCAGGAGACTGGAACAAAGTCCCTACAAATGGTATGGCTCCACGTGCTCCTGGCG 2820

Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 960

Db 2821 GCCCTTTATTTCATTTGCCCTCATGACCTTCGGCAACTACGTCTCTTCAAATTTGTGGTC 2880

Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980

Db 2881 GCCATTCTGGTGGAGGGCTTCCAGCGGAGGAAATCAGCAAAACGGGAAGATGCGAGTGA 2940

Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000

Db 2941 CAGTTAAGCTGTATTTCAGCTGCCTGTCCGACTCCAGGGGGAGATGCCAACAAAGTCCGAA 3000

Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020

Db 3001 TCAGAGCCCCGATTCTTCTCACCCAGCCTGGATGGTGTATGGGGACAGGAAGTGTCTG 3060

Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040

Db 3061 GCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCCTGTGTCGCCCTCTCATC 3120

Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060

Db 3121 ATCCACACGGCCGCCACACCCATGTGCTGCCCAAGAGCACAGACACGGGCCTGGCGAG 3180

Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080

Db 3181 GCGTGGGCCCTGCGTCGCGCCGACACAGCAGCAGCGGGTCCGAGAGCCTGGGCGGCC 3240

Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100

Db 3241 CACGAGATGAAGTCACCGCCACGCGCCGCGAGCTCTCCGCACAGCCCCCTGGAGCGCTGCA 3300

Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120

Db 3301 AGCAGCTGGACCAGCAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAG 3360

Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140

Db 3361 CGGAGAAGCCCAAGTGGAGAGCGCGGTCCCTGTTGTTCGGAGAAGGCCAGGAGCCAG 3420

Qy 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160

Db 3421 GATGAAGAGAGAGCTCAGAAGAGGAGCGGGCCAGCCTCGGGCAGTGACCATCGCCAC 3480

Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180

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Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200

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Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220

Db 3601 GGCAAGTCGGCTTCAGGGCGCCTGGCCCGGCCCTGCGGCTGATGACCCCCCCTGGAT 3660

Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyArgValArgAlaTrpIle 1240

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Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260

Db 3721 CGAGCCGACTCCCTGCCTGCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCT 3780

Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280

Db 3781 CCTCAGTCCAGGTTCCGCCTCTCTGTGTACCCGGATCATCACCCACAAGATGTTTCGACCAC 3840

Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300

Db 3841 GTGGTCTTGTTCATCATCTTCTTAACGTGCATCACCATCGCCATGGAGCGCCCCAAAATT 3900

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Db 3961 TTTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTCGGGGAGCAGGCG 4020

Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360

Db 4021 TACCTGCGGAGCAGTTGGAACGTGCTGGACGGGCTGTGGTGTCTCATCTCCGTCTATCGAC 4080

Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380

Db 4081 ATTCTGGTGTCCATGGTCTCTGACAGCGGCCAACCAAGATCTGGGCATGCTGAGGGTGTG 4140

Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400

Db 4141 CGGCTGCTGCGGACCCCTGCGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTG 4200

1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420  
14201 GTGGGAGACGCTGATGCTCTCACTGAAACCCATCGCAACATTTGTAGTCACTGCTGT 4260  
1421 AlaPhePheIleIlePheGlyIleLeuGlyValClnLeuPheLysGlyLysPheVal 1440  
14261 GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4320  
1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
14321 TGCCAGGCGCAGGATACCAGGAACATCACCAATAAATCGACTGTGCCGAGGCCAGTTAC 4380  
1461 ArgTirValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
14381 CGGTGGTCCGCGCACAAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGTGATGTCCTGTTT 4440  
1481 ValLeuAlaSerLysAspGlyTirValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
1441 GTTTTGGCCTCAAGGATGTTTGGGTGGACATCATGTACGATGGCTGGTGGATGCTGGGC 4500  
1501 ValAspGlnGlnProIleMetAsnHisAsnProTirMetLeuLeuTyrPheIleSerPhe 1520  
14501 GTGGACCAGCAGCCCATCATGAACCAACCCCTGGATGCTGTACTTTCATCTCGTTT 4560  
1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540  
14561 CTGCTCATTTGGCCTCTTTGTCTGAACATGTTTGTGGTGTGGTGGTGGAGAACTTC 4620  
1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeu 1560  
14621 CACAAGTGTGGCAGCACAGGAGGAGAGGAGGCCCGCGGGGGAGGAGAGAGGCCTA 4680  
1561 ArgArgLeuGluLysLysArgArg----- 1568  
14681 CGAAGACTGGAGAAAAGAGAGGAATCTAATGCTGGACGATGTAATTGCTTCCGCGAGC 4740  
1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582  
14741 TCAGCCAGCGCTGCGTCAGAGGCCAGTGCAAACCTTACTACTCGACTACTCCCGCTTC 4800  
1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602  
14801 CGGCTCTCGTCCACCACCTTGTGCACCCACTACCTGGACCTCTTCATCACAGGTGTC 4860  
1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622  
14861 ATCGGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACCGAGCCAGCCCATCTGGAT 4920  
1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642  
14921 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTTCATCTTGTCTGGAGTCAGTTTTC 4980  
1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTirAsnGlnLeuAspLeu 1662  
14981 AAACTTGTGGCCTTGGTTTCCGTGGTCTTCCAGGACAGGTGGAAACCAGCTGGACCTG 5040  
1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsnAlaSer 1682  
15041 GCCATTGTGCTGCTGTCCATCATGGGCATCACGCTGGAGGAATCGAGGTCAACGCTCG 5100  
1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702  
15101 CTGCCCATCAACCCACCATCATCCGCATCATGAGGTGCTGCGCATTTGCCGAGTGTG 5160  
1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722  
15161 AAGCTGCTGAAGATGGCTGTGGGATCGGGCGCTGCTGGACACGGTGTGAGGCCCTG 5220  
1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeu 1742  
15221 CCCAGGTGGGAAACCTGGGACTTCTCTTCATGTTGTTTTCATCTTTGACGCTCTG 5280  
1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762

5281 GGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGCGCTGGGC 5340  
1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782  
5341 CGTCATGCCACCTTTTCGGAACCTTTGGCATGGCCTTCCTAACCCCTCTCCGAGTCTCCACA 5400  
1783 GlyAspAsnTirAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802  
5401 GGTGACAATTGGAATGGCATTTATGAAGGACACCCCTCCGGGACTGTGACGAGGTCCACC 5460  
1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822  
5461 TGTCTACAACACCGTCACTTCGCCTATCTACTTGTGTCTCTCGTGTGACGGCCAGTTT 5520  
1823 ValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842  
5521 GTGCTAGTCAACGTTGGTGTATCGCCGTGTGTATGAAGCACCTGGAGGAGAGCAACAAGGAG 5580  
1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862  
5581 GCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTCAGCCCC 5640  
1863 GlnProHisSerProLeuGlySerProPheLeuTirProGlyValGluGlyProAspSer 1882  
5641 CAGCCCCACTCGCCACTGGGCGAGCCCTTCTCTGGCTGGGTGAGGGCCCCGACAGC 5700  
1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902  
5701 CCCGACAGCCCCAAGCCTGGGCTCTGCACCCAGCGGCCACCGAGATCAGCCTCCCAC 5760  
1903 PheSerLeuGluHisProThr----- 1909  
5761 TTTTCCCTGGAGCACCCACGACAGCAGCTGTTTGACACCATATCCCTGCTGATCCAG 5820  
1909 ----- 1909  
5821 GGCTCCCTGGAGTGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCCAGGGGCCAGCCCC 5880  
1909 ----- 1909  
5881 TCTGCCCTTCCCTTCTGCCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAG 5940  
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5941 ATGGAGGCTCTGTCTCTGACGTGACAGATGTGTCTGAACCGTCTGTCTCTAGCTCTG 6000  
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6001 ACGGTGACTCTTTGCTGATGACATGCACACACTCTTACTTACTGCTCTGGAGAGCAAT 6060  
1910 MetGlnProHisProThrGluLeuProGlyProAspLeuThrValArgLysSerGly 1929  
6061 ATGACGCCCCACCCACGAGCTGCCAGGACCCAGACTTACTGACTGTGCGGAAGTCTGGG 6120  
1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949  
6121 GTCAGCGCAACGCACTCTCTGCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCC 6180  
1950 GluGlyProLeuGlyHisArgGlyTirPglyLeuProLysAlaGlnSerGlySerValLeu 1969  
6181 GAGGGGCCCTGGGACACAGGGCTGGGGCTCCCAAGCTCAGTCAGGCTCCGTCTTG 6240  
1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989  
6241 TCCGTTCACTCCAGCCAGCAGATACCAGCTACATCTGTCAGCTTCCCAAGATGCACCT 6300  
1990 HisLeuLeuGlnProHisSerAlaProThrTirPglyThrIleProLysLeuProProPro 2009  
6301 CATCTGCTCCAGCCCCACAGCGGCCCAACCTGGGGCAACATCCCCAACTGCCCCCCACCA 6360  
2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029

Db 6361 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGCGGCCAGGACGCAATAAGGACTGACTCC 6420

Qy 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049

Db 6421 TTGGACGTTACGGCTCTGGCAGCCGCGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCC 6480

Qy 2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069

Db 6481 CCGCCCTGGCCGGCCCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCAC 6540

Qy 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089

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Qy 2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109

Db 6601 GAACCCAACTGGGCAAGGGCCCTCCAGAGACCAGAGCAGGCTAGAGTTGGACAGGAG 6660

Qy 2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlnGluGluProProSerPro 2129

Db 6661 CTGAGCTGGATTTCAGGAGACCTCTGCCCCCTGGCGGCCAGGAGCCCCCATCCCCA 6720

Qy 2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149

Db 6721 CGGACCTGAAGAAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCTACGTCC 6780

Qy 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169

Db 6781 TGGCTGGATGACGAGGAGACACTTATCGCCGTCAGCTGCCTGGACAGCGGCTCCAA 6840

Qy 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer 2189

Db 6841 CCCACCTGGGCACAGACCCCTCTAACTTGGGGCCAGCCTCTTGGGGGCTGGGAGC 6900

Qy 2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209

Db 6901 CGGCCCAAGAAAAAATCAGCCCGCTAGTATCACCATAGACCCCGGAGAGCAAGGT 6960

Qy 2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229

Db 6961 CCTCGGACCCCGCCAGCCCTGGTATCTGCTCCGAGGAGGGCTCCGTCCAGCGACTCC 7020

Qy 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249

Db 7021 AAGGATCCCTTGGCCTCTGGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAAA 7080

Qy 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266

Db 7081 GATGTGCTGAGTCTCTCCGGTTTATCCTCTGACCCAGCAGACCTGGACCCC 7131

RESULT 2

US-10-757-262-15

; Sequence 15, Application US/10757262

; Publication No. US20040197825A1

; GENERAL INFORMATION:

; APPLICANT: Karicheti, Venkateswarlu

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Eliasof, Scott D.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,

; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,

; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,

; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,

; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,

; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,

; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,

; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

; TITLE OF INVENTION: 55053

; FILE REFERENCE: MPI03-007P1RNMNMIM

; CURRENT APPLICATION NUMBER: US/10/757,262

; CURRENT FILING DATE: 2004-01-14

; PRIOR APPLICATION NUMBER: US 60/440,318

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/444,783

; PRIOR FILING DATE: 2003-02-04

; PRIOR APPLICATION NUMBER: US 60/457,901

; PRIOR FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: US 60/468,775

; PRIOR FILING DATE: 2003-05-08

; PRIOR APPLICATION NUMBER: US 60/471,614

; PRIOR FILING DATE: 2003-05-19

; PRIOR APPLICATION NUMBER: US 60/478,742

; PRIOR FILING DATE: 2003-06-16

; PRIOR APPLICATION NUMBER: US 60/488,529

; PRIOR FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: US 60/491,156

; PRIOR FILING DATE: 2003-07-30

; PRIOR APPLICATION NUMBER: US 60/499,594

; PRIOR FILING DATE: 2003-09-02

; PRIOR APPLICATION NUMBER: US 60/506,332

; PRIOR FILING DATE: 2003-09-26

; NUMBER OF SEQ ID NOS: 136

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 7648

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(7134)

US-10-757-262-15

Alignment Scores:

Pred. No.: 0 Length: 7648

Score: 11815.50 Matches: 2264

Percent Similarity: 95.29% Conservative: 1

Best Local Similarity: 95.25% Mismatches: 1

Query Match: 99.26% Indels: 111

DB: 18 Gaps: 2

US-09-611-257A-37 (1-2266) x US-10-757-262-15 (1-7648)

Qy 1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20

Db 1 ATGGACGAGGAGGAGTGGAGCGGGCCGAGGAGTCGGGACAGCCCCCGGAGCTTCATG 60

Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40

Db 61 CGGCTCAACGACCTGTCTGGGGCCCGGGGCGGGCCGGGTCAGCAGAAAAAGGAC 120

Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60

Db 121 CCGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCCGCGCTGGCCCGGTGTT 180

Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80

Db 181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGGTGTCTCCGACCGTCTGTAAAC 240

Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100

Db 241 CCCTGGTTTGAGCGCATCAGCATGTGGTCAATCCTTCTCAACTGCGTGACCCCTGGGCATG 300

Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120

Db 301 TTCCGGCCATCGGAGGACATCGCCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCCTT 360

Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly 140

Db 361 GATGACTTCATCTTGCCTTCTTTGCGGTGAGATGGTGTGAAGATGGTGGCCTTGGGC 420

Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160

Db 421 ATCTTTGGAAAAAAGTGTACCTGGGAGACACTTGAACCCGGCTGACTTTTTCATCGTC 480

Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180

Db 481 ATCGAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACGTGCTCAGCTTCTCAGCTGTCTCAGG 540  
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTT 600  
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCACGTTGCTGTGATACGCTGCCCATGCTGGCAACGCTCTGCTGCTTCTTCTTC 660  
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCTTCTTCATCTTCGGCATCGTCCGCTCCAGCTGTGGCAGGGCTGCTTTCGGAACCGA 720  
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
Db 721 TGCTTCTTACCTGAGAAATTTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAG 780  
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 781 ACAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCACGCGAGAACGCGCATGCGG 840  
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCCTGCAGAACGCTGCCACCGCTGCGGGGACCGGGGGCGGTGGCCCCACCTTGGCGTCTG 900  
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 901 GACTATGAGGCCTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAAACCGTACTAC 960  
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
Db 961 ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCACTTTGACAACTT 1020  
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1021 GGCTATGCTGGATCGCATCTTCCAGGTATCACCGTGCAGCGTGGAGGGCTGGTGCACATCATG 1080  
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
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Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1141 GTGGGTCTCTTTCATGATCAACCTGTGCTGGTGGTGTGATGTCACGCGAGTTCTCAGAG 1200  
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAGCAGCGGAAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTCTCTGTCCAAAGCC 1260  
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
Db 1261 AGCACCTTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGAGCTGCTCAAGTACCTG 1320  
Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1321 GTGTACATCTCTGTAAGGCAGCCCGCAGGCTGGTCTCAGGTCTCTCGGGCAGCAGGTGTG 1380  
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGGTTGGGTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC 1440  
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 500  
Db 1441 AGCTGCTCTCGCTCCCACCGCGCGCTATCCGTCCACCACTGGTGCACCCACCACCAC 1500  
Qy 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CATCACCACTTACCACTTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCCGGAG 1560  
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
Db 1561 ATCCAGGACAGGGATGCCAATGGGTCCGCGAGGCTCATGTGCCACCACCCCTCGACGCCT 1620

Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db 1621 GCCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1680  
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
Db 1681 TGCCACTTAGAGCCAGTCCCGCTGCCAGGCGCCCCCTCCAGGTCCCCCATCTGAGGCATCC 1740  
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600  
Db 1741 GGCAGGACTGTGGGCAGCGGGGAAGGTGTATCCCAACCGTGACACAGCCCTCCACCGGAG 1800  
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
Db 1801 ACGCTGAAGGAGAAGGCACCTAGTAGAGTGGTGCCTGCCAGTCTGGGCCCCCAACCTCACC 1860  
Qy 621 SerLeuAsnIleProProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db 1861 AGCCTCAACATCCCAACCGGGCCCTTACAGCTCCATGCACAAGCTGTGGAGACACAGAGT 1920  
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACAGGTGCCTGCCAAAGCTCTTGCAGATCTCCAGCCCTTGTCTTGAAGCAGACAGTGA 1980  
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
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Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCGGACCGTGAATGCCTGACTCAGACAGCAGGAGGAGTTTATGAGTTTACACAGGATGCC 2100  
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Db 2101 CAGCACAGCAGCCTCCGGGACCCCCACAGCGGGCGGCAACGGAGCTTGGGCCCCAGATGA 2160  
Qy 721 GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleVal 740  
Db 2161 GAGCCAGCTCTGTGTGGCCTTCTGGAGGGTAAATCTGTGACACCTTCCGAAAGATTGTG 2220  
Qy 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
Db 2221 GACAGCAAGTACTTTGGCCGGGAATCATGATGCCCATCTCTGGTCAACACACTCAGCATG 2280  
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Db 2281 GGCAATCGAATACCAACGAGCAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340  
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800  
Db 2341 GTCTTACACAGCCTCTTTGCCCCGAGATGCTGTGAAGCTGCTTGTGTATGTTGCCCTTT 2400  
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820  
Db 2401 GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTCTATTGTGTCATCAGCGTGTGG 2460  
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
Db 2461 GAGATCGTGGGCAGCAGGGGGGGCGCTGTCCGGTGTGCGGACCTTCCGCTGTATGCGT 2520  
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
Db 2521 GTGCTGAAGCTGGTGGCTTCTCTGCGGGCGCTGCAGCGCAGCTGGTGGTCTCATGAAG 2580  
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
Db 2581 ACCATGGACACGTGGCCACCTTCTGCATGCTGTCTTATGCTCTTTCATCTTCTTCTCAGC 2640  
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900  
Db 2641 ATCTGGGCATGCATCTCTTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGGACACCCCTG 2700



QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrrAlaIleValThrValPheGlnIleLeu 920  
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QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940  
DB 2761 ACCAGGAGGACTGGAACAAAGTCTTACAATGGTATGGCTCCACGTCTCTCTGGCG 2820  
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
DB 2821 GCCCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTTGGTGC 2880  
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980  
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QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000  
DB 2941 CAGTTAAGCTGTATTTCAGCTGCCTGTCGACTCCAGGGGGAGATGCCAACAGTCCGAA 3000  
QY 1001 SerGluProAspPheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020  
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QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040  
DB 3061 GCCTTGGTGTCTCTGGAGAGCACCCGGAGCTGCGGAAGAGCTGTGCCCTCTCATC 3120  
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060  
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QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
DB 3181 GCGCTGGGCCCTGCGTCCGCCCGCACAGCAGCAGCGGGTCCGAGAGCTGGGGCGGCC 3240  
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
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QY 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
DB 3301 AGCAGCTGGACACGAGCGCTCCAGCGGAAACAGCCTCGGCGGTGCACCCAGCCTGAAG 3360  
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln 1140  
DB 3361 CGGAGAAAGCCCAAGTGGAGAGCGGCGTCCCTGTTGTGGGAGAAGGCCAGGAGCCAG 3420  
QY 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
DB 3421 GATGAAGAGGAGAGCTCAGAGAGGAGCGGGCCAGCCCTGCGGCGAGTGACCATCGCCAC 3480  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
DB 3481 AGGGGGTCCCTGGAGCGGAGGCCCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3540  
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
DB 3541 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCCAGGACTGCAAT 3600  
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
DB 3601 GGCAAGTCGGCTTCAGGGCGCCTGGCCGGGCCCTGGCGGCTGTATGACCCCCACTGGAT 3660  
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
DB 3661 GGGGATGACGCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGGTCCGCGCGTGGATC 3720  
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
DB 3721 CGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCTCTGCTCAGCCTACATCTCCCT 3780  
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280

DB 3781 CCTCAGTCCAGGTTCCGCCCTCCTGTGTACCGGATCATCACCAAGATGTTTCGACCAC 3840  
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
DB 3841 GTGGTCTTGTTCATCATCTTCTTAACATGCATCACCATCGCCATGGAGCGCCCCAAAT 3900  
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
DB 3901 GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAAATACATCTTCACCGCAGTC 3960  
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340  
DB 3961 TTTCTGGCTGAATGACAGTGAAGTGGTGGCACTGGGCTGTCTTCGGGAGCAGGCG 4020  
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
DB 4021 TACCTGGGAGCAGTTGGAACGTGCTGGACGGGCTGTTGGTGTCTCATCTCCGTCAACG 4080  
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380  
DB 4081 ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCTGGGCATGCTGAGGGTGTG 4140  
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400  
DB 4141 CGGCTGTCTGGGACCTCGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGTGAAGCTG 4200  
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420  
DB 4201 GTGGTGGAGACGCTGATGTCTCTCACTGAACCCCATCGGCAACATTTAGTTCATCTGTGT 4260  
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
DB 4261 GCCTTCTTCATCATTTTTCGGCATCTTGGGGTGCAGCTCTTCAAGGGAAGTTTTTCGTG 4320  
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
DB 4321 TGCCAGGCGAGGATACCAAGAACATCAACAATAATCGGACTGTGCCAGGCCAGTTAC 4380  
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
DB 4381 CGGTGGTCCGGCACAAAGTACAACTTTGACAACCTTGCCAGGCCCTGATGTCCCTGTTC 4440  
QY 1481 ValLeuAlaSerLysAspGlyTrrValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
DB 4441 GTTTTGGCCTCCAAGGATGTTTGGTGGACATCATGTACGATGGGTGGATGCTGTGGGC 4500  
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520  
DB 4501 GTGGACCAAGCAGCCCATCATGAACCAACACCCCTGGATGTGTCTTTCATCTCTGTTT 4560  
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540  
DB 4561 CTGCTCATTTGTGGCTTCTTTTGTCTGAACATGTTTGTGGGTGTGGTGGAGAACTTC 4620  
QY 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu 1560  
DB 4621 CACAAGTGTCCGCGAGCACCCAGGAGGAAGAGGAGGCCCGCGGCGGAGGAGAGCGCCTA 4680  
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568  
DB 4681 CGAAGACTGGAGAAAAAGAGAAAGGAATCTAATGTGGACGATGTAATTGCTTCCGGCAGC 4740  
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582  
DB 4741 TCAGCCAGCGCTGCGTCAGAAGCCAGTGCACAACTTACTACTCCGACTACTCCCGCTTC 4800  
QY 1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602  
DB 4801 CGGCTCTCTGCTCCACCATTTGTGACCAAGCCACTACCTGGACCTCTTTCATCACAGGTGT 4860  
QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622

Db 4861 ATCGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACCAGCAGCCCCAGATTCTGGAT 4920

Qy 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642

Db 4921 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTTGTCTGGAGTCAGTTTTC 4980

Qy 1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeu 1662

Db 4981 AAACCTTGCGCCCTTGGTTTCGTCGGTCTTCCAGGACAGGTGGAACAGCTGGACCTG 5040

Qy 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682

Db 5041 GCCATTGTGCTGTCTCCATCATATGGGCATCAGCTGGAGGAATCGAGGTCAACGCCCTCG 5100

Qy 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702

Db 5101 CTGCCCATCAACCCACCACCATCATCCGCATCATAGGGTGTGCGCAATGCCCGAGTCTG 5160

Qy 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722

Db 5161 AAGCTGCTGAAGATGGCTGTGGGCATGCGGCCTGCTGTGACACCGTGATGAGGCCCTG 5220

Qy 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742

Db 5221 CCCAGGTGGGAACCTGGGACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5280

Qy 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762

Db 5281 GCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGC 5340

Qy 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782

Db 5341 CGTCATGCCACCTTTTCGAACTTTGGCATGGCTTCTTAACCTCTTCCAGTCTCCACA 5400

Qy 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802

Db 5401 GGTGACAAATTGGAATGGCATATGAGGACACCTCCGGGACTGTGACCAAGGAGTCCACC 5460

Qy 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822

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Qy 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842

Db 5521 GTGCTAGTCAACGTGTGTATCGCCGTGCTGTATGAGCACCTGGAGGAGCAACAAGGAG 5580

Qy 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862

Db 5581 GCCAAGGAGGCGCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTCAGCCCC 5640

Qy 1863 GlnProHisSerProLeuGlySerPropheLeuTrpProGlyValGluGlyProAspSer 1882

Db 5641 CAGCCCCACTCGCCACTGGGCAGCCCTTCTCTGGCTGGGTGAGGSCCCCGACAGC 5700

Qy 1883 ProAspSerProLysProGlyAlaLeuHisProAlaHisAlaArgSerAlaSerHis 1902

Db 5701 CCCGACAGCCCCAAGCCTGGGGCTTGCACCCAGCGGCCACCGGAGATCAGCCTCCCAC 5760

Qy 1903 PheSerLeuGluHisProThr----- 1909

Db 5761 TTTTCCCTGGAGCACCCCAAGCAGGAGCTGTTTGACACCATATCCCTGCTGATCCAG 5820

Qy 1909 ----- 1909

Db 5821 GGTCCCTGGAGTGGGAGCTGAAGCTGATGGACAGCTGGGAGGCCCGAGGGGCCAGCCCC 5880

Qy 1909 ----- 1909

Db 5881 TCTGCCTTCCCTTCTTGCCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAG 5940

Qy 1909 ----- 1909

Db 5941 ATGGAGGCTCTGTCTCTGACGTGAGAGATTGTGTCTGAACCGTCTGCTCTCTAGCTCTG 6000

Qy 1909 ----- 1909

Db 6001 ACGGATGACTTTTGCCTGATGACATGCACACACTCTTACTAGTGCCTGGAGAGCAAT 6060

Qy 1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929

Db 6061 ATGACGCCCCACCCACGGAGCTGCCAGGACAGACTTACTGACTGTGCGGAAGTCTGGG 6120

Qy 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949

Db 6121 GTCAGCCGAACGCACCTCTCTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCC 6180

Qy 1950 GluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeu 1969

Db 6181 GAGGGGCCCTGGGACACAGGGGCTGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCCTTG 6240

Qy 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989

Db 6241 TCCGTTCACTCCAGCCAGCAGATACAGCTACATCTCTGCAGCTTCCCAAGATGCACCT 6300

Qy 1990 HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro 2009

Db 6301 CATCTGCTCCAGCCCCACAGCGCCCAACCTGGGGCACCATTCCCCAACTGCCCCCACA 6360

Qy 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029

Db 6361 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGGGCGCCAGGCAATTAAGGACTGACTCC 6420

Qy 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049

Db 6421 TTGGACGTTTCCGGTCTGGGCAGCCCGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCC 6480

Qy 2050 ProProLeuAlaArgAlaTyrSerPheThrGlyGlnSerSerThrGlnAlaGlnGlnHis 2069

Db 6481 CCGCCCCCTGGCCCGGCTACTCTTCTTGGGGCCAGTCAAGTACCCAGGCACAGCAGCAC 6540

Qy 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089

Db 6541 TCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGGCCAGGCCCA 6600

Qy 2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerSerLeuGluLeuAspThrGlu 2109

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Qy 2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerPro 2129

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Qy 2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149

Db 6721 CGGACCTGAAGAAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCGGGCCTACGTCC 6780

Qy 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169

Db 6781 TGGCTGGATGAGCAGAGGAGACACTCTATCGCCCGTCAGCTGCCCTGGACAGCGGCTCCCA 6840

Qy 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySer 2189

Db 6841 CCCACCTGGGCACAGACCCCTCTAACTTGGGGGCCAGCCCTCTTGGGGGCCCTGGGAGC 6900

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Qy 2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229

Db 6961 CCTCGACCCCGCCAGCCCTGGTATCTGCTCCGAGAGGGGCTCCGTCCAGGACTCC 7020

Qy 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249

Db 7021 AAGGATCCCTTGGCTCTGGCCCCCTGACAGCATGGCTGCTCGCCCTCCCCAAAGAAA 7080



Db 1973 ATCCAGGACAGGATGCCAATGGTCCCGCGGCTCATGTGCCACCAACCCCTCGACGCCT 2032  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db 2033 GCCCTCTCCGGGGCCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2092  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580  
Db 2093 TGCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCCATCTGAGGCATCC 2152  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
Db 2153 GGCAGGACTGTGGGCAGCGGGAAGGTGTATCCACCGTGCACACCGCCCTCCACCGGAG 2212  
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
Db 2213 ACGCTGAAGGAAGGCACTAGTAGAGGTGGTGCACGTCTGGGCCCCCAACCCCTCACC 2272  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
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QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
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QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
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QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2453 GCCGACCGTGAAATGCCTGACTCAGACAGCGAGGCAGTTTATGAGTTCACACAGGATGCC 2512  
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QY 740 lAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMe 760  
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QY 760 tGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIl 780  
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QY 780 eValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPh 800  
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QY 800 eGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTr 820  
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QY 820 pGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetAr 840  
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QY 840 gValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLy 860  
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QY 860 sThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSe 880  
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QY 880 rIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLe 900

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Db 3233 GGCCCTTTTATTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTGTGCTGT 3292  
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QY 980 yGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGl 1000  
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QY 1000 uSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLe 1020  
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QY 1020 uAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIl 1040  
Db 3404 GGCCTTGGTGTCTCCCTGGGAGAGCACCCCGAGCTGCGGAAGAGCCTGTGCCCTCTCAT 3463  
QY 1040 eIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGl 1060  
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QY 1060 uAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAl 1080  
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QY 1080 aHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAl 1100  
Db 3584 CCACGAGATGAAGTCACCGCCAGCGCCGCGAGCTCTCCGACAGCCCTGGAGCGCTGC 3643  
QY 1100 aSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLy 1120  
Db 3644 AAGCAGCTGGACCCAGCAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAA 3703  
QY 1120 sArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluSerGl 1140  
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QY 1140 nAspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHi 1160  
Db 3764 GGATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCTCGGGCAGTGACCATCGCCA 3823  
QY 1160 sArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVa 1180  
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QY 1180 lProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAs 1200  
Db 3884 GCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCGAGACTGCAA 3943  
QY 1200 nglyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAs 1220  
Db 3944 TGGCAAGTCGGCTTCAGGGCGCTGGCCCGGCCCTGGCCCGGCCCTGATGACCCCCACTGGA 4003  
QY 1220 pGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIl 1240  
Db 4004 TGGGGATGACGCGGATGACGAGGGCAACCTGAGCAAAAGGGAAACGGGTCCGCGCGTGGAT 4063  
QY 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260  
Db 4064 CCGAGCCCGACTCCCTGCCTGCCTGCCTCGAGCGAGACTCCTGGTCACTACATCTTCCC 4123



Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280  
Db 4124 TCCTCAGTCCAGGTTCCGCCTCCTGTGTACCGGATCATCACCAAGATGTTTCGACCA 4183  
Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIl 1300  
Db 4184 CGTGGTCCTTGTTCATCATCTTCTCTTAAGTGCATCACCATCGCCATGGAGCGCCCAAAAT 4243  
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320  
Db 4244 TGACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATATCATCTTACCGCAGT 4303  
Qy 1320 lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAl 1340  
Db 4304 CTTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTCGGGGAGCAGGC 4363  
Qy 1340 aTyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360  
Db 4364 GTACCTGCGGAGCAGTTGGAACGTGTGTGACGGGCTGTTGGTGTCTCATCTCCGTATCGA 4423  
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380  
Db 4424 CATTTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCTTGGGCATGCTGAGGGTGCT 4483  
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400  
Db 4484 GCGGCTGCTGCGGACCCTGCGCCCGCTCAGGGTGATCAGCCGGGCGCAGGGGCTGAAGCT 4543  
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420  
Db 4544 GGTGGTGGAGACGCTGATGTCTCTACTGAAACCCATCGGCAACATTTAGTTCATCTCTG 4603  
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440  
Db 4604 TGCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGGGAAGTTTTCGT 4663  
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460  
Db 4664 GTGCCAGGGCGGAGGATACCAGGAACATCACCAATAATCGGACTGTGCCGAGGCCAGTTA 4723  
Qy 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuph 1480  
Db 4724 CCGTGGGTCCGGCACAAAGTACAACTTTGACAAACCTTTGGCCAGGCCCTGATGTCCCTGTT 4783  
Qy 1480 eValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGl 1500  
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Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520  
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Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540  
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Qy 1540 eHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGlu-GluLysArgL 1560  
Db 4964 CCACAAGTGTCCGAGCAGCACAGGAGGAAGAGGAGGCCCGCGCGGGGAGCCAGAAGCGCC 5023  
Qy 1560 euArgArgLeuGluLysLysArgArg-----LysAlaGlnCysL 1573  
Db 5024 TACGAAGACTGGCGAAAAAGAGACCGGACGTAGGAGAACGAGATGGCTGAAGCCCACTGCA 5083  
Qy 1573 ySProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCysThrSerH 1593  
Db 5084 AACCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTCGTCCACCACTTGTGCACCAACC 5143  
Qy 1593 iSyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetG 1613  
Db 5144 ACTACCTGGACCTCTTTCATCACAGGTGTCTCGGGCTGAACGTGGTGCACCATGGCCATGG 5203

Qy 1613 luHistyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheP 1633  
Db 5204 AGCACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGAAGATACATCTTCA 5263  
Qy 1633 hrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPheP 1653  
Db 5264 CTGTCTATCTTGTCTTGGAGTCAAGTTTCAAACCTTGTGGCCTTGGTTTCCGTCGGTTCT 5323  
Qy 1653 heGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleT 1673  
Db 5324 TCCAGGACAGGTGGAACCCAGCTGGACCTGGCCATTGTGTGCTGTCCATCATGGGCATCA 5383  
Qy 1673 hrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleM 1693  
Db 5384 CGCTGGAGGAAATCGAGGTCAACGCTCGCTCGCTGCCCATCAACCCACCATCATCCGCATCA 5443  
Qy 1693 etArgValLeuArgIleAlaArgValLeuLysLeuLysLeuLysMetAlaValGlyMetArgA 1713  
Db 5444 TGAGGGTGTGCGCATTTGCCCGAGTGTGAAGCTGTGAAGATGGCTGTGGGCATCGGG 5503  
Qy 1713 laLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheM 1733  
Db 5504 CGCTGTGACACGGTGATGCAGGCCCTGCCCAGGTGGGGAACCTTGGACTTCTCTTCA 5563  
Qy 1733 etLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysA 1753  
Db 5564 TGTTGTTGTTTTCATCTTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTTGGAGTGTG 5623  
Qy 1753 spGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetA 1773  
Db 5624 ACAGACACACCCCTGTGAGGGCTGGGCCGTGATGCCACCTTTCCGAACCTTTGGCATGG 5683  
Qy 1773 laPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspT 1793  
Db 5684 CCTTCTTAACCCCTCTTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATATTGAAGGACA 5743  
Qy 1793 hrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----IleSerP 1810  
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Qy 1810 roIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleA 1830  
Db 5804 CGCTGTACTTGTGAGCTTCGTGCTCACCGCGCAGTTTCGTGCTCATCAACGTGTGTGTG 5863  
Qy 1830 laValLeuMetLysHisLeuGluLeuSerAsnLysGluAlaLysGluAlaGluLeuG 1850  
Db 5864 CTGTGCTCATGAAGCACCTTGGACGACAGCAACAAGGAGGCGCAGGAGCGCCGAGATGG 5923  
Qy 1850 luAlaGluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProLeuGlyS 1870  
Db 5924 ATGCCGAGCTCGAGCTGGAGATGAAGACCCCTCAGCCCCCAGCCCCACTCGCCACTGGGCA 5983  
Qy 1870 erProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyA 1890  
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Qy 1890 laLeuHisProAlaAlaHisAlaArg-SerAlaSerHisPheSerLeuGluHisProThr 1909  
Db 6044 CTCTGCACCCAGCGGCCACCGCAGGATCAGCCTCCCACTTTTCCCTGGAGCACCCCAACG 6103  
Qy 1909 ----- 1909  
Db 6104 GACAGGCAGCTGTTTGACACCATATCCCTGTGTATCCAGGGCTCCCTGGAGTGGGAGCTG 6163  
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Qy 1909 ----- 1909  
Db 6224 AGCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAGATGGAGGCTCTGTCTCTGACG 6283  
Qy 1909 ----- 1909

Db	6284	TCAGAGATTGTGTCTGAACCGTCCTGCTCTCTAGCTCTGACGGATGACTCTTTGCCTGAT	6343
QY	1910	-----MetGlnProHisProThrGlu	1916
Db	6344	GACATGCACACACTCTTACTTAGTGCCCTGGAGAGCAATATGCAGCCCCACCCACGGAG	6403
QY	1917	LeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu	1936
Db	6404	CTGCCAGACACAGACTTACTGACTGTGCGAAGTCTGGGTGAGCCCGAACGCACTCTCTG	6463
QY	1937	ProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArg	1956
Db	6464	CCCAATGACAGCTACATGTGTGCGCATGGAGCACTGCCGAGGGGCCCTGGGACACAGG	6523
QY	1957	GlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAla	1976
Db	6524	GGCTGGGGGCTCCCCAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCAGCCAGCA	6583
QY	1977	AspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSer	1996
Db	6584	GATACCAGCTACATCCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCCACAGC	6643
QY	1997	AlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGln	2016
Db	6644	GCCCCAACCTGGGCACCATCCCCAAACTGCCCCACAGGACGCTCCCTTTGGCTCAG	6703
QY	2017	ArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGly	2036
Db	6704	AGGCCACTCAGGGCCAGGCAGCAATAAGACTGACTCTCTGGAGCTTTCAGGGTCTGGGC	6763
QY	2037	Ser-ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTy	2056
Db	6764	AGCCCGGAAGACTGCTGGCAGAGGTGAGTGGGCCCTCCCGCCCTGGCCCGGCCTA	6823
QY	2056	rSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysI	2076
Db	6824	CTCTTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGCCACAGCAAGAT	6883
QY	2076	eSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysG	2096
Db	6884	CTCCAAGCACATGACCCCGCCAGCCCTTGCCAGGCCCCAGAACCCAACTGGGGCAAGGG	6943
QY	2096	yProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAs	2116
Db	6944	CCCTCCAGAGACCAGAAGCAGCTTAGAGTTGGACACGGAGCTGAGCTGGATTCAGAGA	7003
QY	2116	pLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTy	2136
Db	7004	CCTCTGCCCTTGGCGGCCAGGAGGAGCCGCCCATCCCCACGGACCTGAAGAGTGCTA	7063
QY	2136	rSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgAr	2156
Db	7064	CAGCGTGGAGGCCACAGAGCTGCCAGCGCGGCTACGTCCTGGCTGGATGAGCAGAGGAG	7123
QY	2156	gHisSerIleAlaValSerCysLeuAspSerGly-SerGlnProHisLeuGlyThrAspp	2176
Db	7124	ACACTCTATCGCCGTCAGCTGCCTGGACAGCGGCTTCCCAACCCCACTGGGCACAGACC	7183
QY	2176	roSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeus	2196
Db	7184	CCTCTAACCTTGGGGGCCAGCCTCTTGGGGGCTGGAGCCGGCCCAAGAAAACTCA	7243
QY	2196	erProProSerIleThrIle-AspProProGluSerGlnGlyProArgThrProProSer	2215
Db	7244	GCCCCGCTAGTATCACCATTAGACCCCCCGAGAGCCAAAGTCTCTCGGACCCCGCCAGC	7303
QY	2216	pro-GlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSe	2235
Db	7304	CCTGGGNTCTGCCTCCGGAGGAGGGCTCCGTCACGCACTCCAAGGATCCCTTGGCCTC	7363
QY	2235	rglyProPro--AspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeu	2254

7364

TGGGCCCCCTGAACAGCATGGCTGCCCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTC

7423

2255

SerGlyLeuSerSerAspProAlaAspLeuAspPro

2266

7424

TCCGGTTTATCTCTGACCCAGCAGACCTGGACCCC

7459

RESULT 4

US-09-383-894-1

; Sequence 1, Application US/09383894

; Publication No. US20030125269A1

; GENERAL INFORMATION:

; APPLICANT: Li, Ming

; TITLE OF INVENTION: T-Type Calcium Channel

; FILE REFERENCE: 004.00191

; CURRENT APPLICATION NUMBER: US/09/383,894

; CURRENT FILING DATE: 1999-08-26

; EARLIER APPLICATION NUMBER: US 60/098,004

; EARLIER FILING DATE: 1998-08-26

; EARLIER APPLICATION NUMBER: US 60/117,399

; EARLIER FILING DATE: 1999-01-27

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 1

; LENGTH: 7129

; TYPE: DNA

; ORGANISM: Rattus sp.

US-09-383-894-1

Alignment Scores:

Pred. No.: 0

Score: 11111.00

Percent Similarity: 94.80%

Best Local Similarity: 93.27%

Query Match: 93.34%

DB: 10

Length: 7129

Matches: 2135

Conservative: 35

Mismatches: 95

Indels: 24

Gaps: 5

US-09-611-257A-37 (1-2266) x US-09-383-894-1 (1-7129)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20

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QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40

Db 61 CAGCTCAACGACCTGTCCGGGCGCGGGCGCGGAGGCGGGCGCGGAGGAC 120

QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60

Db 121 CCGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGCGCTAGCCCGGTGGTT 180

QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80

Db 181 TTTCTTCTACTTGAGCCAGGACAGCCCGCCCGGAGCTGGTGTCTCCGACCGTCTGTAAC 240

QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100

Db 241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCACTTCTCAACTGTGTGACTCTGGGTATG 300

QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120

Db 301 TTCAGGCGGTGTGAGGACATTCGCTGTGACTCCCAAGCGCTGCCGATCCTGCAGGCCCTTC 360

QY 121 AspAspPheIlePheAlaPheAlaValGluMetValLysMetValAlaLeuGly 140

Db 361 GATGACTTCATCTTTGCCCTTCTTGTGTGGAAATGGTGGTGAAGATGGTGGCTTGGGC 420

QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160

Db 421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACCTTTTCATTGTC 480

QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180

Db 481 ATTGCAGGGATGCTGGAGTATTCTGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 540

QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTC 600  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCACATTACTGTGGACACCTTGCCTATGCTGGCAACGTCCTGCTGCTCTGTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCCTTTTTCATCTTTGGCATCGTGGCGTCCAGCTGTGGGCAACGTCCTGCTGCTCTGTTCTTC 720  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
Db 721 TGCTTCCCTCCCGAGAACTTCAGCCTCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 781 ACAGAGAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGA 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCCTGCAGGAGTGTGCCCCACACTGCGTGGGGAAGCGGTGGTGGCCCCACCCTGCACTGTG 900  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCCAGTACTAT 960  
QY 321 ThrAsnCysSerAlaGlyGluHisAsnPropheLysGlyAlaIleAsnPheAspAnile 340  
Db 961 ACCAACTGCTGCGGGCGAGCACAAACCCCTTCAAAGCGGCATCAACTTGCACAACTT 1020  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1021 GGCTATGCCTGGATGCCCATCTTCCAGGTATCACACTGGAGGGCTGGGTGACATCATG 1080  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
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QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTATGTCACGACGAGTTCTCCGAG 1200  
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAACAGCGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAAATGCT 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
Db 1261 AGCACCCCTGGGAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320  
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1321 GTGTACATCCTCCGAAAGCAGCCCGAAGGCTGGCCCCAGGTCTCTAGGGCTATAGGCGTG 1380  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGGCTGGGCTGCTCAGCAGCCCAAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTGGC 1440  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
Db 1441 AGCTGCACTCGCTCACACCGTCTGCTGTGTCCACCACCTGGTCCACCACCATCACCCAC 1500  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCAGAG 1560  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Db 1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTCTACCAACCCCTCTACACCC 1620

QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680  
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
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QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600  
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QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaAserSerGlyProProThrLeuThr 620  
Db 1801 ATACTGAAGATAAAGCACTAGTGGAGGTGGCCCCCAGCCTGGGCCCCCACCCTCAC 1860  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
Db 1861 AGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACGGGAGCCTGCCATAGTCTCTGCAAAATCTCCAGCCCTTGTCTCCAAGGCAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
Db 1981 GCCTGGGGCGGACAGTTGTCTCTACTGTGCCCGGACAGGAGCAGGAGCCAGAGTCC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCTGACCATGTCTGCTGCTGACTCAGACAGCAGGCTGTGTATGAGTTACACAGGACGCT 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719  
Db 2101 CAGCACAGTGACCTCCGGGATCCACAGCGCGGCGGACAGCGGAGCCTGGGCCAGAT 2160  
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739  
Db 2161 GCAGAGCCTAGTTCTGTCTGGCTTCTGGAGGCTGATCTGTGACACATTCGCGAAGATC 2220  
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759  
Db 2221 GTAGATAGCAAAATACTTTGGCCCGGGAATCATGATCGCCCATCTTGGTCAATACACTCAGC 2280  
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779  
Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340  
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799  
Db 2341 ATCGTCTTACCAGCCTCTTCGCCCTGGAGATGCTGTGTAACCTGCTTGTCTACGGTCCC 2400  
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819  
Db 2401 TTTGGCTACATTAAGAAATCCCTACAACATCTTTGATGGTGTCTATTTGGTTCATCAGTGTG 2460  
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839  
Db 2461 TGGGAGATTGTGGCCAGCAGGAGGAGTGGCCTGTTCGGTGTTCGGGACCTTCCGCCCTGATG 2520  
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859  
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QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhePhe 879  
Db 2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCTCATGCTTCTCATCTTCTCATCTTC 2640  
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899  
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QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919

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QY	920	LeuThrGlnGluAspTrrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp	939	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	2761	CTGACTCAGGAAGACTGGAAATAAAGTCTCTACAACGGCATGGCCCTCCACATCGTCTTGG	2820	3841	GACCATGTGGTCTCGTCATCATCTTCTCCTCAACTGTATCACCATCGCTATGGAGCGCCCC	3900
QY	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	2821	GCTGCTCTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG	2880	3901	AAATTGACCCCCACAGCGCTGAGCGCATCTTCTTGACCTCTCCAACTACATCTTTCACG	3960
QY	960	valAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer	979	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrrpCysPheGlyGlu	1338
Db	2881	GTGGCCATTCTGTGAAGGATTCAGGCAGAGGAATCGGCAACGGGAAGATCGGAGT	2940	3961	GCAGTCTTCTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTCTTTGGGGAG	4020
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	2941	GGACAGTTAAGCTGTATTTCAGCTGCTGTCAACTCTCAGGGGGGAGATGCCACCAAGTCT	3000	4021	CAGGCCTACCTGGCAGCAGCTGGAATGTCTGGACGGCTTGTGGTGGTCTCATCTCCGTC	4080
QY	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	3001	GAGTCAGAGCCTGATTCTTTTCGCCAGTGTGGATGGTGGGACAGAAAGAAGCGC	3060	4081	ATCGACATCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGG	4140
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu	1039	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	3061	TTGGCCCTGGTGGCTTTGGGAGAACACCGCGAACTACGGAAGAGCCTTTTGCACCCCTC	3120	4141	GTGCTCGGGCTGCTCGGACCCCTGGTCCACTCAGGCTCATCAGCGGGCCCGAGGACTG	4200
QY	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418
Db	3121	ATCATCCATACGGCTGCGACACCAATGTCACTACCAAGAGTCCAGCACAGGTGTGGGG	3180	4201	AAGCTGGTGTAGAGACTCTGATGTCTATCCCTCAAAACCATTTGGCAACATTTGGTTCATT	4260
QY	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAla	1079	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	3181	GAAGCACTGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCGCTGAGCCTGGAGCT	3240	4261	TGCTGTGCCCTTCTTCATCATTTTTTGAATTTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTC	4320
QY	1080	Ala--HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	3241	GCCCAACATGAGATGAATCTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAGT	3300	4321	TTCGTGTGTGAGGTGAGGACACCCAGGAACATCACTAAACAATCCGACTGCGCTGAGGCC	4380
QY	1099	AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118	1459	SerTyrArgTrrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	3301	GCGGCAAGCAGCTGGACCAAGCGCGCTCCAGCAGGAACAGCCTGGCGCGGCCCGCAGC	3360	4381	AGCTACCGATGGGTCCGGCACAAAGTACAACTTTGACAACTTGGCCAGGCTCTGTATGTC	4440
QY	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu	1138	1479	LeuPheValLeuAlaSerLysAspGlyTrrpValAspIleMetTyrAspGlyLeuAspAla	1498
Db	3361	CTAAAGCGGAGGAGCCCGAGCGGGAGCGGAGTCCCTGCTGTCTGGAGAGGGCCAGGAG	3420	4441	CTGTTGTGTGCTGGCTCCAAGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	4500
QY	1139	SerGlnAspGluGluSerSerGluGluArgArgSerLeuLeuSerProAlaGlySerAspHis	1158	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
Db	3421	AGTCAGGATGAGGAGGAAGTTTCAAGAAGAGACCGCGGCCAGCCCGCAGCAGCAGTAC	3480	4501	GTGGGTGGATCAGCAGCCCATCATGAACCAACCAACCCCTGGATGCTGTATATCTATC	4560
QY	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu	1538
Db	3481	CGCCACAGGGGTCTCTTGGAACTGAGGCCAAGAGTTCCTTTGACCTGCTGACACTCTG	3540	4561	TCCTTCTCTCATCGTGGCTTCTTTGTCTCTGAACATGTTTGTGGCGCTGGTGGTGGAG	4620
QY	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys	1558
Db	3541	CAGGTGCCGGGGCTGCACCGCACAGCCGCGCGGAGCTCTGCCTCTGAGCACCACAGAC	3600	4621	AACCTCCATAAGTGCAGACAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4680
QY	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro	1218	1559	ArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	3601	TGTAATGGCAAGTCCGGCTTCAGGGCGTTTGGCCCGCACCTTGAGGACTGATGACCCCAA	3660	4681	CGACTACGGAGCTGGAGAAAAGAGAAGAAATCTAATGTTGGACGATGTAATGCTTCC	4740
QY	1219	LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238	1569	-----LysAlaGlnCysLysProTrrpTrrpSerAspTrrpSer	1580
Db	3661	CTGGATGGGGATGATGACAATGATGAGGAAATCTGAGCAAGGGGAACGCATACAAAGCC	3720	4741	GGCAGCTCAGCCAGCGCTGCGTCAAGAGCCCGAGTCAAGCCCTACTACTCTGACTACTCG	4800
QY	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle	1258	1581	ArgPheArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1600
Db	3721	TGGGTGAGATCCCGGCTTCTGCTGCTGTCGAGAGCGAGATTCTCTGGTGGCTATATC	3780	4801	AGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCCTACCTGGACCTCTTCATCACT	4860
QY	1259	pheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
				4861	GGTGTCTATCGGGCTGAACGTGGTCTACTATGGCCATTGGCAACATTACAGCAGCCCCAGATC	4920



QY 1621 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer 1640  
DB 4921 CTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGICATCTTTGTCTTTGAGTCA 4980  
QY 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660  
DB 4981 GTTTTCAAACTTGTGGCCTTTGGCTTCCGCCGTTTCTTCCAGGACAGGTGAACAGCTG 5040  
QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1680  
DB 5041 GACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAAT 5100  
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DB 5101 GCTTCGCTGCCATCAACCCACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGA 5160  
QY 1701 ValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720  
DB 5161 GTTCTGAAGCTGTTGAAGATGGCTGTGGGCATCGGGCCTGCTGGACACGGTGATGCAG 5220  
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DB 5221 GCCCTGCCCGAGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATCTTTGCA 5280  
QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760  
DB 5281 GCTCTGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGC 5340  
QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780  
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QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800  
DB 5401 TCCACTGGTGACAACACTGGAATGGTATTATGAAGACACCCCTCCGGGACTGTGACACGAG 5460  
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QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeu 1860  
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QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880  
DB 5641 AGCCCGCAGCCCACTCCCGCTGGGAGCCCTTCTCTGCGCCGGGTGGAGGGTGTG 5700  
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DB 5761 TCGGGCTTCTCCCTTGAGCACCCACCATGGTATGTTACCCACCCGAGGAGGTGCCAGTCCCC 5820  
QY 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937  
DB 5821 CTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGCACTCTCTGCC 5880  
QY 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957  
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DB 5941 TGGGGGCTCCCAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACACGAGAC 6000

QY 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997  
DB 6001 ACCAGCTGCATCTACAGCTTCCCAAAGATGTGCACTATCTGTCTCCAGCCTCATGGGGCC 6060  
QY 1998 ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017  
DB 6061 CCCACCTGGGGCGCCATCCCTAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGG 6120  
QY 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037  
DB 6121 CCTCTCAGGCCCGCAGCAGCAATAAGACTGACTCCCTGGATGTGCAGGGCCTGGGTAGC 6180  
QY 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057  
DB 6181 CGGAAGACCTGTTGTACAGAGGTGAGTGGGCCCTCTCTGCCCTCTGACCCGGTCTCTCATCC 6240  
QY 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077  
DB 6241 TTCTGGGGCGGTTCGAGCATCCAGGTGCAGCAGCGTTCCGGSCATCCAGAGCAAAAGTCTCC 6300  
QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097  
DB 6301 AAGCACATCCGCTGCCAGCCCCCTTGGCCAGGCTGGAAACCCAGCTGGGCCAAGGACCT 6360  
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117  
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DB 6598 AGCCTCGGGGGCCAACTCTTGGGGGTCTTGGAGCCGGCTTAAGAAAAAATCAGCCCCA 6657  
QY 2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217  
DB 6658 CCCAGTATCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCACTCTGGT 6717  
QY 2218 IleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237  
DB 6718 GTCTGCCTCAGGAGGAGGGCGCGCCAGTCACTTAAGGATCCCTCGGTCTCCAGCCCC 6777  
QY 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257  
DB 6778 CTTGACAGCAGCGCTGCCTCACCCCTCCCAAGAAAGACACGCTGAGTCTCTCTGGTTTG 6837  
QY 2258 SerSerAspProAlaAspLeuAspPro 2266  
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RESULT 5

US-09-383-894-3  
; Sequence 3, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004.00191  
; CURRENT APPLICATION NUMBER: US/09/383,894  
; CURRENT FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: US 60/098,004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399

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; EARLIER FILING DATE: 1999-01-27
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; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 7285
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; TYPE: DNA
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; ORGANISM: Rattus sp.
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US-09-383-894-3

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Alignment Scores:		
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Score:	11111.00	Matches:
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US-09-611-257A-37 (1-2266) x US-09-383-894-3 (1-7285)

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QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
Db	217	CAGCTCAACGACCTGTCCGGGGCGGGGGCCGGCAGGGGCGGGGTGCGACGAAAAAGGAC	276
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	277	CCGGGACGCGCGACTCCGAGGCGAGGGGCTGCCGTACCCGGCGTAGCCCCGGTGGTT	336
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
Db	337	TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGACCGTCTGTAAAC	396
QY	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	397	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTCTCAACTGTGTGACTCTGGGGTATG	456
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	457	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCAGCGCTGCCGGATCCTGACGGCCTTC	516
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
Db	517	GATGACTTCATCTTTGCCCTTCTTTGCTGTGAAATGGTGTGAAAGATGGTGGCCTTGGGC	576
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal	160
Db	577	ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATGTTC	636
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	637	ATTGCAGGGATGCTGGAGTATTGCTGGACCTGCAGAACGTCAGCTTCTCCGCGAGTCAGG	696
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	697	ACAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACCGGTGCCAGCATGCGCATTTCTC	756
QY	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	757	GTCAATTACTGCTGGACACCTTGCCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTTCTTC	816
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg	240
Db	817	GTCTTTTTCATCTTTGGCATCGTGGCGCTCCAGTGTGGGCAGGACTGCTTCGCAACCCGA	876
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	877	TGCTTCTCTCCCGAGAACTTCAGCCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG	936
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280

QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
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QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680  
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QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719  
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DB 2317 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGGAAGATC 2376  
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QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859  
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DB 2737 AAGACCATTGGAACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2796  
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DB 2917 CTGACTCAGGAAGACTTGAATAAAGTCCCTTACAACGGCATGGCCTCCACATCGTCTGG 2976  
QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959  
DB 2977 GCTGCTCTTACTTCACTCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3036  
QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979  
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QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999  
DB 3097 GGACAGTTAAGTGTATTTCAGCTGCCTGTCAACTCTCAGGGGGAGATGCCACCAAGTCT 3156

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DB 3877 TGGGTACATCCCGCTTCTGCTTCTGCTGTCGAGAGCGAGATTCTTGGTCCGCTATATC 3936  
QY 1259 PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278  
DB 3937 TTTCTCTCTCAGTCAAGGTTTCGTCTCTGTGTACCCGGATCATCACCCACAAGATGTTT 3996  
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298  
DB 3997 GACCATGTGTCTCTGTCATCATCTTCTCAACTGTATACCATCGTATGGAGCGGCC 4056  
QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318  
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QY 1319 AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu 1338  
DB 4117 GCAGTCTTTCTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTTGGGGAG 4176  
QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358  
DB 4177 CAGGCCTACCTGCGCAGCAGCTGGAATGTGTGGACGGCTTGTGGTGTCTCATCTCCGTC 4236  
QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378

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QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398  
Db 4297 GTGCTGGGCTGCTGCGGACCTCGTCCACTCAGGTCATCAGCGCGGCCAGGACTG 4356  
QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418  
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QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438  
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QY 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478  
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QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498  
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QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518  
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QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLys 1558  
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QY 1559 ArgLeuArgArgLeuGluLysLysArgArg----- 1568  
Db 4837 CGACTACGGAGGCTGGAGAAAAGAGAGGAATCTAATGTTGGACGATGTAATGCTTCC 4896  
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580  
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QY 1581 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600  
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QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620  
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QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1680  
Db 5197 GACCTGGCTATTGTGCTTCTGTCCATCATGGGATCACACTGGAGGAGATTGAGGTCAAT 5256  
QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700  
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QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760  
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QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780  
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QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900  
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QY 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937  
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QY 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997  
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QY 1998 ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017  
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QY 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037  
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QY 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisArgSerHisSerLysIleSer 2077  
Db 6397 TTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAGTCTCC 6456





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Db 1254 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTATTGCCACGCAGTTCTCCGAG 1313  
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1314 ACCAAACAGCGGAGAGTCAGTTCAGTGGGAGACGGTGTACGATTCTGTCCAATGCT 1373  
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440  
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Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
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Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThrGlnProSerSer 480  
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Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
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DB 5445 GACACCCCTCCGGACTGTGACCCAGGAGTCCACCTGCTACAACTGTCTATCTCCCTATC 5504  
QY 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaVal 1831

Db 5505 TACITTTGTCTCTTGGTGTGACGGCCAGTTTGTGCTGGTCAACGTGGTTCATAGCTGTG 5564  
Qy 1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAla 1851  
Db 5565 CTGATGAAGCACCTGGAAGAAGCAACAAAGAGGCAAGGAGGAGGCGGAGCTCGAGGCC 5624  
Qy 1852 GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro 1871  
Db 5625 GAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGCAGCCCC 5684  
Qy 1872 PheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeu 1891  
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Qy 1912 ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer 1928  
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Qy 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948  
Db 5865 GGTGTGACCGCGGACGCACTCTCTGCCAATGACAGCTACATGTGCCGCAATGGAGCACT 5924  
Qy 1949 AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerVal 1968  
Db 5925 GCTGAGAGATCCCTAGGACACAGGGGCTCGGGGCTCCCCAAAGCCAGTCAGGCTCCATC 5984  
Qy 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988  
Db 5985 TTGTCCGTTCACTCCCAACCAGCAGACACCAGTGCATCCTACAGCTTCCCAAGATGTG 6044  
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Qy 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp 2028  
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Qy 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyPro 2048  
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Qy 2049 SerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068  
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Qy 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088  
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Db 6702 GGCTCTCGGCCCCCATGAGTCTCTGGTGTCTGCTCAGGAGGGCGCGCCAGTGAC 6761  
Qy 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248  
Db 6762 TCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCAGGCTGCCTCACCTCCCCAAG 6821  
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US-10-930-301-51  
; Sequence 51, Application US/10930301  
; Publication No. US20050026207A1  
; GENERAL INFORMATION:  
; APPLICANT: Issa, Jean-Pierre  
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: JHU1590  
; CURRENT APPLICATION NUMBER: US/10/930,301  
; CURRENT FILING DATE: 2004-08-30  
; PRIOR APPLICATION NUMBER: US/09/398,522  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 3993  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (373)...(3993)  
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Alignment Scores:  
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Score: 6315.50 Matches: 1207  
Percent Similarity: 98.13% Conservative: 0  
Best Local Similarity: 98.13% Mismatches: 0  
Query Match: 53.05% Indels: 23  
Gaps: 19  
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Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
Db 433 CGGCTCAACGACCTGTCTGGGGCGGGGGCGGGCGGGGTCCGGGTCCAGAGAAAGGAC 492  
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
Db 493 CCGGGCAGCGCGACTCCGAGCGGAGGGGTGCGGTACCGGGCGGTGGCCCGGTGGTT 552  
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
Db 553 TTCTTCTACTTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAAC 612  
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 613 CCCTGGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCGTGACCCCTGGGCATG 672



QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
DB 673 TTCGGCCATCGAGGACATCGCCTGTGACTCCAGCGCTCCGGATCCTGCAGGCCTTT 732  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
DB 733 GATGACTTCATCTTTGGCCTTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC 792  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160  
DB 793 ATCTTTGGGAAAAAGTGTATTACCTGGGAGACACTTGAACCGGCTGACTTTTTCATCGTC 852  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 853 ATCGCAGGGATGTGGAGTACTCGCTGCACCTGCAGAACGTGAGCTTCTCAGCTGTGAGG 912  
QY 181 ThrValArgValIleuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 913 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTT 972  
QY 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
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QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
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QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
DB 1213 TCCTGCAGAGCGTGCACCGCTGCGCGGGAGCGGGCGGTGGCCACCTTTCGGTCTG 1272  
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QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
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QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
DB 1393 GGCTATGCCTGGATGCCATCTTCCAGGTATCATCGCTGGAGGGCTGGTTCGACATCATG 1452  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
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QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
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DB 1753 CGGGTTGGGCTGCTCAGCAGCCCGACACCCCTCGGGGGCCAGAGACCCAGCCAGCAGC 1812  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
DB 1813 AGCTGCTCTCGCTCCACCGCGCCTATCCGTCCACCACCTGGTGACCAACCACCAACCAC 1872  
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
DB 1873 CATCACCACTACTACCCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 1932  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
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DB 2173 ACGCTGAAGAGAGGCACTAGTAGAGGTGGTGCACAGCTCTGGGGCCCCCAACCTCACC 2232  
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; Sequence 8, Application US/10377139  
; Publication No. US20040175761A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKinnon, Roderick  
; APPLICANT: Jiang, Youxing  
; APPLICANT: Lee MacKinnon, Alice  
; APPLICANT: Ruta, Vanessa  
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9  
; CURRENT APPLICATION NUMBER: US/10/377,139  
; CURRENT FILING DATE: 2003-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 6990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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Score: 5496.50 Matches: 1244  
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Best Local Similarity: 51.38% Mismatches: 525  
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DB: 18 Gaps: 60  
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Db 133 GCTGATCCTCATGTCCCAACCCAGACCTGGCGCTATTGCTTCTTCTGCTGCGACAG 192  
QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86  
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QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106  
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Db 313 ATGGACTGCTGTCCGACCGCTGCAAGATCCTGCGAGTCTTTGATGATCATCTTTATC 372  
QY 127 PhePheAlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysCys 146  
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Db 1084 ATCATGTACTAGTGTATGGATGCTCACTCTTCTACAACTTCTATCTTCTCATCTGCTT 1143  
  
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398  
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Db 1144 ATCATAGTGGGCTCTTCTTTCATGATCAACCTGTGCTGCTGTGTATAGCGACCGAGTTT 1203  
  
QY 399 SerGluThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418  
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Db 1204 TCGGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAGCGCGCTACTGTCTCC 1263  
  
QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys 438  
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Db 1264 ---TCCAGCAGGTGGCCAGCTACCGGAGCCTGGCGAGTGTCTACGAGGAGATCTTCCAG 1320  
  
QY 439 TyrLeuValTyrIleLeuArgIysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458  
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Db 1321 TATGTCTGCCACATCTCTGGCAAGGCCAAGCGC-----CGCGCCCTG 1362  
  
QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478  
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Db 1363 GGCCTCTACAGGCGCCTGCAGAGCGGCGCCAGGCCCTGGGCGCGGAGGCCCGGCCCCC 1422  
  
QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis 498  
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Db 1423 GCCAAACCT-----GGGCCCCAC 1440  
  
QY 499 HisHisHisHisHisTyrHis-----LeuGlyAsnGlyThrLeuArgAlaPro 515  
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Db 1441 GCCAAGGAGCCCGGCACCTACCATGGGAAGACTAAGGGTCAGGGA----- 1485  
  
QY 516 ArgAlaSerProGluIleGlnAspArgAspAlaAsn---GlySerArgArgLeuMet--- 533  
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Db 1486 -----GATGAAGGGAGACATCTCGAAGCGCGGCACTTGCAGACT 1524

QY 534 LeuProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerVal 553  
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Db 1525 TTGCATGGGCTGCTCCCT-----GGAAATGATCACTCGGAAGAGAG----- 1569  
  
QY 554 HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPro 573  
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Db 1570 -----CTGTGC-----CCGCAA 1581  
  
QY 574 ArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVal 593  
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Db 1582 CATAGCCCCCTGGATCGACGCCCCACACCTG----- 1614  
  
QY 594 HisThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSer 613  
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Db 1615 ---GTGAGGCCCATCCCCGCCACGCTG----- 1638  
  
QY 614 SerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHis 633  
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Db 1638 ----- 1638  
  
QY 634 LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerPro 653  
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Db 1638 ----- 1638  
  
QY 654 CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg--- 672  
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Db 1639 -----GCTTCCGATCCCCGCCAGCTGCCCTTGTGTGCCAGCATGAG 1677  
  
QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAsp 687  
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Db 1678 GACGGCGCGCGCCCTCGGGCTGGGCGAGCACCGAC---TCGGGCGAGGAGGCTCGGGC 1734  
  
QY 688 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 707  
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Db 1735 TCCGGGAGCTCCGCTGGTGGCGAG-----GACGAGGCGGATGGGACGGGCGCCGAGC 1788  
  
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QY 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739  
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QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759  
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QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779  
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Db 1969 ATGGGATCGAGCACCGACGAGCGCGGAGGAGCTGACCAACATCTCTGGAGATCTGCAAT 2028  
  
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799  
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Db 2029 GTGGTCTTCACGAGCATGTTTGGCTTGGAGATGATCTCTGAAGCTGGCTGCAATTTGGGCTC 2088  
  
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Db 2089 TTCGACTACCTGCGTAACCCCTACAACATCTTCGACAGCATCATTTGTCATCATCAGCATC 2148  
  
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839  
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Db 2209 CGCGTGTGAAACTGGTGGCTTTCATGCTGCCCTGGCGCGCCAGCTCGTGGTGTGCTCATG 2268  
  
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879  
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QY LeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAla 978  
Db 2569 CTGGTGGCCATCCTGGTGGAGGGCTTCAGGCGGAG----- 2604  
QY SerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLys 998  
Db 2605 -----GGTGACGCCAATCGC 2619  
QY SerGluSerGluProAspPheSerProSer----- 1009  
Db 2620 TCCTACTCGACGAGGACCAGAGCTCATCAACATAGAAAGATTGTATAAGTCCAGGAA 2679  
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QY ProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMet 1048  
Db 2740 -----CTGGACCC----- 2748  
QY SerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArg 1068  
Db 2749 AGTCTCCCACTGGGTGGGCACCTAGGTCTGCTGGGGCTGCGGACCTGCCCGCGACTC 2808  
QY Thr-----SerSerSerGlySerAla 1075  
Db 2809 TCACTGCAGCCGACCCCATGTCTGGTGGCCCTGGGCTCCCGAAAGACAGTGTATGTCT 2868  
QY GluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSer 1095  
Db 2869 CTAGGGAGGATGAGCTATGACCAAGCGCTCCCTGTCCAGCTCCGGAGCTCCTACTACGGG 2928  
QY ProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArg 1115  
Db 2929 CCATGGGGCCGACGCGGGCCTGGGCCAGCGCTCGCTCCAGTCCGAC----- 2976  
QY AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu 1135  
Db 2977 -----AGCCTCAAGCACAAGCCCGCTCGCGGAGCATGATGCCCTGCTCTCTGCGGAG 3030  
QY GlyGlnGluSerGlnAspGluGluGluSerSerGluGlu-----GluArgAlaSer 1152  
Db 3031 CGCGCGCGCGCGCGGTCTGCGAGGTTGCGCGGACGAGGGGCGCGCGCGCGCGCA 3090  
QY ProAlaGlySerAspHis----- 1158  
Db 3091 CCCCTGCACACCCACACGCCCCACCATTCATCAGGGCCCCCATCTGGCGCACCGCCAC 3150  
QY ---ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThr 1177  
Db 3151 CGCCACCACCGCGGACGCTGTCCCTCGACACAGGGACTCGGTGACCTGGCCGAGCTG 3210  
QY LeuGlnValProGlyLeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGlu 1195  
Db 3211 GTGCCCGCGGTGGCGGCCACCCCGCGCGCTGGAGGGCGGCGGCGGCGGCGGCGG 3270  
QY HisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAsp 1215

Db 3271 CATGAGGACTGCAATGGCAGGAT-GCCCAGCATCGC---CAAAGACGTCTTCCACCAAGAT 3326  
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Db 3327 GGGCGACCCGGGGATCGCGGGGAGGATGAGGAGAAATCGACTACACCTGTGTCTCCG 3386  
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QY tGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTy 1315  
Db 3567 GGAGCGGCCTCAGATCGAGGCGCGGACCGAACGCACTTTTCTACCGTGTCCCACTA 3626  
QY rIlePheThrAlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCy 1335  
Db 3627 CATCTTACGGCCATCTTCTGTGGCGGAGATGACATTGAAGGATGCTCTCGTGGGCTGTA 3686  
QY sPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValle 1355  
Db 3687 CTTCCGGCAGCAGCGGTACCTACGCAGCAGCTGGAACGTCGTGGATGGCTTTCTTGTCTT 3746  
QY uIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGl 1375  
Db 3747 CGTGTCCATCATCGACATCGTGTGTCCCTGGCCTCAGCCGGGGAGCCCAAGATCTTGGG 3806  
QY yMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAl 1395  
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QY eValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLy 1435  
Db 3927 CGTGCTCATCTGCTGTGCTTCTTTCATCATCTTGGCATCTTGGAGTGCAGCTCTTCAA 3986  
QY sGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCy 1455  
Db 3987 GGGCAAGTTCTACCACTGTCTGGGCGTGGACACCCGCAACATCACCAACCTCGGACTG 4046  
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Db 4107 TCTGATGTCCTCTTGTCTGGCATCCAGGATGGTGGGTGAACATCATGTACAATGG 4166  
QY yLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLe 1515  
Db 4167 ACTGGATGCTGTGCTGTGGACGAGCGCTGTGACCAACCAACCCCTGGATGCTGCT 4226  
QY uTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyVa 1535  
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QY	1575	rTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysThrSerHisTyrLe	1595
DB	4407	CTATGCCACCTATTGTACACCCGGCTGCTCATCCACTCCATGTGCACCCAGCCACTACCT	4466
QY	1595	uAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyr	1615
DB	4467	GGACATCTTTCATCACCTTCATCATCTGCCTCAACGTGGTTCACCATGTCCCTGGAGCACTA	4526
QY	1615	rGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIle	1635
DB	4527	CAATCAGCCCCACGTCCCTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCACCACTGT	4586
QY	1635	epheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAs	1655
DB	4587	CTTTGTGCTGGAGGCTGTGCTGAAGCTGGTGGCATTTGGTCTGAGGGCGCTCTTCAAGGA	4646
QY	1655	pArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlu	1675
DB	4647	CCGATGGAAACCAGCTGGACCTGGCCATTGTGTACTGTCTAGTCAATGGGCATCACCCCTGGA	4706
QY	1675	uGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgVa	1695
DB	4707	GGAGATCGAGATCAATGCGGCCCTGCCCCATCAATCCCACCATCATCCGCATCATGAGGGT	4766
QY	1695	lLeuArgIleAlaArgValLeuLysLeuLysLeuMetAlaValGlyMetArgAlaLeuLe	1715
DB	4767	TCTGCGCATTTGCCCGAGTGTGAAGCTGTTGAAGATGGCCACAGGAATGCGGGCCCTGCT	4826
QY	1715	uAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLe	1735
DB	4827	GGACACGGTGGTCAAGCTTTGCCCCAGGTGGGCAACCTGGGCCCTCCTCTTCATGTCTGCT	4886
QY	1735	uphePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluTh	1755
DB	4887	CTTCTTCATCTATGTGCTCTCGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGA	4946
QY	1755	rHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLe	1775
DB	4947	GAACCCCGTGGAGGGCATGAGCCGGCATGCCACCTTCGAGAACCTTCGGCATGGCCCTTCT	5006
QY	1775	uThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuAr	1795
DB	5007	CACACTCTTCCAGGTCTCCACGGGTGACAACTGGAAACGGGATCATGAAGGACACGCTGG	5066
QY	1795	gAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTyr	1812
DB	5067	GGACTGCACCCACGACGAGCGCAGCTGCCTGAGCAGCCCTGCAGTTTGTGTGCGCCGTGTA	5126
QY	1812	rPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLe	1832
DB	5127	CTTCGTGAGCTTCGTGCTCACCGCGCAGTTTCGTGCTCATCAACGTGGTGGTGGCTGTGCT	5186
QY	1832	uMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGlu	1852
DB	5187	CATGAAGCACCTGGACGACAGCAACAAGGAGGCGCAGGAGGACGCCGAGATGGATGCCGA	5246
QY	1852	uLeuGluLeuGluMet--LysThrLeuSerProGlnProHisSerProLeuGlySerPr	1871
DB	5247	GCTCGAGCTGGAGATGGCCCATGGCCCTGGGCCCTGGCCCGAGGCTGCCTACCGGCTCCCC	5306
QY	1871	oPheLeuTrpProGlyValGluGlyProAsp-----	1881
DB	5307	GGGCGCC---CCTGGC---CGAGGGCCGGAGGGGGGGGGGGGGGGGGGGGACACCGAGGG	5360
QY	1882	-----SerPro-----	1883
DB	5361	CGGCTTGTCCGGCGCTGCTACTCGCCCTGCCCGAGGAGAACCTGTGGTGGACAGCGTCTC	5420
QY	1884	-----AspSerProLysProGlu-----	1889
DB	5421	TTTAATCATCAAGGACTCTTGGAGGGGAGGTGACCATCATCGACACACTGTTCGGGCTC	5480

Qy	1889 yAlaLeuHis-----ProAlaAla-----	1895
Dd	 5481 CATCTTCCACCACACTACTCCTGCCTCGCGGTGCAAGAAAGTGTCACCACGACAAGCAAAGA	5540
Qy	1896 -----HisAlaArgSerAlaSer-----	1901
Dd	 5541 GGTGCAGCTGGCTGAGACGGAGGCCCTTCTCCCTGAACACTCAGACAGGTCTCCTCGTCCCATCCT	5600
Qy	1902 -----HisPheSerLeuGluHisProThrMetGlnPro-----Hi	1913
Dd	 5601 GCTGGGTGACGACCTGAGTCTCGAGGACCCCCACAGCCTGCCACCTGGCCGCAAGACAG	5660
Qy	1913 sProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly-----	1929
Dd	 5661 CAAGGTGAGCTGGACCCACCTGAGCCCATGCGTGTTGGGAGACCTGGGGCAATGCTTCTT	5720
Qy	1930 ----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHisGlySe	1947
Dd	::::: 5721 CCCCTTGTCCTTAACGCCCGTCTCGCCGGATCCAGAGAACTTCTCGTGTGAGATGGAGGA	5781
Qy	1947 rThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySe	1967
Dd	 5781 GATCCCATTTCAACCCCTGTC-----CGTCTCTGG-----CTGAAAACATGACAGCAGTCA	5828
Qy	1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAs	1987
Dd	 5829 AGCACCCCAAGTCCCTTCTCCCGGATGCCTCCAGCCCTCTCCTGCCCCATGCCAGCCGA	5888
Qy	1987 pAlaProHis-----LeuLeuGlnProHisSerAlaProThrTrpGl	2001
Dd	: 5889 GTTCTTCCACCCTGCAGTGCTGTGCCAGCCAGAAAGGCCAATAAGGGCACTGGCACTGG	5948
Qy	2001 yThrIleProLysLeuProProProGly-----ArgSerProLeuAlaGl	2016
Dd	 5949 AACCTTCCCAAGATTGGCTGCAGGGCTCTCTGGGCATCTCTCGGTTCACCAAGGGTCAA	6008
Qy	2016 nArgProLeuArgGlnAlaAlaIleArxThrAspSerLeuAspValGlnGlyLeuGl	2036
Dd	 6009 CTGTACCCTCTCTCCGGCAGGCCACCGGGAGCGACACGTCTCGTTGGAC-----	6054
Qy	2036 ySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTy	2056
Dd	:  6055 -----GCCAGCCCCAGCAGCTCCGGGGCAGCCTGCA	6086
Qy	2056 rSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIl	2076
Dd	::: 6087 GACCACGCTCGAGGACAGCCTGACCCCTGAGCGACAGCCCCCGCGGTGCC-----	6135
Qy	2076 eSerLysHISmetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGl	2096
Dd	::: 6136 -----CTGGGCGCGCGCGCTGTCTCAGGACCCCCGGCGCGCTGTCC-----	6180
Qy	2096 yProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAs	2116
Dd	:  6181 ---CCGCGCGCTCGCGCGCGCTGAGCCTG-----	6207
Qy	2116 pLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTy	2136
Dd	-----CGGGCGCGGGCGCTCTTCAGCCTGCG	6233
Qy	2136 rSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgAr	2156
Dd	::: 6234 GGGCTGCGGGCG-----CATCAGCGCAG	6257
Qy	2156 gHisserIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPr	2176
Dd	 6258 CCACAGCAGCGGGGGCTCC--ACCGCGCGGGCTGCACCCACCGACTCCATGGACCC	6314
Qy	2176 oSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLy	2193
Dd	 6315 CTCGACGAGGCGCGGTGGCGCGGGCGGGGGCGGGGCGGCGGCGGAGCAGCACTCGGA	6374
Qy	2193 sLysLeuSerProSerIleThr-----IleAspProProGluSerGlnGlyPr	2210

Db 6375 GACCCCTACAGACGCTCTCGCTCACCTCCCTCTTCTGCGCGCGCC----- 6420  
Qy 2210 oArgThrProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer-- 2229  
Db 6421 ----CCGCGCGCAGCCCCCGGCTCACGCCCGCCAGGAAGTTTCAGCAGCAGCAGCCT 6476  
Qy 2230 -----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSe 2246  
Db 6477 GCTC 6536  
Qy 2246 rProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPr 2266  
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Qy 2266 o 2266  
Db 6579 G 6579  
RESULT 9  
US-09-935-541-1  
; Sequence 1, Application US/09935541  
; Patent No. US20020150911A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/935,541  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 6816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (192)..(6716)  
US-09-935-541-1  
Alignment Scores:  
Pred. No.: 0 Length: 6816  
Score: 5492.50 Matches: 1236  
Percent Similarity: 60.30% Conservative: 213  
Best Local Similarity: 51.44% Mismatches: 506  
Query Match: 46.14% Indels: 449  
DB: 9 Gaps: 55  
US-09-611-257A-37 (1-2266) x US-09-935-541-1 (1-6816)  
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50  
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Db 324 GGTGATCCTCATGTCCACACCCAGACCTGGCGCCTATTGCGCTTCTTCTGCTGCGGACAG 383  
Qy 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgIle 86  
Db 384 ACCACGAGCCCCCGAACTGGTGTCATCAAGATGGTGTGCAACCCCGGTGTTGAATGTGTC 443  
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Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126  
Db 504 ATGGACTGCTGTCTCCGACCGCTGCAAGATCCTGCAGGTCTTTGATGACTTTCATCTTATC 563

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Qy 147 TyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166  
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Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186  
Db 684 TACTCCCTGGACCTTCAGAACATCAACCTGTGAGCCATCCCGACCGTGGCGTCTCTGAGG 743  
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206  
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Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226  
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Qy 227 IleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246  
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Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300  
Db 1044 CCGCTCAAAGGAGCAG-----GGCCGTGAGTGTGCTGCTGCCAGGACGACGTCTAC 1094  
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318  
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QY 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538  
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QY 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis 558  
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QY 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726  
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QY 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744  
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QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680  
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QY 1913 ----HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929  
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; Sequence 1, Application US/10425800  
; Publication No. US20030180886A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
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; PRIOR APPLICATION NUMBER: US/09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 6816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
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Alignment Scores:  
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Score: 5492.50 Matches: 1236  
Percent Similarity: 60.30% Conservative: 213  
Best Local Similarity: 51.44% Mismatches: 506  
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QY 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66  
Db 324 GCTGATCCTCATGTCCACACCCAGACCTGGCGCCTATTGCTTCTTCTGCTGCGACAG 383  
QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgile 86  
Db 384 ACCACCAAGGCGGAACTGGTGCATCAAGATGGTGTGCAACCCCGTGGTTGAATGTGTC 443

Qy	87	SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp	106
Db	444	AGCATGCTGGTGATCCTGCTGAACCTGCGTGACACTTGGCATGTACCAGCGCTGCGACGAC	503
Qy	107	IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla	126
Db	504	ATGGACTGCTGCGGACCGCTGCAAGATCCTGCGAGGTCTTTGATGACTTCATCTTTATC	563
Qy	127	PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys	146
Db	564	TTCTTTGCCATGGAGATGGTGCTCAAGATGGTGGCCCTGGGATTTTGGCAAGAAGTGC	623
Qy	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu	166
Db	624	TACCTCGGGGACACATGGAAACCGCTGGATTCTTCATCGTCATGGCAGGATGGTCGAG	683
Qy	167	TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg	186
Db	684	TACTCCCTGGACCTTCAGAAACATCAACCTGTACGCCATCCGACCGTGCGCGTCTTGAGG	743
Qy	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206
Db	744	CCCCTCAAAGCCATCAACCGCGTGCCAGTATGCGGATCCTGGTGAAACCTGCTCCTGGAC	803
Qy	207	ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly	226
Db	804	ACACTGCCCATGTCTGGGAATGTCTGTCTGTCTGTCTTCTTCTTCTTCTTCTTCTTGGC	863
Qy	227	IleValGlyValGlnLeuTrpAlaGlyLeuLeuAsnArgCysPheLeuProGluAsn	246
Db	864	ATCATAGGTGTGCAGCTTGGGGGGCTGTCTGCTGCTAAACCGCTGTCTTCTGAGGAGAAC	923
Qy	247	PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu	266
Db	924	TTACCATACAAGGGGATGTGGCCTTGGCCCCCATCTACCGCGGAGGAGGATGATGAG	983
Qy	267	SerPropheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro	286
Db	984	ATGCCCTTCATCTGCTCCCTGTGGGGGACAAATGGGATAATGGGTGCCATGAGATCCCC	1043
Qy	287	ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	1044	CGGCTCAAGGAGCAG-----GGCCGTGAGTGTGCTGTCTCCAGGACGACGTCTAC	1094
Qy	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln	318
Db	1095	GACTTTGGGGCGGGCGCCAGGACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGT	1154
Qy	319	TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp	338
Db	1155	TACTACAAATGTGTGCCGACCGGCGAGCCCAACCCCAAGGTTGCCATCAACTTTGAC	1214
Qy	339	AsnIleGlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAsp	358
Db	1215	AACATCGGTTATGCTTGGATTGTCTATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAG	1274
Qy	359	IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPhelIleTyrPheIleLeuLeu	378
Db	1275	ATCATGTACTACGTGATGGATGCTCACTCTCTTCTACAACTTCATCTACTTCACTCTGCTT	1334
Qy	379	IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe	398
Db	1335	ATCATAGTGGGCTCCTTCTTCTCATATCAACCTGTGCGCTCGTTGTGCATAGCGACCCAGTTC	1394
Qy	399	SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer	418
Db	1395	TCGAGACCAAGCAACGGGAGCACCGGCTGATGTGGAGCGCGGACGCTACCTGTGCTC	1454
Qy	419	AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluLeuLeuLys	438
Db	1455	---TCCAGCAGGTTGGCCAGCTACGCGGAGCCTGGCGACTGTCTACGAGGAGATCTTCAG	1511

QY	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaA	458
Db	1512	TATGTCTGCCACATCTCTGCGCAAGCCAAAGCGC-----CGCGCCCTG	1553
QY	459	GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro	478
Db	1554	GGCCTCTACAGGCCCTGCAGAGCCGCGCCAGGCCCTGGGC-----	1595
QY	479	SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis	498
Db	1595	-----	1595
QY	499	HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer	518
Db	1595	-----	1595
QY	519	ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer	538
Db	1596	-----CCGGAG	1601
QY	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis	558
Db	1602	GCCCCGGCC-----CCCGCCAAACCTGGGCC-----CAC	1631
QY	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu	578
Db	1632	GCCAAG-----GAGCCCCGGCACTACCAAGCTGTCCCCGCAACATAGCCCCCTGGAT	1682
QY	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro	598
Db	1683	GCGACGCCCCACACCTG-----GTGACGCCCATC	1712
QY	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr	618
Db	1713	CCCCGCCACGCTG-----	1724
QY	619	LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr	638
Db	1724	-----	1724
QY	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658
Db	1724	-----	1724
QY	659	SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg-----	672
Db	1725	-----GCTTCCGATCCCGCCAGCTGCCCTTGTGTCCAGCATGAGGACGGCGCGGCCCC	1778
QY	673	AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla	692
Db	1779	TCGGGCCTGGGCACGACCGAC--TCGGGCCAGGAGGGCTCGGGCTCCGGGAGCTCCGCT	1835
QY	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712
Db	1836	GGTGGCGAG-----GACGAGGCGGATGGGGACGGGCCCGGAGCAGCGAGGACGGAGCC	1889
QY	713	GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-----	726
Db	1890	TCCTCAGAACTGGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCGGATGGGGCGGTCTGGCTG	1949
QY	727	-----AlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr	744
Db	1950	TGCGGGGATGTGTGGCGGGAGACGCGAGCCCAAGCTGCGCGGCATCGTGGACAGCAAGTAC	2009
QY	745	PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr	764
Db	2010	TTCAACGGGGCATCATGATGGCCATCTCTGGTCAACACCGTCAGCATGGGCATCGAGCAC	2069
QY	765	HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer	784
Db	2070	CACGAGCAGCCGGAGGAGTGACCAACATCCTGGAGATCTGCAATGTGGTCTTCCACCAGC	2129
QY	785	LeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys	804



QY	1480	eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValG1	1500
DB	4208	TGTCTGGCATCCAAGGATGGTTGGGTGAACATCATGTACAATGGACTGGATGCTGTTC	4267
QY	1500	yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh	1520
DB	4268	TGTGGACCAGCAGCGCTGTGACCAACCACACCCCTGGATGCTGCTGTACTTCATCTCCTT	4327
QY	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh	1540
DB	4328	CCTGCTCATCGTCAGCTTCTTTGTGCTCAACATGTTTGTGGGTGTCGTGGTGGAGAACCT	4387
QY	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLe	1560
DB	4388	CCACAAGTGCCCGCAGCACCCAGGAGCTGAAGAGGCACGGCGGTGAGGAGAAGCGCT	4447
QY	1560	uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe	1580
DB	4448	GCGGCGCTGGAGAAGAAGCGCGGAAGGCCACGCGGTGCCCTACTATGCCACCTATTG	4507
QY	1580	rArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh	1600
DB	4508	TCACACCCGGCTGCTCATCCACTCCATGTGTGCACGAGCCACTACCTGGACATCTTCATCAC	4567
QY	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI1	1620
DB	4568	CTTCATCATCTGCCTCAACGTGGTCAACCATGTCCCTGGAGCACTACAATCAGCCACGTC	4627
QY	1620	eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe	1640
DB	4628	CCTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCACCACTGTCTTTGTGTGGAGGC	4687
QY	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe	1660
DB	4688	TGTGCTGAAGCTGGTGGCATTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACCACT	4747
QY	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
DB	4748	GGACCTGGCCATTGTGCTACTGTCTAGTCATGGGCGCATCACCTGGAGGATCGAGATCAA	4807
QY	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
DB	4808	TGCGGCCCTGCCCATCAATCCCACCATCATCCGCATCATGAGGGTTCTGCGCATGCCCCG	4867
QY	1700	gValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG1	1720
DB	4868	AGTGTGAAGCTGTTGAAGATGGCCACAGGAATGCGGCCCTGCTGGACACGGTGGTGCA	4927
QY	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuphePheAl	1740
DB	4928	AGCTTTGCCCCAGGTGGCAACCTTGGGCGCTCCTCTTCATGCTGCTCTTCTTCATCATGC	4987
QY	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1	1760
DB	4988	TGCTCTCGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTGCGAGGG	5047
QY	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
DB	5048	CATGAGCCGGCATGCCACCTTCGAGAACTTCGGGCATGGCTTCCTTCACACTCTTCCAGGT	5107
QY	1780	lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspG1	1799
DB	5108	CTCCACGGGTGACAACTGGAAACGGGATCATGAAGGACACGCTGCGGGACTGCACCCACGA	5167
QY	1799	nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa	1817
DB	5168	CGAGCGCAGCTGCCTGAGCAGCGCTGCAGTTTGTGTGCGCGGTGTACTTTCGTGAGCTTCGT	5227
QY	1817	lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG1	1837
DB	5228	GCTCACCGCGCAGTTTCGTGCTCATCAACGTTGGTGGTGGTGTCTCATGAAGCACCTGGA	5287

1837	QY	uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMe	1851
5288	Db	CGACAGCAACAAGGAGCGCAGGAGACGCCGAGATGGATGCCGAGCTCGAGCTGGAGAT	5347
1857	QY	t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGln	1876
5348	Db	GGCCCATGGCCTGGCCCTGGCCCGAGGCTGCCTACCGGCTCCCGCGGCGCC---CCTGG	5404
1876	QY	yValGluGlyProAspSerProAsp	1884
5405	Db	C---CGAGGCGGGAGGGCGGGCGGGGGCGGACACCGAGGGGGGCTGTGTCCGGCG	5461
1885	QY	-----SerProLysProGlyAlaLeu	1891
5462	Db	CTGCTACTCGCCTGCCAGGACTCCTTGGAGGGGGAGCTGACCATCATCGACAACCTGTC	5521
1892	QY	-----HisProAlaAlaHisAla	1897
5522	Db	GGGCTCCATCTCCACCACTACTCTCTCGCCTGCCGGCTGCAAGAAGTGTACCCACGACAA	5588
1898	QY	-----ArgSerAla	1901
5582	Db	GCAAGAGGTGCAGCTGGCTGAGACGGAGGCTTCTCCCTGAACCTCAGACAGGTCTCTCGTC	5641
1901	QY	r-----HisPheSerLeuGluHisProThrMetGlnPro	1912
5642	Db	CATCCTGCTGGTGACGACCTGAGTCTCGAGGACCCACAGCCTGCCACCTGGCCGCA	5701
1913	QY	-----HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly	1929
5702	Db	GGACAGCAAGGTGAGCTGGACCCACCTGAGCCCATCGTGTGGGAGACCTGGCGGAATG	5761
1930	QY	-----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHis	1945
5762	Db	CTTCTTCCCTTGTCTCTACGGCGCTCTCGCCGGATCCAGAGAACTCTCTGTGTGAGAT	5821
1945	QY	sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe	1965
5822	Db	GGAGGAGATCCCAATCAACCTGTGTC---CGGTCTCTGG---CTGAAACATGACAG	5869
1965	QY	rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr	1985
5870	Db	CAGTCAAGCACCCCAAGTCCCTTCTCCCGGATGCCTCCAGCCCTCTCTCTGCCCATGCC	5929
1985	QY	oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh	1999
5930	Db	AGCCGAGTTCTTCCACCCCTGCAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGG	5989
1999	QY	rTrpGlyThrIleProLysLeuProProProGly-----ArgSerProLe	2014
5990	Db	CACCTGGAACCTCCCAAGATTGGCTGCAGGGCTCTCTGGGCATCTCTCGGTTCACCAAG	6049
2014	QY	uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGl	2034
6050	Db	GGTCAACTGTACCTCTCTCCGCGCAGGCCACCGGGAGCGACACGTCTGGTGGAC	6101
2034	QY	yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaAr	2054
6102	Db	-----GCCAGCCCCAGCAGCTCCCGGGCGCAG	6127
2054	QY	gAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSe	2074
6128	Db	CCTGCAGACCACGCTCGAGGACAGCCTGACCTTGAGCGACAGCCCCCGCGGTGCC----	6182
2074	QY	rLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGl	2094
6183	Db	-----CTGGGGCCCGCCCGCTGCTCCAGGACCCCGCGCGCGCTGTC	6226
2094	QY	yLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe	2114
6227	Db	C-----CCCGCGCTGCGCGCGCTGAGCCTG-----	6254
2114	QY	rGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLy	2134



Db 6255 -----CGCGCGCGGGCCTCTTCAG 6274  
QY 2134 sCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluG1 2154  
Db 6275 CCTGCGGGGCTGCGGGCG-----CATCA 6298  
QY 2154 nArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyTh 2174  
Db 6299 GCGCAGCCACAGCAGCGGGGCTCC---ACCAGCCCGGGCTGCACCCACCACTCCAT 6355  
QY 2174 rAspProSerAen-----LeuGlyGlyGlnProLeuGlyProGlySerArgPr 2191  
Db 6356 GGACCCCTCGACGAGGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6415  
QY 2191 oLysLysLysLeuSerProProSerIleThr-----IleAspProProGluSerG1 2208  
Db 6416 CTCGGAGACCTCAGCAGCCTCTCGCTCACCTCCCTCTTCTGCCCCCGCCCC----- 6467  
QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAs 2228  
Db 6468 -----CGCGCGCCAGCCCCCGCCTCACGCCCGCCAGGAAGTTCAGCAGCACCAG 6517  
QY 2228 pSer-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSe 2244  
Db 6518 CAGCCTGGCGCCCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCGCG 6577  
QY 2244 rProSerProLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264  
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QY 2264 uAspPro 2266  
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RESULT 11  
US-09-935-541-3  
; Sequence 3, Application US/09935541  
; Patent No. US20020150911A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/935,541  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: 09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 6855  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (192)..(6755)  
US-09-935-541-3  
Alignment Scores:  
Pred. No.: 0 Length: 6855  
Score: 5484.00 Matches: 1237  
Percent Similarity: 59.93% Conservative: 211  
Best Local Similarity: 51.20% Mismatches: 507  
Query Match: 46.07% Indels: 462  
DB: 9 Gaps: 56  
US-09-611-257A-37 (1-2266) x US-09-935-541-3 (1-6855)  
QY 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50  
Db 264 CAGCCCGGACCCCGGAGCCCCCATCTCCCGCCAGCGCCTGGAGGAGCCTCTGGATGA 323

QY 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66  
Db 324 GCTGATCTCATGTCCACACCCAGACCTGGCGCCTATTGCCTTCTTCTGCCTGCGACAG 383  
QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86  
Db 384 ACCACCAAGCCCGGAACTGGTGCATCAAGATGGTGTGCAACCCCGTGGTTTGAATGTGTC 443  
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106  
Db 444 AGCATGTGGTGATCTGTGTAACCTGCGTGACACTTGGCATGTACCAGCCGTCGACGAC 503  
QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAla 126  
Db 504 ATGGACTGCTGCTCCGACCGCTGCAAGATCCTGCAGGTCTTGTATGATCATCTTATC 563  
QY 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146  
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QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166  
Db 624 TACCTCGGGGACACATGGAACCGCTGGATTTCTTCATGCTGCGAGGGATGGTGGAG 683  
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186  
Db 684 TACTCCCTGGACCTTCAGAACATCAACCTGTGAGCCATCCGACCGCTGCGCGTCTGAGG 743  
QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206  
Db 744 CCCCTCAAAGCCATCAACCCGCTGCCAGTATCGGGATCTGGTGAACCTGCTCTCTGGAC 803  
QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226  
Db 804 ACCTGCCCATGCTGGGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863  
QY 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246  
Db 864 ATCATAGGTGTGCAGCTCTGGCGGGGCTGCTGCGGTAACTGCTGCTGCTGCTGCTGCTGCT 923  
QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266  
Db 924 TTCACCATCAAGGGGATGTGGCTTGCCCTTGCCCATATACTACACGCGGAGGAGGATGATGAG 983  
QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286  
Db 984 ATGCCCTTTCATCTGCTCCCTGTGCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCC 1043  
QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300  
Db 1044 CCGCTCAAGGAGCAG-----GGCCGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318  
Db 1095 GACTTTGGGGCGGGCGGCCAGACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGT 1154  
QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338  
Db 1155 TACTACAATGTGTGCCGACGGGCGAGCGCAACCCCAAGGGTGCCATCAACTTTGAC 1214  
QY 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358  
Db 1215 AACATCGGTTATGCTTGGATTGTCTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAG 1274  
QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378  
Db 1275 ATCATGTACTACGTGATGGATGCTCACTCTCTTCTACAACTTCATCTACTTCTCTGCTT 1334  
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398  
Db 1335 ATCATAGTGGGCTCCTTCTTTCATGATCAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1394



Db 2970 TATGACCAGCGTCCCTGTCCAGCTCCGGAGCTCTACTACGGGCCATGGGCGGCAGC 3029

Qy 1101 SerSerTrpThrSerArgSerArgSerLeuGluArgAlaProSerLeuLys 1120

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Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGlu---GlyGlnGluSer 1139

Db 3072 CACAAGCCGCTCGCGGAGCATGATGCTCTCTGCGGAGCGCGCGCGGCC 3131

Qy 1140 GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157

Db 3132 CGGGTCTGGAGGTTGCCGCGGACGAGGGCGCGCGCGCGCGCCGCGCACACCCA 3191

Qy 1158 His-----ArgHisArgGly 1162

Db 3192 CACGCCCCACCATTCATCACGGGCCCATCTGGCGCACCGGCCACCGCGCGG 3251

Qy 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182

Db 3252 ACGCTGTCCCTCGACAAACAGGAGTCTGGTGGACCTGGCGGAGCTGGTCCCGCGGTGGC 3311

Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200

Db 3312 GCCCACCCCGCGCGCTGGAGGGCGCGCAGCGCGCGCGCGCGCATGAGGACTGCAAT 3371

Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220

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Qy 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIl 1240

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Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260

Db 3488 CGACGTCTATAAGCCCGACTGGTGGAGGTCGCGAAGACTGGTGTCTACCTCTCTC 3547

Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280

Db 3548 TCCCGAGAACAGGTTCCGGTCTGTGTGACACCATTAATGGCCACAAACTCTTCGACTA 3607

Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIl 1300

Db 3608 CGTCGTCTGGCTTCATCTTTCTCACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3667

Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320

Db 3668 CGAGCGCGGACGACCGAAGCATCTTCTCACCGTGTCCAACATACATCTTACGGCCAT 3727

Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340

Db 3728 CTTCTGGGCGAGATGACATTGAAGTAGTCTCGTGGCGCTGTACTTTCGGCGAGCAGGC 3787

Qy 1340 aTyrLeuArgSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360

Db 3788 GTACCTACGCAGCAGCTGGAACGTGTGTGGATGGCTTTCTTGTCTTCGTCTCCATCATCGA 3847

Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380

Db 3848 CATCGTGGTGTCCCTGCCTCAGCCGGGGAGCCAAAGATCTTGGGGGTCTCTCCGAGTCTT 3907

Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400

Db 3908 GCGGCTCTCGCACCCCTACGCCCCCTTGGGTGTATCAGCCGGCGCGCGCGGCTTGAAGCT 3967

Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420

Db 3968 GGTGGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGCTG 4027

Qy 1420 sAlaPheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440

Db 4028 TGCCTTCTTCATCATCTTTGGCATCTTGGGAGTGCAGCTCTTCAAGGGCAAGTTCTTACCA 4087

Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460

Db 4088 CTGTCTGGCGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCACTA 4147

Qy 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480

Db 4148 CCGTGGGTCCATCACAAATACAACTCGACAACCTGGGCCAGGCTCTGATGTCCCTCTT 4207

Qy 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGl 1500

Db 4208 TGTCTGGCATCCAAGGATGGTTGGGTGAACATCATGTACAATGGACTGGATGCTTTCG 4267

Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520

Db 4268 TGTGGACCAAGCAGCTGTGACCAACCAACACCCCTGGATGTGTACTTTCATCTCTT 4327

Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540

Db 4328 CCTGTCTCATCTCAGCTTCTTTGTGTCTCAACATGTTTGTGGGTGTCTGTGGAGAACTT 4387

Qy 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLe 1560

Db 4388 CCACAAGTGCCTGGCAGCACCCAGGAGGCTGAAGAGGCACCGCGCGTGTGAGGAGAACGGCT 4447

Qy 1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580

Db 4448 GCGCGCTGTGAGAGAAAGCGCGCAAGGCCAGCGGCTGCGCTACTATGCCACCTATTG 4507

Qy 1580 rArgPheArgLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600

Db 4508 TCACACCCCGCTGTCTCATCCACTCCATGTGCACCAGCCACTACCTGGACATCTTTCATCAC 4567

Qy 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIl 1620

Db 4568 CTTTCATCATCTGCCTCAACGTGTGTCCACTGTCCCTGGAGCACTACAATCAGCCCACTC 4627

Qy 1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640

Db 4628 CCTGGAGACAGCCCTCAAGTACTTGCAACTATATGTTCCACTGTCTTTGTGTGGAGGC 4687

Qy 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660

Db 4688 TGTGTGAAGCTGGTGGCATTTGTGTGAGCGCTTCTTCAAGGACCGATGGAAACAGCT 4747

Qy 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680

Db 4748 GGACCTGGCCATTGTCTACTGTCTAGTCAATGGGCATCACCTGGAGGAGATCGAGATCAA 4807

Qy 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700

Db 4808 TCGCGCCCTGCCCATCAATCCCACCATCATCCGCATCATGAGGGTTCTGCGCATTTGCCG 4867

Qy 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720

Db 4868 AGTGTGAAGCTGTTGAAGATGGCCACAGGAATGCGGGCCCTGTGTGGACACGGTGTGCA 4927

Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740

Db 4928 AGCTTTGCCCGCAGGTGGCAACCTGGGCCCTCTCTTTCATGTGTCTTCTTTCATCTATGC 4987

Qy 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760

Db 4988 TGCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTCGAGGG 5047

Qy 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780

Db 5048 CATGAGCCCGCATGCCACCTTCGAGAACTTCGGCATGGCCCTTCTTCCACATCTTTCAGGT 5107

Qy 1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspGl 1799

Db 5108 CTCCACGGGTGACAACTGGAAACGGGATCATGAAGGACACCGTGGGGACTGCACCCACGA 5167





Query Match:	46.07%	Indels:	462
DB:	16	Gaps:	56

US-09-611-257A-37 (1-2266) x US-10-425-800-3 (1-6855)

QY	31	ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly	50
DB	264	CAGCCCGGACCCCGAGCCCGCCCATCTCCCGCCAGGCCCTGGAGGAGCCTCTGGATGGA	323
QY	51	-----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln	66
DB	324	GCTGATCCTCATGTCCACACCCAGACCTGGCGCCTATTGCCCTTCTTCTGCCTGCGACAG	383
QY	67	AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgIle	86
DB	384	ACCACGAGCCCGGAACTGGTGCATCAAGATGGTGTGCAACCCGTTTGAATGTGTC	443
QY	87	SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp	106
DB	444	AGCATGCTGGTATCCTGCTGAACCTGCGTACACTTGGCATGTACCAGCCGTGCGACGAC	503
QY	107	IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAla	126
DB	504	ATGGACTGCCCTGTCCGACCGCTGCAAGATCCTGCAGGCTTTTGATGACTTTCATCTTTATC	563
QY	127	PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys	146
DB	564	TTCTTTGCCATGGAGATGGTGTCTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAAAGTGC	623
QY	147	TyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu	166
DB	624	TACCTCGGGGACACATGGAACCGCTGGATTTCTTCATCGTCATGGCAGGGATGGTCGAG	683
QY	167	TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValAlaArgThrValArgValLeuArg	186
DB	684	TACTCCCTGGACCTTCAGAACATCAACCTGTGCAGCCATCGCACCGTGCCTGCTGAGG	743
QY	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206
DB	744	CCCCTCAAAGCCATCAACCGCGTGCCAGTATGCGGATCTGGTGAACTGCTCTCTGGAC	803
QY	207	ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly	226
DB	804	ACACTGCCCCATGCTGGGAATGTCTGTGCTGCTGCTTCTTGTCTTCTTCTTCTTCTTGGC	863
QY	227	IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn	246
DB	864	ATCATAGGTGTGCAGCTCTGGCGGGCCTGCTGCGTAACCGCTGCTTCTCTGGAGGAGAAC	923
QY	247	PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu	266
DB	924	TTCAACCATACAAGGGATGTGGCCTTGCCCCCATATACAGCCGGAGGAGGATGATGAG	983
QY	267	SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro	286
DB	984	ATGCCCTTCATCTGCTCCCTGTCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCC	1043
QY	287	ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu-----	300
DB	1044	CGCTCAAGGAGCAG-----GGCCGTGAGTGTGCTGCTGCCAAGGACGACGCTCTAC	1094
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln	318
DB	1095	GACTTTGGGGCGGGGCCAGGACCTCAATGCCAGCGGCCTCTGTGTCAACTGGAAACCGT	1154
QY	319	TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp	338
DB	1155	TACTACAAATGTGTGCCGCGGGCAGCGCCCAACCCCAAGGGGTGCCATCAACTTTGAC	1214
QY	339	AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp	358
DB	1215	AACATCGGTTATGCTTGGATGTTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAG	1274

QY	359	IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu	378
DB	1275	ATCATGTACTACGTGATGCTCACTCCCTCTACAACCTTCACTCTACTCTATCTATCTGCTT	1334
QY	379	IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe	398
DB	1335	ATCATAGTGGGCTCTCTTCTCATGATCAACCTGTGCCTCGTTGTATAGCGACCCAGTTC	1394
QY	399	SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer	418
DB	1395	TCGGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAGCGGCGCTACTGTCTCC	1454
QY	419	AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys	438
DB	1455	---TCCAGCACGGTGGCCAGCTACGCCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAG	1511
QY	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla	458
DB	1512	TATGTCTGCCACATCTCTGCGCAAGGCCAAGCGC-----CGCGCCCTG	1553
QY	459	GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThrGlnPro	478
DB	1554	GGCCTCTACCAGGCCCTGCAGAGCCGGCGCCAGGCCCTGGGC-----	1595
QY	479	SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis	498
DB	1595	-----	1595
QY	499	HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer	518
DB	1595	-----	1595
QY	519	ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer	538
DB	1596	-----CCGGAG	1601
QY	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis	558
DB	1602	GCCCCGGCC-----CCGCCAAACCTGGGCC-----CAC	1631
QY	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGlu	578
DB	1632	GCCAAG-----GAGCCCCGGCACTACCAGCTGTGCCCGCAACATAGCCCCCTGGAT	1682
QY	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro	598
DB	1683	GGCAGCCCCCACACCTG-----GTGAGCCCCATC	1712
QY	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr	618
DB	1713	CCCGCCACGCTG-----	1724
QY	619	LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr	638
DB	1724	-----	1724
QY	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658
DB	1724	-----	1724
QY	659	SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg-----	672
DB	1725	-----GCTTCGATCCCGCAGCTGCCCTGTGTCAGCATGAGGACGGCCGGGCC	1778
QY	673	AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla	692
DB	1779	TCGGGCTGGGCAGCACCGAC--TCGGGGCAGGAGGGCTCGGGCTCCGGAGCTCCGCT	1835
QY	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712
DB	1836	GGTGGCGAG-----GACGAGCGGGATGGGACCGGGGCCCGGAGCAGCAGGAGGCC	1889
QY	713	GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-----	726



QY	1400	uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy	1420
DB	3968	GGTGGTGGAGACACTCATCTCCTCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGCTG	4027
QY	1420	sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa	1440
DB	4028	TGCCTTCTTCATCATCTTTGGCATCCTGGGAGTGCAGCTCTTCAAGGGCAAGTTCTATCCA	4087
QY	1440	lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy	1460
DB	4088	CTGTCTGGGCGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCAACTA	4147
QY	1460	rArgTIPValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh	1480
DB	4148	CCGCTGGGTCCATCAACAATACAACCTTCGACAACTGGGCCAGGCTCTGATGTCCCTCTT	4207
QY	1480	eValLeuAlaSerLysAspGlyTIPValAspIleMetTyrAspGlyLeuAspAlaValG1	1500
DB	4208	TGTCTGGCATCCAAAGATGGTTGGTGAACATCATGTACAATGGACTGGATGCTGTGTC	4267
QY	1500	yValAspGlnGlnProIleMetAsnHisAsnProTIPMetLeuLeuTyrPheIleSerPh	1520
DB	4268	TGTGACCCAGCAGCCTGTGACCAACCACCAACCCCTGGATGCTGCTGTACTTTCATCTCCTT	4327
QY	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh	1540
DB	4328	CCTGCTCATCGTCAGCTTCTTTGTGCTCAACATGTTGTGGTGTCTGTTGGAGAACTT	4387
QY	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe	1560
DB	4388	CCACAAGTGCCCGCAGCACCCAGGAGCTGAAGAGGCACGGCGCTGAGGAGAACGGCT	4447
QY	1560	uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe	1580
DB	4448	GCGGCGCTGGAGAAGAGCGCGGAGGCCAGCGGCTGCCCTACTATGCCACCTATTG	4507
QY	1580	rArgPheArgLeuLeuValHisLeuLeuCysThrSerHisTyrLeuAspLeuPheIleTh	1600
DB	4508	TCACACCCGGCTGCTCATCCACTCCATGTGTGCCAGCCACTACCTGGACATCTTCATCAC	4567
QY	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIl	1620
DB	4568	CTTTCATCATCTGCCCTCAACGTGGTCAACCATGTCCCTGGAGCACCTACAATCAGCCACGTC	4627
QY	1620	eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe	1640
DB	4628	CCTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCCACCACTGTCTTTGTGTGGAGGC	4687
QY	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTIPAsnGlnLe	1660
DB	4688	TGTGCTGAAGCTGGTGGCATTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACCACT	4747
QY	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
DB	4748	GGACCTGGCCATTGTGCTACTGTCTAGTCACTGGGCATCACCTGGAGGAGATCGAGATCAA	4807
QY	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
DB	4808	TGCGGCCCTGCCCATCAATCCACCATCATCCGCATCATGAGGGTTCTGCGCATGTCGCCG	4867
QY	1700	gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG1	1720
DB	4868	AGTGTGAAGCTGTTGAAGATGGCCACAGGAATGCGGCCCTGCTGGACACGCTGGTGCA	4927
QY	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
DB	4928	AGCTTTGCCCCAGGTGGGCAACCTGGGCCCTCCTTTCATGTGCTCTTCTTCATCTATGC	4987
QY	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1	1760
DB	4988	TGCTCTCGGGGTGGAGTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTGCGAGGG	5047

QY	1760	yLeuGlyArgHisAlaThrPheArgAsnPhGlyMetAlaPheLeuThrLeuPheArgVa	1780
DB	5048	CATGAGCCGGCATGCGACCTTCGAGAACTTCGGCATGGCCTTCCTCACACTCTCCAGGT	5107
QY	1780	lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys--AspG1	1799
DB	5108	CTCCACGGGTGACAACTGGAACGGGATCATGAAGGACACGTCGGGGACTGACCCACGA	5167
QY	1799	nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa	1817
DB	5168	CGAGCGCAGCTGCCTGAGCAGCCTGCAGATTGTGTGCGCGCTGTACTTCGTGAGCTTCGT	5227
QY	1817	lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG1	1837
DB	5228	GCTCACC CGCAGTTCGTGCTCATCAACGTGGTGGTGGTGTGCTCATGAAGCACCTGGA	5287
QY	1837	uGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuLeuGluMe	1857
DB	5288	CGACAGCAACAAGGAGGCGCAGGAGGACGCGAGATGGATGCCGAGCTCGAGCTGGAGAT	5347
QY	1857	t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG1	1876
DB	5348	GGCCCATGGCCCTGGCCCTGGCCCGAGGCTGCCTACCGGCTCCCCGGGGCGCC---CCTGG	5404
QY	1876	yValGluGlyProAsp-----	1881
DB	5405	C---CGAGGCGCGGAGGGGCGGGCGGCGGCGGCGGCGGCGGCTGTGCGCGCG	5461
QY	1882	-----SerPro-----	1883
DB	5462	CTGCTACTCGCCTGCCCGAGGAACTGTGTGGTGGACAGCGTCTCTTTAATCATCAAGGA	5521
QY	1884	-----AspSerProLysProGlyAlaLeuHis-----	1892
DB	5522	CTCCTTGGAGGGGAGCTGACCATCATCGACAACCTGTGGGGCTCCATCTTCCACCACCTA	5581
QY	1893	-----ProAlaAla-----	1895
DB	5582	CTCCTCGCCTGCGGCTGCAAGAAGTGTCAACCACGACAAGCAAGAGGTGCAGCTGGCTGA	5641
QY	1896	-----HisAlaArgSerAlaSer-----HisPh	1903
DB	5642	GACGGAGGCCCTTCTCCCTGAACTCAGACAGTCTCTGTCATCTCTGCTGGGTGACGACCT	5701
QY	1903	eSerLeuGluHisProThrMetGlnPro-----HisProThrGluLeuPr	1918
DB	5702	GAGTCTCGAGGACCCACAGCCTGCCCACTGGCCGCAAGACAGCAAGGGTGAGCTGGA	5761
QY	1918	oGlyProAspLeuLeuThrValArgLysSerGly-----ValSerArgTh	1933
DB	5762	CCCACCTGAGCCCATCGTGTGGGAGACCTGGGCGGAATGCTTCTTCCCTGTCTCTCTAC	5821
QY	1933	rHisSerLeuProAsn--AspSerTyrMetCysArgHisGlySerThrAlaGluGlyPr	1952
DB	5822	GGCCGTCTCGCCGATCCAGAGAACTTCTTGTGTGATGGAGGAGATCCCATTCACCC	5881
QY	1952	oLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi	1972
DB	5882	TGTC-----CGGTCTGG-----CTGAAACATGACAGCAGTCAAGCACCCCCAAGTCC	5929
QY	1972	sSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHis-----	1990
DB	5930	CTTCTCCCGGATGCTCCAGCCCTCTCTGCCCATGCCAGCCGAGTCTTCCACCCTGCG	5989
QY	1991	-----LeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe	2006
DB	5990	AGTGCTGCCAGCCAGAAAGGCCCAAGAAAGGGCACTGGCACTGGAAACCTCCCAAGAT	6049
QY	2006	uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr	2021
DB	6050	TGGCTGCAGGGCTCTGGGCATCTCTGCGGTACCAAGGGTCAACTGTACCTCTCTCCG	6109
QY	2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe	2041

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Db      6110 GCAGGCCACGGGAGCGACACGTCGTCGAC----- 6140
QY      2041 uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyG1 2061
Db      6141 -----GCCAGCCCGCAGCAGCTCCCGCGGCGAGCCTCGACACCGCTCGAGGA 6187
QY      2061 nSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMetTh 2081
Db      6188 CAGCCTGACCTGAGCGACAGCCCGCGGTGCC-----CTGGG 6226
QY      2081 rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr 2101
Db      6227 GCCGCCCGCGCTGCTCCAGGACCCCGCGCGCTGTCC-----CCGCCGCTCG 6277
QY      2101 gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProG1 2121
Db      6278 CCGCGCGCTGAGCCTG----- 6293
QY      2121 yGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaG1 2141
Db      6294 -----CGCGCGCGGCTCTTCAGCCTGCGGGGCTCGCGGCG-- 6332
QY      2141 nSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVa 2161
Db      6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358
QY      2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
Db      6359 CTCC---ACCAGCCGGGTGCACCCACACGACTCCATGGACCCCTCGGACGAGGG 6415
QY      2179 -LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPr 2198
Db      6416 CCGCGGTGGCGGGCGGGCGGGCGGCGGAGCACTCGGAGACCCCTCAGCAGCCT 6475
QY      2198 oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSe 2215
Db      6476 CTCGCTCACCTCCCTCTTCTGCCCGCGGCC-----CCGCGCGCCAGC 6517
QY      2215 rProGlyIleCysLeuArgArgAlaProSerSerAspSer-----LysAs 2231
Db      6518 CCGCGCCTCACCGCCCGCCAGGAGTTCAGCAGCAGCAGCAGCCTGGCGCCCGCGCG 6577
QY      2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa 2251
Db      6578 CCCCCAGCGCGCGCCCTGGCCCCACGCGCTGGCCCGGAGCCCTCGTGGCGCGCGGAC-- 6635
QY      2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db      6636 -----CGCAGCAAGGACCCCGCGCGCGCGCGCGGCGGACCG 6665
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RESULT 13
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12
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Alignment Scores:
Pred. No.: 0
Score: 5418.50
Percent Similarity: 60.47%
Best Local Similarity: 51.57%
Query Match: 45.52%
DB: 9

US-09-611-257A-37 (1-2266) x US-09-935-541-12 (1-6503)

QY      27 GlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46
Db      320 GGAATCACTGAGCAGCCGGGGCCCGGAGTCCCTCCATCCCTCCAGGCTCGAGGAG 379
QY      47 GluAlaGluGly-----LeuProTyrProAlaLeuAlaProValPhePhe 62
Db      380 CCATTGGAAGGAACCAACCTGACGTCACACATCCAGACCTGGCTCCTGTTGCTTCTTC 439
QY      63 TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82
Db      440 TGCCTGCGCCAGACACGAGCCCGGAACTGGTGCATCAAGATGGTTTGTAAACCGGTGG 499
QY      83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db      500 TTCGAGTGTGTGAGCATGCTGGTTATTCTGCTGAACCTGTGTGACCTGGGATGTACCAG 559
QY      103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
Db      560 CCATGTGATGACATGGAGTGCCTGTCCGACCGCTTGAAGATCCTGAGGCTCTTCGATGAC 619
QY      123 PheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyIlePhe 142
Db      620 TTCATCTTCATCTTCTTCCATGGAGATGGTGTCTTAAGATGGTGGCCCTGGGCATTTT 679
QY      143 GlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAla 162
Db      680 GGCAAGAGTGTCTACCTCGGAGACACATGGAACCGCTGGATTCTTCTTCTTCATGTGCA 739
QY      163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
Db      740 GGGATGGTTGAGTACTCTCTGGACCTACAGAACATCAACCTGTGAGCATCCGCACTGTG 799
QY      183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
Db      800 CGTGTCTGAGGCTCTCAAAGCCATCAACCGTGTACCCAGCATCGGATCCTGGTGAAC 859
QY      203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhe 222
Db      860 CTGCTGCTCGACACGCTGCCCATGTCTGGGAGACGTCTCTCTGCTCTGTTCTTCGTC 919
QY      223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe 242
Db      920 TTCATCTTCGGCATCATTTGGCGTGCAGCTCTGGGAGGCTGTGAGGCTGCCCCCTTATTA 979
QY      243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
Db      980 CTGGAAGAGAACTTCACCATACAAAGGGGATGTGGCCCTGCCCCCTTATTAACCAACCA 1039
QY      263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
Db      1040 GAGGATGACGAGATGCCCTTTATCTGCTCCCTGACTGGGGACAATGGCATCATGGGCTGC 1099
QY      283 ArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db      1100 CACGAGATCCCCCACTGAAGAGAGCAG-----GGCCGGGAATGCTGCTGTCCAAA 1150
QY      301 -----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysVal 314
Db      1151 GATGATGTGTATGACTTCGGGGCGGGCGCCAGGACCTCAACGCCAGCGGTCTGTGCGTC 1210
QY      315 AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAla 334
Db      1211 AACTGGAACCGCTACTACACGTCTGCCGACCGGGCAACGCCAACCTCACAAGGGCGCC 1270
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QY 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354  
Db 1271 ATCAACTTTGACAACATTGGCTATGCCGGATTGTGATTTTCCAGGTGATCACTCTGAA 1330  
QY 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374  
Db 1331 GGCTGGTGGAGATCATGTACTATGTGATGGACGCACATTCTTACAACTTTCATCTAC 1390  
QY 375 PheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuCysLeuValIle 394  
Db 1391 TTCATTCTGCTCATCATAGTGGCTCCTTCTTCATGATCAACTTGTGCCTCGTTGTCATA 1450  
QY 395 AlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414  
Db 1451 GCAACCCAGTTCTCTGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAACGCCAG 1510  
QY 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434  
Db 1511 CGTACCTGTCC--TCCAGCACGGTGGCCAGTTACGCTGAGCCCGGTGATTGCTATGAG 1567  
QY 435 GluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnVal 454  
Db 1568 GAGATCTTCCAATATGTCTGTACATCCTTCGAAAGCCAGCCCGCTGCCCTAGGCCCTC 1627  
QY 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474  
Db 1628 TACCAGGCCCTGCAGAACCGG----- 1648  
QY 475 GluThrGlnProSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeu 494  
Db 1648 ----- 1648  
QY 495 ValHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAla 514  
Db 1648 ----- 1648  
QY 515 ProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu 534  
Db 1649 -----CGCCAGGCCCATGGGC----- 1663  
QY 535 ProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHis 554  
Db 1664 -----CCGGGACACCCAGCC-----CCTGCCAAGCCTGGGCC----- 1696  
QY 555 SerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArg 574  
Db 1697 -----CATGCCAAG-----GAGCCAGCCACTGCAAGCTGTGCCCCAGCAC 1738  
QY 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594  
Db 1739 AGCCCCCTGGAC-----CCACACTCCCCAC 1762  
QY 595 ThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSer 614  
Db 1763 ACATGGTGCAGCCC----- 1777  
QY 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMethHisLys 634  
Db 1777 ----- 1777  
QY 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys 654  
Db 1778 -----ATCTCTGCCATT 1789  
QY 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672  
Db 1790 CTGGCCTCTGAC-----CCAGCAGCTGCCCTCACTGCCAGCAGGCA 1834  
QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSer 688  
Db 1835 GGCAGGGCGCCTCTGGCCTGGGCAGCACTGAC---TCAGGCCAGGAAGGCTCAGGTTCT 1891

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Db 1892 GGTGGCTCTGCAGAGCCGAAGCCAATGGGATGGACTCCAGACAGTGGATGGSGTC 1951  
QY 707 pProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe 724  
Db 1952 TCCTCGGACCTGGGAAGGAGGAGGAACAGGAGCGGG-----CAGCCCAGACTG 2002  
QY 724 rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTy 744  
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QY 764 rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe 784  
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Db 2773 GGACCAGAGCTCATCCAATTTGGAGGAGTTTGACAAGCTCCAGAGGGCCTGGACAACAG 2832  
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QY 1066 -----SerArgArgThrSerSerSe 1072  
Db 2944 CCTCTACTGCAGCCAGACCCGGTACTGGTGGCCCTAGACTCTCGGAAAGCAGTGTCTAT 3003  
QY 1072 rGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSe 1092  
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QY 1092 rProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSe 1112  
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QY 1112 rLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLe 1132  
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QY 1150 ----ArgAlaSerProAlaGlySerAspHis----- 1158  
Db 3220 AACTCGCACCGCCCTGCTGCTCCACACGCGCACCCAGCGCACCATGGACCCACCT 3279  
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Db 3280 GGCACACCGTACCGCACACCCGCGGACTCTGTCCCTTGATACACAGGACTCTGTGA 3339  
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Db 4117 GCAGCTTTTCAAAGGCAAGTTCTTACCATTTGTTGGGAGTGGACACCCGAAACATCACCAA 4176  
QY 1451 nLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAs 1471  
Db 4177 CCGATCTGACTGCGTGGCGGCCCACTACCGCTGGTGGTGCATCACAATACAACTTTGACAA 4236  
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QY 1631 ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr 1651  
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QY 1691 gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMe 1711  
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QY 1731 uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG1 1751  
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QY 1887 sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi 1907  
Dd 5437 CCCTGGT----- 5443  
QY 1907 sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal----- 1925  
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QY 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941  
Dd 5503 TGGGGCTCGGGGCGAGGATCGGGAGGGGAGGTGTGGAGGC---GACACCGAGAGTCA 5559  
QY 1941 rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuPr 1961  
Dd 5560 CCTGTGCCG----- 5569  
QY 1961 oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrl 1981  
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QY 1981 eLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGl 2001  
Dd 5570 -----CACTGCTATTCTCCAGCCCGAGAGACCCTGTGG-- 5602  
QY 2001 yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021  
Dd 5603 -----CTGGACAG 5610  
QY 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041  
Dd 5611 CGTCTCTTTAATCATCAAGGACTCCTTGGAG-----GGGGAGCTGACCAT 5655  
QY 2041 uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTyrSerPheTrpGly 2060  
Dd 5656 CATTGACAACCTGTCTGGTCCGTCTTCCACCCTACGCTCAGCCCTGACGGCTGTGGCAA 5715  
QY 2061 GlnSerSerThrGlnAlaGlnHisSerArgSer-----HisSerLysIleSer 2077  
Dd 5716 GTGTACCATGACAAGCAAGAGACAGGTCTTTCATCCATCCTGTGGGGGATGACCTGAGT 5775

QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097  
Dd 5776 -----CTTGAGGACCCACCGCCTGCCCA-----CAGGGCCCC 5808  
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117  
Dd 5809 AAGGAGAGCAAG-----GGTGAACTA 5829  
QY 2118 LeuProProGlyGlnGluGluProProSerProArgAspLeuLysCysTyr--- 2136  
Dd 5830 GAGCCTCG-----GAGCCCATGCAGGCTGGAGACCTGGATGAATGCTTTTGG 5877  
QY 2137 -----SerVal----- 2138  
Dd 5878 CCCTTTGCCAAGCAGCCAGTGTCCACAGGCCAGAGAGCCTGTGTGGAGATGGGGC 5937  
QY 2139 ---GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgArgHi 2157  
Dd 5938 CATTCCATTCAACCTGTCCAG-----TCCTGGCTCAAAACACGAGAGACGCCA 5985  
QY 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170  
Dd 5986 AGCACCCACAGAGCCCTTTCTCCCGGATGGCTCCAGCCCTCTCTGTAGATGCCTGCTGA 6045  
QY 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGl 2188  
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Dd 6106 AACCTTGCCCAAGATTGCACCTCAG-----GGGTCTCTG 6138  
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QY 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248  
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RESULT 14

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; Sequence 12, Application US/10425800  
; Publication No. US20030180886A1  
; GENERAL INFORMATION  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGilvern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/10/425,800  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US/09/404,650  
; PRIOR FILING DATE: 1999-09-23  
; NUMBER OF SEQ-ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 6503  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-10-425-800-12

Alignment Scores:  
Pred. No.: 0 Length: 6503  
Score: 5418.50 Matches: 1212  
Percent Similarity: 60.47% Conservative: 209  
Best Local Similarity: 51.57% Mismatches: 446  
Query Match: 45.52% Indels: 484  
DB: 16 Gaps: 53

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US-09-611-257A-37 (1-2266) x US-10-425-800-12 (1-6503)
QY 27 GlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46
Db 320 GGAATCACTGAGCAGCGGGGCCCCGGAGTCCCCCTCCATCCCTCCAGGCTGGAGGAG 379
QY 47 GluAlaGluGly-----LeuProTyrProAlaLeuAlaProValValPhePhe 62
Db 380 CCATTGGAAGGAACCAACCCCTGACGCTCCACATCCAGACCTGGCTCCCTGTGCTTCTTC 439
QY 63 TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82
Db 440 TGCCTGCGCCAGACCACGAGCCGACGCGAACTGGTGATCAAGATGGTTTGTAAACCCGCTGG 499
QY 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 500 TTCGAGTGTGTGAGCATGCTGGTTATTCTGCTGAACCTGTGTGACCCCTGGGATGTACCAG 559
QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
Db 560 CCATGTGATGACATGGAGTGCCTGTGCGACCGTTGCAAGATCCTGCAGGTCTTCGATGAC 619
QY 123 PheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePhe 142
Db 620 TTCATCTTCATCTCTTTGGCCATGGAGATGGTCTTAAGATGGTGGCCCTGGGCAATTTT 679
QY 143 GlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAla 162
Db 680 GGCAAGAAGTGTACTACCTCGGAGACACATGGAAACCGCCTGGATTTCTTCATTTGTCATGGCA 739
QY 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
Db 740 GGGATGGTTGAGTACTCTCTGGACCTACAGAACATCAACCTGTGACCCATCCGCACTGTG 799
QY 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
Db 800 CGTGTCTCGAGGCTCTCAAAGCCATCAACCGTGTACCCAGCATCGGATCCTCGTCTTC 859
QY 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhe 222
Db 860 CTGCTGCTCGACAGCTGCCATGTGGGAACGTGTCTCCTGCTCTGTTCTTCTGCTCTTC 919
QY 223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe 242
Db 920 TTCATCTTCGGCATATTGGCGTGCAGCTCTGGCAGGCGCTGTACGGAACCGCTGCTTC 979
QY 243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
Db 980 CTGGAAGAGAACTTCACCATACAAGGGGATGTGGCCCTGCCCTTATTACCAACCCAGAG 1039
QY 263 AsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
Db 1040 GAGGATGACGAGATGCCCTTTATCTGCTCCCTGACTGGGGAACAATGGCATCATGGGCTGC 1099
QY 283 ArgSerValProThrLeuArgGlyAspGlyGlyProProCysGlyLeu----- 300
Db 1100 CACGAGATCCCCCCTGAGGAGCAG-----GGCCGGGAATGCTGCCTGTCCAAA 1150
QY 301 -----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysVal 314
Db 1151 GATGATGTGTATGACTTCTGGGGCGGGGCGGCGGAGACCTCAACGCCAGCGGTCTGTGCGTC 1210
QY 315 AsnTrpAsnGlnTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAla 334
Db 1211 AACTGGAACCGCTACTACAACGTCTGCCGACGGGCAACGCCAACCTCACAAGGGCGCC 1270
QY 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354
Db 1271 ATCAACTTTGACAACATTGGCTATGCCGGGATGTGATTTTCCAGGTGATCACTCTGGAA 1330
QY 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374
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	QY	724	rValLeuAlapheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTy	744
	Dd	2003	TGTGGG-GATGTGTGCCCGAGACACGAAAAAAGCTGCGGGGCATCGTGGACAGAAGTA	2061
	QY	744	rPheGlyArgGlyIleMetIleAlalaileLeuValAsnThrLeuSerMetGlyIleGluty	764
	Dd	2062	CtTTCAACAGAGGTATCATGATGGCTATCCTGGTGAAACACAGTCAGCATGGCCATCGAGCA	2121
	QY	764	rHisGluGlnProGluGluThrAsnAlaLeuGluIleSerAsnIleValPheThrSe	784
	Dd	2122	CCACGAACAGCCCAGAGACTGACCACAATCCTGGAGATCTGCAATGTGGTCTTCACCAG	2181
	QY	784	rLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPropHeGlyTyrIleLy	804
	Dd	2182	TATGTTTTGCCCTGGAGATGATCCTGAAAACCTGGCCCGCTTTGGGCTCTTCGACTACCTGCG	2241
	QY	804	sAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGL	824
	Dd	2242	GAAACCTTACAACATCTTTGACAGCATCATCGTCATCATCAGCATCTGGGAAATCGTGGG	2301
	QY	824	yGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLe	844
	Dd	2302	GCAGCGGACGGTGGCTGTCTGTGTCGCACCTTCCGGTTGCTGCGGTGCTGAAGCT	2361
	QY	844	uValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAs	864
	Dd	2362	GGTGGCTTCATGCCGCGCTGCGGCGCACGCTCGTGTCTCATGAAGACCATGGACAA	2421
	QY	864	nValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMe	884
	Dd	2422	CGTGGCCACCTTCTGCATGCTACTCATGCTGTTCATCTTTCAGCATCCTTGGGAT	2481
	QY	884	tHisLeuPheGlyCysLysPheAlaSerGluArgSp---GlyAspThrLeuProAspAr	903
	Dd	2482	GCATACTTTGGCTGCAAATTTCAGCCTCCGCACGACGGGAGACACCGTTCTCTGACAG	2541
	QY	903	gLysAsnPheAspSerLeuLeuTriAlaIleValThrValPheGlnIleLeuThrGlnGL	923
	Dd	2542	GAAGAACCTTCGATTCTTACTGTGGCCATCGTGCACAGTGTCCAGATCCTCACTCAGGA	2601
	QY	923	uAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTy	943
	Dd	2602	GGACTGGAACTGTCTGTACAATGGCATGGCCCTCCACCCCCCTGGGCTCCCTCTA	2661
	QY	943	rPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLe	963
	Dd	2662	TTTTGTTGCCCTCATGACCTTTGGCAACTACGTTCTCTTCAATCTCCTGGTGGCTATCCT	2721
	QY	963	uValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe	983
	Dd	2722	GGTAGAGGGTTTCCAGGCTGAG-----	2743
	QY	983	rCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPr	1003
	Dd	2744	-----GGTGTGTGTAATCGTTCTCTGCTCTGATGA	2772
	QY	1003	oASPpheSerProser-----LeuaspGlyAs	1013
	Dd	2773	GGACCAGAGCTCATCCAATTTGGAGGAGTTTGACAAGCTCCAGAGGGCCTGGACAACAG	2832
	QY	1013	pGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHISproGluLeuArgLy	1033
	Dd	2833	TAGAGATCTCAAGCTCTGCCCAATACCCATGACACCCCAATGGACAC-----	2878
	QY	1033	sSerLeuLeuProProLeuIleIleHisthrAlaAlaThrPrometSerLeuProLysSe	1053
	Dd	2879	-----CTGGACCCT-----AGCCTCCCT-----	2896
	QY	1053	rThrSerThrGlyLeuGlyGluAlaLeuGlyProAla-----	1065
	Dd	2897	-----CTGGGTGCGCATCTGGGTCTCTGCTGGTFACCATGGGTACTGCCCCCG	2943

[illegible]

Db	3997	TATCAGCCGGCCCTGGGCTGAAGCTGGTGGTAGAGACGCTCATCTCCTCCCTCAAGCC	4056
QY	1411	oileGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVa	1431
Db	4057	CATTGGGAACATCGTCTCATCTGCTGCTTCTTTCATCATCTTCGGCATCTCTGGGGT	4116
QY	1431	lGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAs	1451
Db	4117	GCAGCTTTTCAAAGCAAGTTCTACCATTTGTTGGAGTGGACACCGAAACATCACCAA	4176
QY	1451	nLysSerAspCysAlaGluAlaSerTyrArgTirpValArgHisLysTyrAsnPheAspAs	1471
Db	4177	CCGATCTGACTGCTGGCGGCCAACTACCGCTGGGTGCATCACAATACAACTTTGACAA	4236
QY	1471	nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTirpValAspIl	1491
Db	4237	CCTGGGCCAGGCATTGATGTCCCTCTTTGTCTGGCCTCCAAGGACGGCTGGGTGAACAT	4296
QY	1491	eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr	1511
Db	4297	CATGTATAATGAATAGATGCTGTTGCTGTGGACAGCAGCCAGTCAGCAACCAACCC	4356
QY	1511	oTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe	1531
Db	4357	CTGGATGCTACTGTACTTTCATTTCTGCTCATCGTCAGCTTCTTTGTGCTCAACAT	4416
QY	1531	tPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGl	1551
Db	4417	GTTTGTGGCGTGGTCTGGAGAACTTCCACAAGTCCGGCAGCACCCAGGAGGTGAGGA	4476
QY	1551	uAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgLysAlaGl	1571
Db	4477	GGCGCGGAGCGTGAGGAGAAACGGCTCGCGCGCTGGAAAGAGCGCGTAAGGTCA	4536
QY	1571	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCysTh	1591
Db	4537	GAGSCTGCCCTACTATGCTACCTACTGTCCCAAGGCTGCTCATCCACTCCATGTGCAC	4596
QY	1591	rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl	1611
Db	4597	CAGCCACTACCTGGACATCTTTCATTTACCTTTCATCATCTGCCTCAATGTTGTCAACATGTC	4656
QY	1611	aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl	1631
Db	4657	CCTGGAGCACTACAACCGCCTACATCCCTAGAGACAGCCCTTAAGTACTGCAACTACAT	4716
QY	1631	ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr	1651
Db	4717	GTTTCAACCACTGCTTTGTGTGGAGGCTGTGCTGAAGCTGTTGGCATTTGGCCTGAGCG	4776
QY	1651	gPheGlnAspArgTirpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGl	1671
Db	4777	TTTCTTCAAGGACCGATGGAAACAGCTGGACCTGGCCATTGTGCTGTGCTCCGTCACTGGG	4836
QY	1671	yIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr	1691
Db	4837	CATCACACTGGAGGAGATCGAGATCAATGCCGCCCTTCCCATCAACCCCACTCATCCG	4896
QY	1691	gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMe	1711
Db	4897	TATCATGCGGTCTTCGATATCGCCCGGGTGTGAAGCTATTGAAGATGGCCACAGGAAT	4956
QY	1711	tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe	1731
Db	4957	GCGGGCCCTGCTGGACACAGTGTACAGGCTCTGCCCCAGGTGGCAACCTGGCCCTGCT	5016
QY	1731	uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGl	1751
Db	5017	CTTCATGCTGCTTCTTTCATCTATGCTGCTCTGGAGTGGAGCTCTTCGAAAGCTGGT	5076
QY	1751	uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGl	1771

5077	CTGCAATGACGAGAACCCGCTGTGAGGGCATGAGCCGGCAGCCACCTTTTGAAACTTCGG	5136
1771	yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy	1791
5137	CATGGCCTTCCTCACGCTCTTCCAGGTCTCCACAGCGGATAACTGGAATGGAATATGAA	5196
1791	sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il	1808
5197	GGACACCCCTGCGAGACTGTACCCCATGATGAGCGCAGCTGCCTAAGCAGCCTGCAGTTGT	5256
1808	eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa	1828
5257	GTACCCGCTCTACTTTGTGAGCTTCGTGCTCACAGCTCAGTTTCGTGCTCATCAACGTGT	5316
1828	lIleAlaValLeuMetLyHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGl	1848
5317	GGTGGCCGTGCTGATGAACATCTGGATGACAGCAACAAGAGGAGCCAGGAGGATGCAGA	5376
1848	uLeuGluAlaGluLeuGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr	1867
5377	GATGGATGCTGAGATCGAGCTGGAGATGGCCCATGGCCCTCGGCCCTGCCCT-----	5428
1867	oLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLy	1887
5429	-----GGCCCTG	5436
1887	sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi	1907
5437	CCCTGGT-----	5443
1907	sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal----	1925
5444	-CCCTGCCCTGCCCTGCCCTGTGCTGGCCCGAGGCTGCCACTAGTTTCACC	5502
1926	-----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy	1941
5503	TGGGGCTCCGGGCGAGGATCGGGAGGGCAGGTCTGTGAGGC---GACACCGAGAGTCA	5559
1941	rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuPr	1961
5560	CCTGTGCCG-----	5569
1961	oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrl	1981
5569	-----	5569
1981	eLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGl	2001
5570	-----CACTGCTATTCTCCAGCCAGGAGACCCTGTGG--	5602
2001	yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr	2021
5603	-----CTGGACAG	5610
2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe	2041
5611	CGTCTCTTTAATCATCAAGGACTCCTTGGAG-----GGGAGCTGACCAT	5655
2041	uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTyrSerPheTrpGly	2060
5656	CATTGACAAACCTGTCTGGGTCCGTCTTCCACCACCTACGCCTCACCTGACCGGTGGCAA	5715
2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer	2077
5716	GTGTCAACCATGACAAGCAAGAGACAGGTCTTTCATCCATCCTGTCTGGGGGATGACCTGAGT	5775
2078	LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro	2097
5776	-----CTTGAGGACCCACGGCCTGCCCA-----CAGGGCCCC	5808
2098	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117
5809	AAGGAGAGCAAG-----GGTGAACATA	5829

QY 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyr--- 2136  
Db 5830 GAGCCTCG-----GAGCCCATGCAGGCTGGAGACCTGGATGAATGCTTTGG 5877  
QY 2137 -----SerVal----- 2138  
Db 5878 CCCTTTGCCAAGCAGCCAGTGTCCACAGGCCCCAGAGAGCCCTGTGTGCGAGATGGGGC 5937  
QY 2139 ---GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgHi 2157  
Db 5938 CATTCATTCAACCTGTCCAG-----TCCTGGCTCAAAACACGAGAGCCCA 5985  
QY 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170  
Db 5986 AGCACCCAGAGCCCTTCTCCCCGGATGGCTCCAGCCCTCTCTGTAGATGCCTGTGA 6045  
QY 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyProGl 2188  
Db 6046 GTTCTTCCACCTGTGTCTGCCAGCCAGAGGGGCGAGGACCGGCATGATGTCAGG 6105  
QY 2188 ySerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGl 2208  
Db 6106 AACCTGCCCAAGATTGCATTTCAG-----GGGTCTCTG 6138  
QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228  
Db 6139 GGCATCGCTGAGTCAACCGAGTGTCACTGCACCCCTCTTGGCGCAGGCTACTGTGAGTGA 6198  
QY 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248  
Db 6199 CACGTCC-----TTGGATGCCAGTCTAGCAGCTCAGCGGGCAGCCTACAGACCACACT 6252  
QY 2248 sLysAspValLeuSerLeuSer 2255  
Db 6253 GGAAGACAGTCTGACTCTGAGT 6274

RESULT 15

US-09-030-482B-18  
; Sequence 18, Application US/09030482B  
; Patent No. US20020009772A1  
; GENERAL INFORMATION:  
; APPLICANT: Snutch, Terry  
; TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED  
; TITLE OF INVENTION: PROBES, CELL LINES AND METHODS  
; FILE REFERENCE: 38109-20007.00  
; CURRENT APPLICATION NUMBER: US/09/030,482B  
; CURRENT FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: US 60/039,204  
; PRIOR FILING DATE: 1997-02-28  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 5562  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(5562)  
; OTHER INFORMATION: Human alpha-1 partial sequence from BAC BK206c7  
US-09-030-482B-18

Alignment Scores:

Pred. No.:	3,25e-316	Length:	5562
Score:	3959.50	Matches:	908
Percent Similarity:	54.89%	Conservative:	158
Best Local Similarity:	46.76%	Mismatches:	361
Query Match:	33.26%	Indels:	515
DB:	9	Gaps:	42

US-09-611-257A-37 (1-2266) x US-09-030-482B-18 (1-5562)

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QY 40 AspProGlySerAlaAspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProVal 59  
Db 289 CCTGAGGCACAGGCCACGTATACAGCAGGGTGCACCCCGCCACGGCGATCCCCACC 348  
QY 60 ValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCys 79  
Db 349 TGCTGCTTTGCTCTTGAC-----TTGGTGTGC 375  
QY 80 AsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGly 99  
Db 376 ACG---TGTTTGAATGTGTACGATGCTGGTATCCTGTAACCTGCTGACACTTGGC 432  
QY 100 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 119  
Db 433 ATGTACCAGCCGTGCGACGACATGGACTGCCTGTCCGACCGCTGCAAGATCCTGCAGGTC 492  
QY 120 PheAspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeu 139  
Db 493 TTTGATGACTTCATCTTTATCTTTTTCCTGATGAGATGGTGTCAAGATGGTGGCCCTG 552  
QY 140 GlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIle 159  
Db 553 GGGATTTTGGCAAGAAGTGTCTACCTCGGGACACATGGAAACCGCTGGATTTCTTCATC 612  
QY 160 ValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaVal 179  
Db 613 GTCATGGCAGGC-----AACATCAACCTGTGAGCCATC 645  
QY 180 ArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIle 199  
Db 646 CGCACCGTGGCGTCTCTGGACACACTGCCCATGTGGGGAATGTCTGTCTGTCTTC 705  
QY 200 LeuValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuCysPhe 219  
Db 706 CTGGTGAACCTGCTCTGGACACACTGCCCATGTGGGGAATGTCTGTCTGTCTTC 765  
QY 220 PheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsn 239  
Db 766 TTTGTCTTCTTCATCTTTGGCATCATAGGTGTGAGCTTGGGGGGGCTGTGCTGCTAAC 825  
QY 240 ArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyr 259  
Db 826 CGCTGCTTCTGAGGAGAACTTACCACATACAAGGGGATGTGGCCTTGCCTCCCATACTAC 885  
QY 260 GlnThrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMet 279  
Db 886 CAGCCGGAGGAGGATGATGAGATGCCCTTCATCTGCTCCCTGTGGGGCGACAATGGGATA 945  
QY 280 ArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGly 299  
Db 946 ATGGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG-----GGCCGTGAGTGTGTC 996  
QY 300 Leu-----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr--- 312  
Db 997 CTGTCCAGGACGACGTCTACGACTTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1056  
QY 313 ---CysValAsnTrpAsnGlnTyrThrAsnCysSerAlaGlyGluHisAsnProPhe 331  
Db 1057 CTCTGTGCAACTGGAACCGTTACTACAATGTGTGCCGCGACGGGCGAGCCCAACCCAC 1116  
QY 332 LysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIle 351  
Db 1117 AAGGGTGCCATCAACTTTGACAACATCGGTTATGCTTGGATGTGATCTTCCAGGTGATC 1176  
QY 352 ThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsn 371  
Db 1177 ACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGATGATGATGATGATGATGAT 1236  
QY 372 PheIleTyrPheIleLeuLeuIleIle----- 380

Db 1237 TTCACTACTTCTATCTGCTTATCATAAAGTGAGCTCATCCACCTCGTTCATGCTGACTGC 1296  
QY 380 ----- 380  
Db 1297 AGCTTCAGCACAGCACAGTCCCCAAAATGTCAAGGTGATTCACTCCCAGGAGTCGCTGCT 1356  
QY 380 ----- 380  
Db 1357 GAATCCCTGCTGCGAGACTCTAGCTCCTCAGTCATCACTGATGAGGCTGAGCCATG 1416  
QY 380 ----- 380  
Db 1417 GAGAACCTCTCTGGCGGCACCTCCAAGGGGATGAAAGCTATCTGCTCAGGCTGGCCGCG 1476  
QY 380 ----- 380  
Db 1477 AGCCAAAGTTCACTCCAGGCTCAGCAAAATGCTGGGAGGGGCTGGGCCCTGAAAGCCTG 1536  
QY 380 ----- 380  
Db 1537 GAAACTGGAGAGAGCCCCCACTCTGTGGAGCCCTCGGGGCCACAAGAGATGGGATCCCCAA 1596  
QY 381 -----ValGlySerPhePhe 385  
Db 1597 TGCCAAACAGGGCAGCCTCTCCCCCTTCATTTCATGCAAGCACAGGTGGGCTCTCTTCTTC 1656  
QY 386 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 405  
Db 1657 ATGATCAACCTGTGCTCGTTGTATAGCGACCCAGTTCGCGAGACCAAGCAACGGGAG 1716  
QY 406 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 425  
Db 1717 CACCGGCTGATGCTGGAGCAGCGCGCAGCTACCTGTCC---TCCAGCACGGTGGCCAGC 1773  
QY 426 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 445  
Db 1774 TACGCCGAGCCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCTGCGC 1833  
QY 446 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeu 465  
Db 1834 AAGGCCAAGCGC-----CGCGCCCTGGGCTCTACCAGGCCCTGCAG 1875  
QY 466 SerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSerSerCysSerArgSer 485  
Db 1876 AGCCGGCGCAGGCCCTGGGCGCGGAGGCCCGGCCCGCCCAACCT----- 1923  
QY 486 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 505  
Db 1924 -----GGGCCCCAGCCCAAGGAGCCCGCCACTAC 1953  
QY 506 HisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAsp 525  
Db 1954 CCTCTCAGAGTCTGGGAATCGATTCTTGGGAGGCAAGCAGAGAAGATGCACGCTCAGAGCT 2013  
QY 526 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProAlaLeuSerGlyAla 545  
Db 2014 GCC-----GCCACCCGTCCTCGGGTGCCAGC 2040  
QY 546 ProProGly---GlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGlu 564  
Db 2041 CATCCAGGGCTGGGCTCGGAGGAGGCC----- 2067  
QY 565 ProValArgCysGlnAlaProProArgSerProSerGluAlaSerGlyArgThrVal 584  
Db 2068 CCAGAGCTGTGC-----CCGCAACATAGCCCCCTGGATGCGACGCCCCACACCCCTG 2118  
QY 585 GlySerGlyLysValTyrProThrValHisThrSerProProProGluThrLeuLysGlu 604  
Db 2119 -----GTGCAGGCCCATCCCGCCACGCTG----- 2142  
QY 605 LysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThrSerLeuAsnIle 624

Db 2142 ----- 2142  
QY 625 ProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys 644  
Db 2142 ----- 2142  
QY 645 GlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyAlaCysGlyPro 664  
Db 2143 -----GCTTCGGATCCC 2154  
QY 665 AspSerCysProTyrCysAlaArg-----AlaGlyAlaGlyGluVal 678  
Db 2155 GCCAGCTGCCCTTGCTGCCAGCATGAGGACGGCGCGGCCCTCGGGCTGGGCGAGCACC 2214  
QY 679 GluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGln 698  
Db 2215 GAC---TCGGGCCAGGAGGGCTCGGGCTCCGGGAGCTCCGCTGGTGGCGAG-----GAC 2265  
QY 699 AspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyPro 718  
Db 2266 GAGCGGATGGGACGGGGCCGGAGCAGCGAGGAGCCCTCTCAGAACTGGGGAAG 2325  
QY 719 AspAlaGluProSerSerValLeu-----AlaPheTrpArg 730  
Db 2326 GAGGAGGAGGAGGAGGAGGAGCGGATGGGGCGGTGTGGTGTGCGGGGATGTGTGGCGG 2385  
QY 731 LeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMet 750  
Db 2386 GAGACGGCAGCCAAGCTGCGCGGCATCGTGGACAGCAAGTACTTCAACCGGGGCATCATG 2445  
QY 751 IleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGlu--- 769  
Db 2446 ATGGCCATCCTGTTCAACACCGTCAGCATGGGCATCGAGCACCCAGCAGCAGCCAGTGCA 2505  
QY 770 -----GluLeuThrAsnAlaLeuGlu 776  
Db 2506 GCGCAGCCGGCGCGGCTGCGGGAGAGGACAAATCCAGACCTTTGTCATGACCCCTCAAG 2565  
QY 777 -----IleSerAsnIleVal 781  
Db 2566 GCCCCTTGTCTGTGTACAACGTCCCTTCAACAGGCCAGGGTGTCTCTGCCATCCAGTG 2625  
QY 781 ----- 781  
Db 2626 ACTCCACCCCATACAGCCCATGGCGCATGGAGACAGAAAGCAGGACAGGATGTGAA 2685  
QY 782 -----PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeu 795  
Db 2686 GAAGSACCAGGACAACGAAGCAGTGACATGTTTGCCTGGAGATGATCTCTGAAGCTGGCT 2745  
QY 796 ValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal 815  
Db 2746 GCATTTGGGCTCTTCGACTACCTGCGTAACCCCTTACAACATCTTCGACAGCATCATGTC 2805  
QY 816 ValIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThr 835  
Db 2806 ATCATCAGCATCTGGGAGATCGTGGGGCAGGCGGACGGTGGGCTGTCCGTGCTGGGACC 2865  
QY 836 PheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeu 855  
Db 2866 TTCCGGCTGCTGCGCGTGTGAAACTGGTGGCTTCATGCCTGCCCTGCCGCGCCAGCTC 2925  
QY 856 ValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPhe 875  
Db 2926 GTGGTGTCTCATGAAGACCATGGACAACGTGGCCACCTTCTGCATGTCTGCTCATGTCTTC 2985  
QY 876 IlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArg 895  
Db 2986 ATCTTCATCTTCAGCATCTTGGGATGCATATTTTGGCTGCAAGTTCAAGTTCAGCCTCCG 3045  
QY 896 Asp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleVal 914  
Db 3046 GAACTGGAGACACGGTGCCCGACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGTC 3105



QY 915 ThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAla 934  
DB 3106 ACTGTGTTCCAGATCCTCACCCAGGAGGACTGGAACGTCTCTTACAAATGGCATGGCC 3165  
QY 935 SerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVal 954  
DB 3166 TCCACTTCTCCCTGGGCCTCCCTACTTTGTGCGCCCTCATGACCTTCGGCAACTATGTG 3225  
QY 955 LeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnAlaGlu---GluIleSer 973  
DB 3226 CTCCTTCAACCTGTGTGGTGGCCATCCTGTGGAGGGCTTCCAGGCGGAGGTGACTGTGGTC 3285  
QY 974 LysArgGluAspAla----- 978  
DB 3286 TTGGCAGAGGAAGACACCCACAGGGCCTGCGAAAGACTGGGGGAGGAGAGGTGGCCCTG 3345  
QY 979 -----SerGlyGlnLeuSerCysIleGlnLeuPro 988  
DB 3346 GATGGGGGAGGGCTGCAATTCAAACTTCTAGCAGGCAACCTATCC---CTAAGGAGGGG 3402  
QY 989 ValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPheSerPro 1008  
DB 3403 GTTGCTGATGAGGTGGTGACGCCAAATCGCTCTACTCGGACGAGGACCAGAGCTCATCC 3462  
QY 1009 Ser-----LeuAspGlyAspGlyAspArgLysLys 1018  
DB 3463 AACATAGAAAGATTGTATAAGCTCCAGGAAGGCCTGGACAGCAGCGGAGATCCCAAGCTC 3522  
QY 1019 CysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProPro 1038  
DB 3523 TGCCCAATCCCATGACCCCAATGGGCAC-----CTGACCC 3561  
QY 1039 LeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeu 1058  
DB 3562 -----AGTCTCCCACTGGGTGGGCACCTAGTCTCT 3591  
QY 1059 GlyGluAlaLeuGlyProAla----- 1065  
DB 3592 GCTGGGGCTGGGGACCTGCCCCCGACTCTCACTGCAGCGCGACCCCATGTGTGGTGCC 3651  
QY 1066 -----SerArgArgThrSer----- 1070  
DB 3652 CTGGGCTCCGAAAGAGAGCGTGTCTCTAGGGAGGATGAGCTATGACCAGCGCTCC 3711  
QY 1071 -----SerSerGlySerAlaGluProGlyAlaAlaHisGluMetLys 1084  
DB 3712 CTGGTGGGTGTCTTAGAGCCACAGCGGGGGTGCAGGCTGCTTTGGGCACCTGTGGCCC 3771  
QY 1085 SerPro-----ProSerAla 1089  
DB 3772 CAGCCGTGGGTGTGCCTGTGGGGCGTGCACCCGAAACGGGAACCTCTTCCAGTCCAGCTCC 3831  
QY 1090 ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSer 1109  
DB 3832 CGGAGCTCTACTACGGGCCATGGGGCCGACGCGGGCCTGGGCCAGCCGTCGCTCCAGC 3891  
QY 1110 ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArg 1129  
DB 3892 TGGAAC-----AGCCTCAAGCACAAAGCGCCCGTTCGGCGGAGCATGAG 3933  
QY 1130 SerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGluGlu 1148  
DB 3934 TCCCTGTCTCTCGCGAGCGCGCGGGCGCGCCGGGTCTGCGAGGTTGCGCGGACGAG 3993  
QY 1149 -----GluArgAlaSerProAlaGlySerAspHis----- 1158  
DB 3994 GGGCCCGCGGGCCGACCCCTGCACACCCACCCACCCACCCACCTTCATCACGGGCC 4053  
QY 1159 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSer 1171  
DB 4054 CATCTGGCGCACCGCCACCGCCACCGCCCGGACGCTGTCCCTCGACAAACAGGACTCG 4113

QY 1172 PheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg--- 1190  
DB 4114 GTGACCTGGCCGAGCTGGTGGCGCGGTGGCGGCCACCCCGGGCCGCTTGGAGGCGG 4173  
QY 1191 ---GlySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1209  
DB 4174 GCAGGCCCGGCCCGGGCATGAGGACTGCAATGGCAGGATGCCAGCATCGCCAAAGAC 4233  
QY 1210 ArgAlaLeuArgProAspAspProProLeuAspGlyAspAspAlaAspAsp----- 1226  
DB 4234 GTCCTTACCAAGATGGCGGACCCGCGGGGATCGCGGGGAGGATGAGGAGAAATCGACTAC 4293  
QY 1227 -----GluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
DB 4294 GTGAGTGGGGGGGGCGGAAAGGGACCTGACCCCTGTGTCTCCGCGTCCGCAAGATGATC 4353  
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260  
DB 4354 GACGTCTATAAGCCCGACGTGGTGGAGGTCCGCGAAGACTGGTCTGTCTACCTCTTCTCT 4413  
QY 1261 ProGlnSerArgPheArg-----LeuLeuCys----- 1269  
DB 4414 CCCGAGAACAGGCTCAGGGATCTGGGTGGTAAGCCTCAGTGCAGGAAAGGTGGGT 4473  
QY 1270 -----HisArgIleIleThrHisLys 1276  
DB 4474 GACCTCGTGGTGTGGGTGTATGGTCAGAGGAGGCGGAGCCAGACCATATTATGCCCAAAA 4533  
QY 1277 MetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGlu 1296  
DB 4534 CTCTTCGACTACGTCTCTGGCCTTCATCTTTCTCACTGCATCACCATCGCCCTGGAG 4593  
QY 1297 ArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIle 1316  
DB 4594 CGGCCTCAGATCGAGCGCGGACGACCGAACGCATCTTTCTCACCGTGTCCAACATACATC 4653  
QY 1317 PheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPhe 1336  
DB 4654 TTCACGGCCATCTCGTGGCGGAGATGACATTGAAGGTAGTCTCGTGGGCTGTACTTTC 4713  
QY 1337 GlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIle 1356  
DB 4714 GCGGAGCAGCGGTACCTACGCGACGAGTGAACGTGTGTGGATGGCTTTCTTGTCTCGTG 4773  
QY 1357 SerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMet 1376  
DB 4774 TCCATCATCGACATCGTGGTGTCTCTGGCCTCAGCCGGGGAGCCAAAGATCTTGGGGGTC 4833  
QY 1377 LeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGln 1396  
DB 4834 CTCCGAGTCTTGGGCTCCTGCGCACCCCTACGCCCTTGTGTGTATCAGCCGGGCGCGG 4893  
QY 1397 GlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleVal 1416  
DB 4894 GGCCTGAAGCTGGTGGTGAGACACTCATCTCCTCCCTCAAGCCCATCGGCAACATCGTG 4953  
QY 1417 ValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGly 1436  
DB 4954 CTCATCTGCTGTGCTTCTTTCATCATCTTTGGCATCTTGGAGTGCAGCTCTTCAAGGC 5013  
QY 1437 LysPhePheValCysGlnGlyAspThrArgAsnIleThrAsnLysSerAspCysAla 1456  
DB 5014 AAGTTCTACCACTGTCTGGGCGGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATG 5073  
QY 1457 GluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeu 1476  
DB 5074 GCCGCCAACTACCGTGGGTCCATCACAATAACAACCTTCGACAACCTGGGCCAGGCTCTG 5133  
QY 1477 MetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeu 1496  
DB 5134 ATGTCCTCTTTGTCTGCGCATCCAAAGGATGGTGGGTGAACATCATGTACAATGGACTG 5193  
QY 1497 AspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyr 1516

Db	5194	GATGCTGTGCTGTGGACGAGCCTGTGACCAACCAACCCCTGGATGCTGTAC	5253
Qy	1517	PheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValVal	1536
Db	5254	TTCATCTCTCTCCTGCTCATCGTCAGCTTCTTTTGIGGTCACATGTTTGGGTGTCGTG	5313
Qy	1537	ValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGlu	1556
Db	5314	GTGGAGAACTTCCACAAGTGCCGCGCAGCACCCAGGAGGTGAAGAGGCACGCGCGCGTGAG	5373
Qy	1557	GluLysArgLeuArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyr	1576
Db	5374	GAGAAGCGGCTGCGGCGCCTGGAGAAGAAGCGCCGGAAGGCCCCAGCGGCTGCCCTACTAT	5433
Qy	1577	SerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAsp	1596
Db	5434	GCCACCTATTGTCACACCCCGGCTGCTCATCCACTCCATGTGCACCCAGCCACTACCTGGAC	5493
Qy	1597	LeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGln	1616
Db	5494	ATCTTCATCACCTTCATCATCTGCCTCAACGTTGGTCAACCATGTCCCTGGAGCACTACAAT	5553
Qy	1617	GlnPro	1618
Db	5554	CAGCCC	5559

Search completed: April 16, 2005, 19:01:36  
Job time : 3081 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 16, 2005, 02:17:06 ; Search time 14253 Seconds  
(without alignments)  
6051.613 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKDVLSLGLSSDPADLDP 2266

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-O=/cgn2 1/USPTO.spool/US09611257/runat 13042005 170153 164/app query.fasta\_1.2439  
-DB-EST\_QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09611257\_QCGN 1 1 9104 @runat 13042005 170153 164 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703.5	14.3	6636	3 BC043482	BC043482 Mus muscu
2	1683.5	14.1	6035	3 BC051413	BC051413 Mus muscu
3	1382.5	11.6	1076	4 BM479323	BM479323 AGENCOURT
4	1314.5	11.0	879	7 CF548698	CF548698 AGENCOURT
5	1290.5	10.8	5666	9 AY416501	AY416501 Mus muscu
6	1281.5	10.8	1064	4 BM451648	BM451648 AGENCOURT
7	1257	10.6	793	6 CA319705	CA319705 UI-M-FW0-
8	1223.5	10.3	5943	9 AY416499	AY416499 Homo sapi
9	1216	10.2	711	5 BM950154	BM950154 UI-M-EH0p

10	1215.5	10.2	771	5 BU058818	BU058818 UI-M-FR0-
11	1215.5	10.2	990	4 BI905383	BI905383 603167426
12	1212.5	10.2	784	7 CF742232	CF742232 UI-M-HB0-
13	1187.5	10.0	810	5 BU709095	BU709095 UI-M-EW0-
14	1185	10.0	736	4 BI160856	BI160856 602864778
15	1183	9.9	939	4 BI736618	BI736618 603361089
16	1178	9.9	973	2 BF783704	BF783704 602109506
17	1174	9.9	4675	3 AK083220	AK083220 Mus muscu
18	1140.5	9.6	777	6 CA945335	CA945335 UI-M-FD0-
19	1136	9.5	6822	9 AY406058	AY406058 Mus muscu
20	1132	9.5	715	7 CF745071	CF745071 UI-M-GV0-
21	1130	9.5	676	4 BI917129	BI917129 603181539
22	1130	9.5	843	5 BQ180375	BQ180375 UI-M-EX0-
23	1129.5	9.5	6813	9 AY406056	AY406056 Homo sapi
24	1116.5	9.4	777	5 BU708898	BU708898 UI-M-FI0-
25	1107.5	9.3	710	5 BU704267	BU704267 UI-M-F00-
26	1104	9.3	952	7 CF584866	CF584866 AGENCOURT
27	1103.5	9.3	845	6 CA327685	CA327685 UI-M-FY0-
28	1101	9.2	707	7 CN216936	CN216936 RJA002G02
29	1092.5	9.2	918	6 CD557381	CD557381 AGENCOURT
30	1084	9.1	647	6 CB518482	CB518482 UI-M-GH0-
31	1081	9.1	693	5 BM949227	BM949227 UI-M-EG0p
32	1074	9.0	708	5 BQ179746	BQ179746 UI-M-EW0-
33	1068.5	9.0	710	7 CR576255	CR576255 CR576255
34	1065.5	9.0	727	5 BQ443110	BQ443110 UI-M-EV0-
35	1058.5	8.9	731	7 CN534628	CN534628 UI-M-HS0-
36	1055.5	8.9	803	6 CB245297	CB245297 UI-M-FY0-
37	1051	8.8	773	4 BI249987	BI249987 60295228
38	1025	8.6	640	6 CB056097	CB056097 NISC_jj12
39	1024	8.6	588	2 BE781203	BE781203 601469131
40	1018.5	8.6	684	5 BU262763	BU262763 603374462
41	1012	8.5	726	5 BQ042267	BQ042267 UI-M-EQ0-
42	1012	8.5	772	6 CB524438	CB524438 UI-M-FY0-
43	1006	8.5	707	5 BU612176	BU612176 UI-M-EW0-
44	995	8.4	1134	2 BF179657	BF179657 601806048
45	993	8.3	957	4 BG298038	BG298038 602396253

ALIGNMENTS

RESULT 1  
BC043482  
LOCUS BC043482 6636 bp mRNA linear HTC 19-NOV-2003  
DEFINITION Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,  
mRNA (CDNA clone IMAGE:5369391); containing frame-shift errors.  
ACCESSION BC043482  
VERSION BC043482.1 GI:28175783  
KEYWORDS HTC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 6636)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,  
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,  
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences





Db 1122 CTGGCCAGGACCCAAACGGTGGCATCACGAACCTTCGACAATTTTCTTTGCCATGCTAAC 1181

Qy 346 ailePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAl 366

Db 1182 TGTGTTCCAGTGATTACCATGAAGGCTGGACAGACGCTCTACTGGATGCAGGATGC 1241

Qy 366 aHisSerPhe--TyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePh 385

Db 1242 CATGGGGTATGAGCTGCCCTTGGGTGTACTTTGTGAGCCTTGTTCATCTTTGGGTCTTCTT 1301

Qy 385 eMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGln---- 403

Db 1302 TGTCTCAACCTTGTGCTTGGAGTCTTAAGCGGGGAGTTCTCAAGGAAAGAGAAAGGC 1361

Qy 404 -----ArgGluSerGlnLeuMetArgGluGlnArgVa 414

Db 1362 AAAAGCAGGAGTGACTTTTCAGAAAGCTTCGGGAGAGCAGCAGATGGAAGACCTTCG 1421

Qy 414 lArgPheLeu-----SerAsnAl 420

Db 1422 GGGCTACCTGGACTGGATCACACAGGCTGAGGAGTTAGACCTTCATGACCCCTCAGTAGA 1481

Qy 420 aSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLe 440

Db 1482 CGGCAACTTGGCTTCTCTTGGTGAAGAGGA----- 1512

Qy 440 uValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVa 460

Db 1513 -----CGGGCGGGCCA 1523

Qy 460 lArgValGlyLeuLeuSerSerProAlaProLeuGlyGly-----GlnGluTh 476

Db 1524 TCGTAGGCAACTCAATTCTGGCCCGCTTCATTCTAGCCCTGATGTGATGGCCCTCCTG 1583

Qy 476 rGlnProSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHi 496

Db 1584 AAACCCAGACCAAGCCTGC-----AGCCACCCTAGGCTTGCCCCAAATCT----- 1629

Qy 496 sHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProAr 516

Db 1630 -----GGATCAGGG-----CACAG 1643

Qy 516 gAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPr 536

Db 1644 AATCTCAACCCAGATTTCAG-----ATACAAAGACTCCAACCTAGTTCC 1685

Qy 536 oProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPh 556

Db 1686 TTGTCCCTTAGATTGACCCCTAATTCTGCCACCAAGC-----CACTCT-- 1728

Qy 556 eTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerPr 576

Db 1729 -----TCTCAGTTACAACCTATCCCCCACAGGGCCACAACGT----- 1764

Qy 576 oSerGluAlaSerGlyArgThrValGly--SerGlyLysValTyrPro-----ThrVal 593

Db 1765 -TCAGAGCTGACCAATAGGAGGCGCGGACGGCTGCGATGTTTCAGCCACTCTACTCGCTC 1823

Qy 594 HisThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSer 613

Db 1824 CACACACT-CCACCAGCAGCCACG-----CCAGCC 1852

Qy 614 SerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHis 633

Db 1853 TCCCAGCCAGTGACACTGGC-TCCATGACAGACACCCCTGGAGAT----- 1896

Qy 634 LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerPro 653

Db 1897 -----GAGGATGAAGAGAGGGGACCATGGCTAGTGTACACGCTGCCTAAACAAG 1947

Qy 654 CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAla 673

Db 1948 ATTATGAAAAACA-----AGGATCTCGCCCACTTCCGCGGAGCC 1986

Qy 674 GlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaVal 693

Db 1987 AACCGGGT----- 1995

Qy 694 TyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGln 713

Db 1996 -----CTCCGT-----GCACGCTGCCGC 2013

Qy 714 ArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTyrArgLeuIleCys 733

Db 2014 CGGGCGGTCAAGTCCAACGCC-----TGCTACTGG----- 2043

Qy 734 AspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIle 753

Db 2044 -----GCTGTACTGTTGCTCGTC 2061

Qy 754 LeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsn 773

Db 2062 TTCCTCAACACGTTGACCATAGCTTCAGAGCACCATGGCAGCCTTTGTGGCTCACCCAG 2121

Qy 774 AlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLys 793

Db 2122 ACCAAGAGTATGCCAACAAAGTTCTGCTCTGCCTCTTCACTGTGGAGATGCTCTCAAA 2181

Qy 794 LeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAsp----- 811

Db 2182 CTGTACGGCCTGGGCCCTCTGTCTACGTTGCCTCCTTTTCAACCCGCTTTGACTGCTTC 2241

Qy 812 -----GlyValIleValValIleSerValTyrPheGluIleValGlyGlnGlnGlyGly 828

Db 2242 GTGGTCTGTGGGGCATCTTAGAAACCACTTTGTGTGAGGTGGGGCCATGCAGCCTCTT 2301

Qy 829 GlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeu 848

Db 2302 GGCATCTCAGTGCTCCGATGTGTACGTCTCCTCAGGATCTTCAAGGTCAACGAGGACTGG 2361

Qy 849 ProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPhe 868

Db 2362 GCATCCCTGAGCAATCTGGTGGCATCTTTGTCTCAATTCATGAAGTCCATCGCCTCCTTG 2421

Qy 869 CysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGly 888

Db 2422 CTGCTTCTCCTCTTTCTCTTCATCATCATCTTCTCCCTGCTTGGCATGCAGCTGTTGGG 2481

Qy 889 CysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSer 908

Db 2482 GGCAAGTTCAACTTTGACCAG-----ACCCACACCAAGAGGAGCACCCTTTGATACC 2532

Qy 909 LeuLeuTyrAlaIleValThrValPheGlnIleLeuThrGlnGluAspTyrAsnLysVal 928

Db 2533 TTTCCCCCAAGCCCTCCTCACTGTCTTTTCAGATCCTGACTGGTGAGGATTGGAACGTTGTC 2592

Qy 929 LeuTyrAsnGlyMetAlaSer-----ThrSerSerTyrAlaAlaLeu 942

Db 2593 ATGTATGATGGTATCATGGCTACGGTGGGCCCTTCTTCCCAGGATGCTGGTGGCTGTT 2652

Qy 943 TyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIle 962

Db 2653 TATTTTCATCATCCTCTTTCATGTGTGGCAACTACATCCTGCTGAACGCTGTTTCTTGGCCATT 2712

Qy 963 LeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeu 982

Db 2713 GCCGTGGATAACCTAGCCAGC----- 2733

Qy 983 SerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGlu 1002

Db 2734 -----GGGGATGCAGGCACCTGCCAAA----- 2754

Qy 1003 ProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeu 1022

Db 2755 -----GACAAGGCGCAGAGAGAAGAGC----- 2775



Db 4554 GGACATTTCATCAAGTCTTTCCAGGCTTGCCCTATGTG-----GCACCTTCTCATAG 4604

Qy 1733 etLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCys- 1752

Db 4605 CAATGATATTCTCTCATCTATGCAGTCATTCGATGCAGATGTTGGCAAGGTGGCTCTTC 4664

Qy 1753 --AspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyM 1772

Db 4665 AGGACGGCACGCAG-----ATAAATCGAAACAACAATTTCCAGACCTTCCGC 4712

Qy 1772 etAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysA 1792

Db 4713 AGGCTGTGCTGCTTCTGTTTCAGGTGTGCCACTGGTGAGGCTGGCAAGAGATAATGCTAG 4772

Qy 1792 spThrLeu-----ArgAspCysAspGlnGluSer-----T 1802

Db 4773 CCAGCCTTCCAGGAAATCGATGTGACCCCTGAGTCTGACTTTGGCCCCAGGCGAGGAATTA 4832

Qy 1802 hrCysTyrAenThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP 1822

Db 4833 CCTGT---GGTAGCAGTTTTTGCATCGTCTACTTTCATCAGCTTCTTTATGCTCTGTGCCT 4889

Qy 1822 heValLeuValAenValIleAlaValLeuMet----- 1833

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Qy 1834 -----LysHisLeuGluGluSerAenLysGluAlaLysGluGluA 1847

Db 4950 ATTGGTCTATCCTGGGACCCCAACCACTTGATGAATTC---AAGAGGATCTGGTCTGAAT 5006

Qy 1847 laGluLeuGluAlaGluLeuGluLeuGlu-----MetLysThrL 1860

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Qy 1860 euSerProGln-----ProHisSer----- 1866

Db 5067 TCCAGCCCCCATTTGGGATTGTGAAAGCTATGCCCAACCGAGTGGCTGCAAGAGACTCG 5126

Qy 1867 -----ProLeuGlySerProPhe-----LeuT 1874

Db 5127 TGGCAATGAATGTGCCCTCAACTCAGA-TGGAACAGTGACATTCAACGCTACACTCTTT 5185

Qy 1874 rpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisProA 1894

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Qy 1894 laAla-----HisAlaArgSerAlaSerHisPheSerLeuGlu----- 1906

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Qy 1907 --HisProThrMetGln-----ProH 1913

Db 5306 GTCATCCCTCCTCCCGATGAGGAGGAGGTCACTGTGGGAAAATTTCTATGCCACATTCCTG 5365

Qy 1913 isProThrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgT 1933

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Qy 1933 hrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProL 1953

Db 5420 AGAGAGGC---CCCAACAAGCACATCTCTGCCCTCCAGGCTGGTCTAAGGAG---CCTG 5473

Qy 1953 eu-----GlyHisArgGlyT 1958

Db 5474 CAGGACTTGGGTCTGAGATCCGTCAAGCCCTCACCTATGACACTGAGGAAGAAGAGGAA 5533

Qy 1958 rpGlyLeuProLysAlaGlnSerGly-----Serv 1968

Db 5534 GAGGAAGAGGAGGAGTGGGTGAGGAGGCTGAGGAAGAGGAGGAGTGAACAACCCAGAACCA 5593

Qy 1968 alLeuSerValHisSerGlnProAlaAspThrSerTyr-----Ile- 1981

Db 5594 TACAAAGACTCCATAGACTCTCCCAAGCCCCCAATCTCGATGGAACTCTAGGATTTTCGGTGTCT 5653

RESULT 2  
BC051413  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

BC051413 6035 bp mRNA linear HTC 19-NOV-2003  
Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,  
mRNA (cDNA clone IMAGE:6493332), containing frame-shift errors.  
BC051413  
BC051413.1 GI:30802106  
HTC.

Qy 1982 LeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGly 2001

Db 5654 CTACCTGTAAAGGAGAAACTTCCAGATTCTCTCAACTGGCCGAGTGATGATGGG 5713

Qy 2002 ThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArg 2021

Db 5714 CTGGTCCCAACTCCAGGCAGCCAGTGTGATACAGGCTGGCTCCCAACACACAGGAGA 5773

Qy 2022 GlnAlaAlaIle-----ArgThrAspSerLeuAspValGlnGlyLeu 2035

Db 5774 AGCTCTGGGTTTTCATGTTCACTATCCCGAAGAGGAAGTATTCAGCTCAAGGGAAT 5833

Qy 2036 GlySerArgGlu-----AspLeuLeu 2042

Db 5834 CAAGGGCAGGACAATCAGAATGAGGAACAGGAAGTCCCTGACTGGACTCCTGACCTGGAT 5893

Qy 2043 AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSer 2062

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Qy 2063 SerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro 2082

Db 5942 -----TCCAGCAACACACGTAAACGGGCACCATGTGCCACGCCGACGTTTGTGCC 5992

Qy 2083 ProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProGluThrArgSer 2102

Db 5993 CCCACGCCTGCA-----GGTCGGAAGCCCTCTTTCACCATCCAG 6031

Qy 2103 SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProGly--- 2121

Db 6032 TGCTGTCAACGCCAGGCGAGTGTGAA-----GATTACCTATCCCAAGGCACC 6079

Qy 2122 -----GlyGlnGluGluProProSerProArgAspLeuLysCysTyrSerVal 2138

Db 6080 TACCATCGTGGACGGACCTCAGGACCAAGC----- 6109

Qy 2139 GluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSer 2158

Db 6110 -----AGGGCTCAGGGTTCTCTGGGAGCCCTCTCAGAAAGGTCGA 6151

Qy 2159 IleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn 2178

Db 6152 CTGCTATATATGCC-----CCCTGTGTGTGGTGGAGGAATCTACA 6190

Qy 2179 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProPro 2198

Db 6191 GTGGGTGAAGGATACCTTGGC-----AAACTTGGCGGCCCA 6226

Qy 2199 SerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSer 2215

Db 6227 CTGCGTACCTTCACTGTCTGCAAGTGCCTGG-AGCTCATCCGAATCCCAGCCACGCCAA 6285

Qy 2216 ProGlyIleCys-----LeuArgArgArgAlaProSer 2226

Db 6286 GAGGGCAGTGTGACAGTTTGGTGGAGGCTGTGTCTCATCTCCGAAGG-----CCTAGG 6339

Qy 2227 SerAspSerLysAspProLeuAlaSerGlyPro-----ProAspSerMetAlaAla 2243

Db 6340 TCTCTTTGCCCAAGACCCACGATTTGTGGCCCTGGCCCAAGCAGGAGATTGCAGATGCATG 6399

Qy 2244 SerProSerPro 2247

Db 6400 TCACCTGACCCT 6411

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 6035)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 6035)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (25-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc.mgc@nhgri.nih.gov">nisc.mgc@nhgri.nih.gov</a> Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
FEATURES	Location/Qualifiers
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ORIGIN	

Alignment Scores:			
Pred. NO.:	1.99e-105	Length:	6035
Score:	1683.50	Matches:	616
Percent Similarity:	38.15%	Conservative:	331
Best Local Similarity:	24.82%	Mismatches:	752
Query Match:	14.14%	Indels:	786
DB:	3	Gaps:	86
US-09-611-257A-37 (1-2266) x BC051413 (1-6035)			
QY	1	MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20
Db	18	ATGTCGGAATCTGAAGTCGGGAAGATACAACCCAGAGCCAGTCCAGCCAAT	71
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyPro	38
Db	72	-----GGGACTGGCCCTGGCCCTGAATGGGGCTCTGTCT	107
QY	39	LysAspPro-----GlySerAlaAspSerGluAlaGluGlyLeuProTyrPro	54
Db	108	GGGCTCCAACTGTGGGACTGATACCAAGGGGGCTCAGGCTGGGACCCCAAGA	167
QY	55	-----AlaLeuAlaProValPhePheTyrLeu	64
Db	168	AGGACCAGCACAAACAAGACTGTGGCGTGGCC	206
QY	65	SerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnPro	81
Db	207	AGTGTCTCAGAGATCACCTCGAGCGCTCTTCTGCCTCACCCCTACTAATCCCAT	266
QY	82	-----Trp-----PheGluArgIleSerMetLeuValIleLeu	92
Db	267	TCCTGCATCAGCATTGTAGAGTGAAGCCTTTGATATTCTCATCTCTGACAATCTTT	326
QY	93	LeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGln	112
Db	327	GCCAACTCGTGGCATTGGGGTATATATATCCCTTCCCTGAGGAGCACTCCAACACTGCT	386
QY	113	ArgCysArgIleLeuGlnAlaPheAspAspPheIlePhe---AlaPhePheAlaValGlu	131
Db	387	AACCACAACTTGGACAGGTA-----GAATACGTGTTCTCTGGTGATTTTACCGTGGAG	440
QY	132	MetValValLysMetValAlaLeuGly---IlePheGlyLysLysCysTyrLeuGlyAsp	150
Db	441	ACAGTGCTCAAGATCTAGCCTATGGGTGGTGTCTCCATCCCGCGCTATATTCGCAAT	500
QY	151	ThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAsp	170
Db	501	GGCTGGAACCTGCTCGACTTCATCATCGTCTGGTGGGCTGTTTTCAGCGTGTCTGGAA	560
QY	171	Leu-----GlnAsnValSer	175
Db	561	CAAGGACCTGGCGGCAGGAGATGCCCGCATACTGGAGAAAGCCAGGAGCTTCGAT	620
QY	176	PheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPro	195
Db	621	GTAAGGCACCTGCGGCATTTAGGGTGTCTACGACCTCTAAGGCTAGTGTCTGGGGTCCC	680
QY	196	SerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeu	215
Db	681	AGTCTGCACATAGTGTCAATTCATCATGAAGCGCTTGTCCCGTGTCTGCACATTGCC	740
QY	216	LeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGly	235
Db	741	CTGTTGGTGTCTTCTCGTCATTATCATTTACGCCATCATCGGACTCGAGCTATTCTCGGA	800
QY	236	LeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeu	255
Db	801	CGATGCACAAGACATGCTACTTC-----CTGGGATCTGATATG	839
QY	256	GluArgTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArg	275
Db	840	GAA-----GCAGAGGAGGAGCCCATCACCT-----	863



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QY 276 GluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGly 295
Db 864 -----TGTGCATCT-----TCTGGCTCTGGG 884
QY 296 ProProCysGlyLeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsn 315
Db 885 CGTTCATGCACACTGAAC----- 902
QY 316 TrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnPropheLysGlyAlaIle 335
Db 903 -----CATACCGAGTGC CGCGGCGCTGGCCAGGACCAACGGTGGCATCACG 950
QY 336 AsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGly 355
Db 951 AACCTCGACAATTTTCTTTGCCATGCTAACTGTGTCCAGTGATTACCATGGAAGGC 1010
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Db 1011 TGGACAGACGCTCTACTGGATGCAGGATGCCATGGGGTATGAGCTGCCCTTGGGTGTAC 1070
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Db 1071 TTTGTGAGCCTTGTTCATCTTTGGTCTCTTTGTCTCCTCAACCTTGTGTGGATCCTA 1130
QY 395 AlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414
Db 1131 AGCGGGAGTTCTCCAAGGAAAGAGAAAAGGCAAAAGCACGAGGTGACTTTTCAGAAGCTT 1190
QY 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434
Db 1191 CGG-----GAGAAGCAGCAGATGGAAGAA 1214
QY 435 GluLeuLeuLysTyrLeuValTyrIleLeuArg----- 445
Db 1215 GACCTTCGGGGCTACCTGGACTGGATCACACAGGCTGAGGAGTTAGACCTTCATGACCCC 1274
QY 446 LysAlaAlaArgArgLeuAlaGlnValSer-ArgAlaAlaGlyValArgValGlyLeuLe 465
Db 1275 TCAGTAGACGGCAACTTGGCTTCTTGCTGAAGAGGACGGCGGGCCATCGGCCACAA 1334
QY 465 uSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSerSerCysSerArgse 485
Db 1335 CTGTCAGAGCTGACCAATAGGAGC-----GCGACGGCTGCGAT----- 1374
QY 485 rHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTy 505
Db 1374 ----- 1374
QY 505 rHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAs 525
Db 1375 -----GGTTCAGCCACTCTACTCGCTCCACACT----- 1404
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Db 1405 -----CCACCAGCAGCCAGCCAGCC----- 1425
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Db 1425 ----- 1425
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Db 1425 ----- 1425
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QY 605 sAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThrSerLeuAsnIlePr 625
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QY 645 nSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyAlaCysGlyProAs 665
Db 1496 TAGCTGTACACGCTGCCATAACAAGATTATGAAACA-----AG 1534
QY 665 pSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgGluMe 685
Db 1535 GATCTGCCGCCACTTCGCCCGAGCCAAACCGGGT----- 1568
QY 685 tProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLe 705
Db 1569 -----CT 1570
QY 705 uArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerVa 725
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Db 1608 ---TGCTACTGG----- 1616
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QY 820 pGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetAr 840
Db 1850 GGAGGTGGGGCCATGCAGCCTTTGGCATCTCAGTGTCCGATGTGTACGTCTCTCTCAG 1909
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QY 900 uProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLe 920
Db 2081 CACCAAGAGGAGCACCTTTGATACCTTCCCCCAAGCCCTCCTCACTGTCTTTCAGATCCT 2140
QY 920 uThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer----- 935
Db 2141 GACTGGTGAGGATTGGAACGTTGTATGATGATGATGATGATGATGATGATGATGATGATG 2200
QY 936 ---ThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVa 954
Db 2201 CTTCCAGGGATGCTGGTGTGTATTATTTCATCATCTCTTCTCATCTGTGTGGCACTACAT 2260
QY 954 lLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLy 974
Db 2261 CCTGTGAACGTTTCTTGGCCATTGCGTGGATACCTAGCCAGC----- 2306
QY 974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGl 994
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QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMet--- 1719
Db ::::|||||
3908 ---GTCAAGTCTCTAGTAAGGTGAGGGGATCCGCACACTGCTCTGGACATTATCAAG 3964

QY 1720 -----GlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePhe 1737
Db ::::|||||
3965 TCTTTCCAGGCTTGCCTATGTG-----GCACCTTCTCATAGCAATGATATCTTC 4015

QY 1738 IlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCys---AspGluThrHis 1756
Db ::::|||||
4016 ATCTATGCAGTCAATTGGCATGCGATGTTTGGCAAGGTGGCTCTTCAGGACGGCAGCAG 4075

QY 1757 ProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThr 1776
Db ::::|||||
4076 -----ATAAATCGAAACAACAATTTCCAGACCTTTCCGCAGGCTGTGTGCTT 4123

QY 1777 LeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeu----- 1794
Db ::::|||||
4124 CTGTTTCAGGTGTCCTACTTTCATCAGCTTCTTATGCTCTGTGCTTCTCTGATATAAAT 4183

QY 1795 ArgAspCysAspGlnGluSer-----ThrCysTyrAsnThr 1806
Db ::::|||||
4184 AATCGATGTGACCTTGAGTCTGACTTGGCCCGGAGGAATTTACCTGT---GGTAGC 4240

QY 1807 ValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsn 1826
Db ::::|||||
4241 AGTTTGGCCATCGTCTACTTTCATCAGCTTCTTATGCTCTGTGCTTCTCTGATATAAAT 4300

QY 1827 ValValIleAlaValLeuMet----- 1833
Db ::::|||||
4301 CTCCTTGTGGTGTAAATCATGGAATACTTTGATTACCTAACCCAGAGATTGGTCTATCCTG 4360

QY 1834 -----LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAla 1851
Db ::::|||||
4361 GGACCCACCACCTTGATGAATTC---AAGAGGATCTGGTCTGAATATAGACCCCGGAGCC 4417

QY 1852 GluLeuGluLeuGlu-----MetLysThrLeuSerProGln--- 1863
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4418 AAGGGCCGATCAAGCACCTTGGATGTGGTTGCCCTGTGCTGAGACGCATCCAGCCCCCATTTG 4477

QY 1864 -----ProHisSer----- 1866
Db ::::|||||
4478 GGATTTGGAAGCTATGCCCCACACCGAGTGGCTGCAAGAGACTCGTGGCAATGAATGTG 4537

QY 1867 ProLeuGlySerProPhe-----LeuTrpProGlyValGlu 1878
Db ::::|||||
4538 CCCCTCACTCAGA-TGGAACAGTGACATTCAACGCTACACTCTTTGCCCTGTGTGGCGAC 4596

QY 1879 GlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAla----- 1895
Db ::::|||||
4597 ATCCCTGAAGATCAAGACAGAGGAAACCTGGATCAAGCCAACCCAGGAGCTTCGGATGGT 4656

QY 1896 HisAlaArgSerAlaSerHisPheSerLeuGlu-----HisProThrMet 1910
Db ::::|||||
4657 CATCAAAAAGATCTGGAAGCGGATAAAGCAGAAATTTGTGGATGAGGTATCCCTCCTCC 4716

QY 1911 Gln-----ProHisProThrGluLeu 1917
Db ::::|||||
4717 CGATGAGGAGGAGTCACTGTGGGAAAATTTCTATGCCACATTCTGTATCCCAAGATTATT 4776

QY 1918 ProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db ::::|||||
4777 -----CCGAAAATTCGGAGAGGAAGAAAGGGGCTACTAGGAAGAGAGGC---CCC 4827

QY 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu----- 1953
Db ::::|||||
4828 AACAAAGCACATCCTCTGCCCCTCCAGGCTGGTCTAAGGAG---CCTGCAGGACTTGGGTCC 4884

QY 1954 -----GlyHisArgGlyTrpGlyLeuProLys 1962
Db ::::|||||
4885 TGAGATCGTCAAGCCCTCACCTATGACACTGAGGAAGAAGAGGAAAGAGAGAGGAGCAGT 4944
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RESULT 3  
BM479323

LOCUS

DEFINITION

BM479323 1076 bp mRNA linear EST 05-FEB-2002  
AGENCOURT 6418725 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:5502230  
5', mRNA sequence.

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QY 1963 AlaGlnSerGly-----SerValLeuSerValHis 1972
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4945 GGGTCAGGAGGCTGAGGAAGAGAGAGCTGAGAACACCCAGAACCATACAAGACTCCAT 5004

QY 1973 SerGlnProAlaAspThrSerTyr-----Ile-LeuGlnLeuProly 1986
Db ::::|||||
5005 AGACTCCAGCCCCCAATCTCGATGGAACCTTAGGATTTTCGGTGTCTCTACCTGTTAAGGA 5064

QY 1986 sAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe 2006
Db ::::|||||
5065 GAAACTTCCAGATTCTCTCTCAACTGGGCCGAGTGATGATGATGGCTGGCTCCCAACTC 5124

QY 2006 uProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIle-- 2025
Db ::::|||||
5125 CAGGCAGCCAGTGTATACAGGTGGCTCCCAACCCACAGGAGAAGCTCTGGGGTTTT 5184

QY 2026 -----ArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlu-- 2039
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5185 CATGTTCACTATCCCGAAGAAAGATATTTCAGCTCAAGGGAACCTCAAGGGCAGGACAA 5244

QY 2040 -----AspLeuLeuAlaGluValSerGl 2047
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5245 TCAGATGAGGAACAGGAAGTCCCTGACTGGACTCTCTGACTGGATGAGCAGGCCGGGAC 5304

QY 2047 yProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGl 2067
Db ::::|||||
5305 TCCTTCGAACCCAGTCTCTTTTACCA---CCTCACTGG-----TCCCA 5343

QY 2067 nGlnHisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysPr 2087
Db ::::|||||
5344 GCAACACGTAAACGGGCACCATGTGCCACGCCGACGTTTGTGTCCTCCACGCTGCA-- 5401

QY 2087 oGlyProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAs 2107
Db ::::|||||
5402 -----GGTCGAAGCCCTCTTCCATCCAGTGTCTGCAACGCCA 5442

QY 2107 pThrGluLeuSerTrpIleSerGlyAspLeuLeuProProGly-----GlyGl 2123
Db ::::|||||
5443 GGGCAGTTGTGAA-----GATTACCTATCCAGGACCTACCATCGTGGACG 5490

QY 2123 nGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCy 2143
Db ::::|||||
5491 GACCTCAGGACCAAGC----- 5506

QY 2143 sGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCy 2163
Db ::::|||||
5507 ---AGGGCTCAGGGTTCCTGGGCAGCCCTCTCCTCAGAAGGGTCTGACTGTATATGCC-- 5560

QY 2163 sLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGlyGlnPr 2183
Db ::::|||||
5561 -----CCCTGTGTGGTGGAGGAATCTACAGTGGGTGAAGGATA 5601

QY 2183 oLeuGlyGlyProGlySerArgProLysLysLeuSerProProSerIleThr----- 2201
Db ::::|||||
5602 CCTTGGC-----AAACTTGGCGGCCCACTGCGTACCTTCAC 5637

QY 2202 ---IleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCys-- 2219
Db ::::|||||
5638 CTGCTGCAAGTGCCTGG-AGCTCATCCGAATCCAGCCACCGCAAGAGGGGCGAGTGTG 5696

QY 2220 -----LeuArgArgAlaProSerSerAspSerLysAs 2231
Db ::::|||||
5697 ACAGTTTGGTGGAGGCTGTGCTCATCTCCGAAGG-----CCTAGGTCTCTTTGCCCAAG 5750

QY 2231 pProLeuAlaSerGlyPro-----ProAspSerMetAlaAlaSerProSerPro 2247
Db ::::|||||
5751 ACCCAGCATTTGTGGCCCTGGCCCAAGCAGGAGATTGCGATGTCATGTCACCTGACCT 5808
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ACCESSION BM479323 GI:18528365  
VERSION BM479323.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1076)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM12140 row: a column: 15  
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Pred. No.: 1.13e-85 Length: 1076  
Score: 1382.50 Matches: 286  
Percent Similarity: 90.37% Conservative: 5  
Best Local Similarity: 88.82% Mismatches: 15  
Query Match: 11.61% Indels: 16  
DB: 4 Gaps: 3  
US-09-611-257A-37 (1-2266) x BM479323 (1-1076)  
QY 1447 ArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLys 1466  
Db 3 AGGAACATCACCATAAATCGGACTGTGCCGAGGCCAGTACCGGTGGTCCGCACAAG 62  
QY 1467 TyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp 1486  
Db 63 TACAACCTTGACAAACCTTGCCAGGCCCTGATGCTCTGTTCTGTTGGCCTCCAAGGAT 122  
QY 1487 GlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIle 1506  
Db 123 GGTGGGTGGACATCATGTACGATGGGCTGGATGCTGGGCGTGGACCGAGCCCATC 182  
QY 1507 MetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhe 1526  
Db 183 ATGAACCACAAACCCCTGGATGCTGTACTTTCATCTCGTTCCTGCTCATTTGGCCTTC 242  
QY 1527 PheValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHis 1546  
Db 243 TTTGTCTGAACATGTTTGTGGGTGGTGGTGGAGAACTTCCACAAGTGTGGCAGCAC 302  
QY 1547 GlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuLysLys 1566  
Db 303 CAGGAGGAAGAGGAGGCCCGGGGAGGAGAGCGCCTACGAAGACTGGAGAAAAG 362  
QY 1567 ArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuVal 1586

Db 363 AGAAGAAAGCCAGTGCAGAACCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTCGTC 422  
QY 1587 HisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsn 1606  
Db 423 CACCACCTTGTGCACCCAGCACTACCTGGACCTTTCATCACAGGTGTCACTGGGCTGAAC 482  
QY 1607 ValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLys 1626  
Db 483 GTGTGCACCATGGCCATGGAGCACTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542  
QY 1627 IleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAla 1646  
Db 543 ATCTGCAACTACATCTTCACTGTCTCTTGTCTTGGAGTCAGTTTCAAACTTGTGGCC 602  
QY 1647 PheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeu 1666  
Db 603 TTTGGTTTCCGTGGTCTTCCAGGACAGGTGGAAACAGCTGGACCTGGCCATTGTGCTG 662  
QY 1667 LeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsn 1686  
Db 663 CTGTCCATCATGGGCATCAGCTGGAGGAATCGAGGTCAACGCCTCGCTGCCCATCAAC 722  
QY 1687 ProThrIleIleArgIle-MetArgValLeuArgIleAlaArgValLeuLysLeuLeu-L 1706  
Db 723 CCCACCATCATCCGCATCATTTGAGGTGCTGCGCATTGCCCGAGTGTGAAGTGTCTGAA 782  
QY 1706 ysMetAlaValGlyMet-ArgAlaLeuLeuAspThrValMetGlnAla--LeuProGlnV 1725  
Db 783 AAATGCGTGTGGGCATGCGGCGCGCTGCTGGACACCGTGTATGCACGCCCTGTCCCCGGT 842  
QY 1725 alGlyAsnLeuGlyLeuLeuPheMet-----LeuLeuPhePheIlePheAlaAlaLeuG 1743  
Db 843 GGGGAAACCTGGGGACCTTTTCTCCAGGCCGTTGGTGTTCATCCCTCGCGCTCCTG 902  
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Db 903 GCGCCGTGCAGCCTCTTTTGGAGAA-----CCTTGAAG 937  
RESULT 4  
CF548698  
LOCUS CF548698 879 bp mRNA linear EST 22-SEP-2003  
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IMAGE:7018586 5', mRNA sequence.  
ACCESSION CF548698  
VERSION CF548698.1 GI:34885530  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus.  
REFERENCE 1 (bases 1 to 879)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement:  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM14738 row: j column: 24  
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Location/Qualifiers  
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN
Alignment Scores:
Pred. No.: 4.47e-81 Length: 879
Score: 1314.50 Matches: 255
Percent Similarity: 94.79% Conservative: 18
Best Local Similarity: 88.54% Mismatches: 13
Query Match: 11.04% Indels: 2
DB: 7 Gaps: 1

US-09-611-257A-37 (1-2266) x CF548698 (1-879)

QY 1486 AspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnPro 1505
Db 1 GACGGATGGTGGACATCATGTATGATGGACTGGATGCTGCGAATTGACCAGCCCA 60

QY 1506 IleMetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAla 1525
Db 61 GTGATGAATTACAACCTTGGATGCTGCTATATTTTCATCTCATTTTGTGTTGGCA 120

QY 1526 PhePheValLeuAsnMetPheValGlyValValValGluValAsnPheHisLysCysArgGln 1545
Db 121 TTTTGTGCTCAACATGTTTGGTGTGGTGGTGGAGAACTTCCATAAGTGCCGGCAG 180

QY 1546 HisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLys 1565
Db 181 CATCAGGAGGAGGAGGAGCGAAGACGGGAGAAAGAGGCTCCGAGGATGGAGAAA 240

QY 1566 LysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeu 1585
Db 241 AAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300

QY 1586 ValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeu 1605
Db 301 ATCCATCAGATCTGTACAAGTCATATTGGAATTTGTTTATTACTGGGTTCATGGATTG 360

QY 1606 AsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeu 1625
Db 361 AATGTTATCACTATGGCAATGGAGCACTATCAGCAACCCAGGATTTGGTTGAAGCTCTA 420

QY 1626 LysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuVal 1645
Db 421 AAAATCTGTAATTACATCTTTACCTCATTTTTCGTAATCTGGGTGCAAAATGATA 480

QY 1646 AlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleVal 1665
Db 481 GCTTTTGGCTTCGGCGATTCTTTAAAGACAGGTGGAACCAAGTTGGATCTGGCCATCGTT 540

QY 1666 LeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIle 1685
Db 541 CTTCTCTCCATCATGGGAATCACACTGGAAGAGATTGAAGTCAATGCATCACTGCCCAT 600

QY 1686 AsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeu 1705
Db 601 AACCCCAACAATCATCCGAATAATGAGGGTCTTGGGATTGCTCGGGTCTGAAGTTATTA 660

QY 1706 LysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnVal 1725
Db 661 AAGATGGCAGTCGGTATCGAGCCCTGCTGGATACGGTTCTGCAAGCGCTTTCTCAAGTG 720

QY 1726 GlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGlu 1745
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1746 LeuPheGlyAspLeuGluCysAspGluThrHisProCysGlu-GlyLeuGlyArgHisAl 1765
Db 781 CTTTTTGGTGACTTAAAGAGCACTGGATCCCATCCCTGTGAAGGTCTTTGGCAGACTTGC 840

QY 1765 aThrPheArgAsn---PheGly 1771
Db 841 CACTTTTCAAGGAATTTTCGGG 862

RESULT 5
AY416501
LOCUS
DEFINITION
Mus musculus SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,
AY416501
ACCESSION
AY416501.1 GI:39772461
VERSION
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5666)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 5666)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Location/Qualifiers
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Alignment Scores:
Pred. No.: 4.47e-78 Length: 5666
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Percent Similarity: 36.71% Conservative: 305
Best Local Similarity: 23.22% Mismatches: 713
Query Match: 10.84% Indels: 723
DB: 9 Gaps: 77

US-09-611-257A-37 (1-2266) x AY416501 (1-5666)

QY 25 LeuSerGlyAlaGlyGlyArgProGlyProGlyProGlySerAlaGluLysAspProGlySerAla 44
Db 204 CTACGGGGACATCCCGCAAGCGCTGGTTGGTTCC-----CCTGGAGGACTT 251

QY 45 -AspSerGluAlaGluGlyLeuProTyr-----CCGTACTATTTCAGCGAGAAAACCTTTTGTAGTATAAA 53
Db 252 TGAC-----CCGTACTATTTCAGCGAGAAAACCTTTTGTAGTATAAA 293

QY 54 -----ProAlaLeuAlaProValValPhePh 62
Db 294 CAGAGGGGAAAACCTCTCTTCAGATTTAGCGCCACTCCTCGCTG-----TA 338

QY 62 eTyrLeuSerGlnAspSerArgProArgSerTyrPheCysLeuArgThrValCysAsnProTr 82
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Db	399	CTTC	AGCAT	GATCAT	GTGC	ACCAT	CTCT	GACCA	ACTGT	GTAT	TCAT	GACT	TTTAGTAA	458									
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Db	546	C-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	593	
Qy	156	pPhe	Phe	Ile	Val	Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Ph	176	
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Qy	196	rMet	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu	Pro	Met	Leu	Gly	Asn	Val	Leu	Le	216	
Db	708	CCT	GAAG	ACA	ATCG	TGG	CGCC	CTCAT	CCAG	TCTGT	GAGA	AGCTGT	GCAG	ACGT	GTAT	GAT	767						
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Db	828	CCT	TCG	AA	CA	AGT	GTGT	CGT	GTG	GGCC	CA	TAA	AACT	CAAC	-----	-----	-----	-----	-----	-----	-----	867	
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QY	455	rArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnG1	475
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QY	535	roProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisS	555
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QY	575	erProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThr-----	592
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QY	593	-----ValHisThrSerProProProGluThrLeuLysGluLysA	606
Db	1602	GTCGCTGCTCAGCATCCCGAGGCTCGCCCTTCTCTTCCCGACACACAGCAAAA-----	1654
QY	606	laLeuValGluValAlaAlaSerSerGlyProProThrLeuThrSerLeuAsnIleProp	626
Db	1655	-----GCAGCATCTTCAGCTTTCGGGGTCTCGACGGTTCCGGGACCCCGG	1700
QY	626	roGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSerThr-----	641
Db	1701	TTCGGAGAACGAGTTCCG-----CAGACGACGAGCACAGCACAGTGGAGGA	1745
QY	642	-----GlyAlaCysGlnSerSerCysLys-----	649
Db	1746	AAGTGAGGCGCGCGGACTCGCTCTTTCATCCCGATCCGCGCCCGGAGCGCCGACAGCAG	1805
QY	650	-----IleSerSerProCysLeuLysAlaAspSerGlyAlaC	662
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QY	662	ysGlyPro-----AspSerCysProTyrCysAlaArgAla-----GlyAlaG	676
Db	1866	GCGGCGCAGCGTGAAACGCAACAGACAGCACCGTGGACTGCAATGGCGTGGTGTCTCATCGG	1925
QY	676	lyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluP	696
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QY	696	heThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerL	716
Db	1983	-----	1983
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VERSION
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  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
AUTHORS
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
JOURNAL
  Tissue Procurement: ATCC
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM12116 row: h column: 02
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  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH_MGC 67"
  /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
  Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
  Average insert size 1.75 kb. Library constructed by Life
  Technologies."
ORIGIN
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Pred. No.: 1.22e-78 Length: 1064
Score: 1281.50 Matches: 272
Percent Similarity: 76.36% Conservative: 9
Best Local Similarity: 73.91% Mismatches: 16
Query Match: 10.77% Indels: 71
DB: 4 Gaps: 6
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  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 793)
REFERENCE
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
```









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Db 4888 CTGATCAAAAGCGCCAAAGGGATTGTCACCTGCTCTTTCCTTAAATGATGTCTTGCCT 4947  
Qy 1724 GlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGly 1743  
Db 4948 GCCCTGTTCAACATCGGCCTTCTGCTCTTCTGTCATGTCATCTCTCCATTTTGGG 5007  
Qy 1744 ValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg 1763  
Db 5008 ATGTCCAATTTGCATATGTGAAGCACGAG-----GCTGGTATCGATGAC 5052  
Qy 1764 HisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGly 1783  
Db 5053 ATGTTCAACTTTGAGACATTTGGCAACAGCATGATCTGCCTGTTTCAAATCACAACTCA 5112  
Qy 1784 AspAsnTrpAsnGlyIleMetLysAspThrLeuArg-----AspCys-----Asp 1798  
Db 5113 GCTGGTGGGATGGCCTGCTGCTGCCCATCTAAACCGCCCCCTGACTGCAGCCTAGAT 5172  
Qy 1799 GlnGlu-----SerThrCysTyrAsnThrValIleSerProIle 1811  
Db 5173 AAGGAACACCCAGGAGTGGCTTTAAGGGAGATTGTGGGAACCCCTCAGTGGGCATCTTC 5232  
Qy 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal 1831  
Db 5233 TTTCTTTGAAGCTACATCATCTCTTTCCTAATTGTCGTGAACATGTACATGCGCATC 5292  
Qy 1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGlu-----GluAlaGlu 1848  
Db 5293 ATCTCGGAGAACTTCAGTGTAGCCACAGAGGAAGTGCAGACCCCTCTGAGTGAGGATGAC 5352  
Qy 1849 LeuGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProLeu 1868  
Db 5353 TTTGAGACCTTCTATGAG-----5370  
Qy 1869 GlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysPro 1888  
Db 5371 -----ATCTGGGAGAGTTCGAC---CCCCATGCCACCCAGTTTCATTGAGTAC 5415  
Qy 1889 GlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisPro 1908  
Db 5416 TGTAAAGCTGGCAGACTTTGCAGATGCC-----TTGGAGCATCTCT 5454  
Qy 1909 ThrMetGlnProHisProThr-----GluLeuProGlyProAspLeuThrValArg 1926  
Db 5455 CTCGGAGTGCCCAAGCCAAATACCATTTGAGCTCATCGCTATGATCTGCCAATGGTG--- 5511  
Qy 1927 LysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGly 1946  
Db 5512 ---AGCGGG---GATCGCATCCACTGCTTG-----GACATCCT-TTTTGCCTTCACCAA 5558  
Qy 1947 SerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGly 1966  
Db 5559 GCG-----GGTCTGGGAGATAGCGGGGAGTTGGACATCTCCTCGGCAGCAGATGGA 5609

Qy 1967 SerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLys 1986  
Db 5610 AGAGCGGTC--GTGGCATCCAATCCTTCCAAAGTGTCTTAC----- 5649  
Qy 1987 AspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeu 2006  
Db 5650 -----GAGCCAATCACAAACCACTGGTCGCGCAAG 5679  
Qy 2007 ProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArg 2026  
Db 5680 CAGGAGGAGGTATCTGCAGTGGTCTCTGCAGCGTGGCTACCGGGACATTTGGCAAGCGG 5739  
Qy 2027 -----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040  
Db 5740 GGCTTCATCTGCAAAAGACAACTTCTAATAAGCTGGAGAATGGAGGCACACACCGGGAG 5799  
Qy 2041 LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGly 2060  
Db 5800 -----AAAAAGAGAGCACCCTCATACAGCCTCCCTCCCTCTATGACAGTGAAC 5853  
Qy 2061 GlnSerSerThrGlnAlaGlnGlnHisSer-----ArgSerHisSerLysIle 2076  
Db 5854 AAACCTGAAAGAGAGAAACAGCAGCGGGCAGAGGAAGGAAGGAAGGAAGGAAGGAAGGA 5913  
Qy 2077 SerLysHisMet 2080  
Db 5914 CAAAAGAGGTC 5925

RESULT 9  
BM950154  
LOCUS  
DEFINITION  
IMAGE:5686589 5', mRNA sequence.  
BM950154  
VERSION  
KEYWORDS  
SOURCE  
MUS musculus (house mouse)  
ORGANISM  
MUS musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 711)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.  
Location/Qualifiers  
1..711  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5686589"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 18.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP\_EHOp"  
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded

cdNA was size selected according to mRNA size fraction,  
ligated with EcoR I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA  
tail, is CAGCCACGAC. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institute of Mental Health  
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN  
Alignment Scores:  
Pred. No.: 2.32e-74 Length: 711  
Score: 1216.00 Matches: 236  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 10.22% Indels: 0  
DB: 5 Gaps: 0

US-09-611-257A-37 (1-2266) x BM950154 (1-711)  
Qy 1582 PheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGly 1601  
Db 3 TTCCGGCTCCTCGTCCACCACCTGTGTACCGCCACTACCTGGACCTCTTCATCATGGT 62  
Qy 1602 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu 1621  
Db 63 GTCATCGGGTGAATGTGTGTCACGATGGCCATGGAACATTACCAGCAGCCCCAGATCCTG 122  
Qy 1622 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerVal 1641  
Db 123 GACGAGGCTCTGAAGATCTGCAACTACATCTTTACCGTCATCTTTGTCTGGAGTCAGTA 182  
Qy 1642 PheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAsp 1661  
Db 183 TTCAAACCTTGTGGCTTCGGCTTCGCCGGTCTTCCAGGACAGGTGGAACCCAGCTGGAC 242  
Qy 1662 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsnAla 1681  
Db 243 CTGGCTATTGTGCTTCTGTCCATCATCGGCATCACGCTGGAAGAGATTGAGGTCAATGCT 302  
Qy 1682 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1701  
Db 303 TCACTGCCCATCAACCCACCATCATCCGTATCATGAGGGTGTCCGCTATGTCGAGTT 362  
Qy 1702 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAla 1721  
Db 363 CTGAAGCTGTTGAAGATGGCTGTGGGCATCGGGCACTGCTGGACACGGTGTGTCAGGCC 422  
Qy 1722 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAla 1741  
Db 423 CTGCCCCAGGTGGGAACCTGGGACTTCTCTCATGCTATTTATTTTCATCTTTGCAGCT 482  
Qy 1742 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1761  
Db 483 CTGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTG 542  
Qy 1762 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1781  
Db 543 GGCCGCGCATGCCACCTTTAGGAACCTTTGGTATGGCTTTCTGACCCCTTTCGAGTCTCC 602  
Qy 1782 ThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSer 1801  
Db 603 ACTGTGACAACTGGAATGTTATTATTAAGGAGACACCCCTCCGGGACTGTGACCAAGATCC 662  
Qy 1802 ThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheVal 1817  
Db 663 ACCTGCTACAACACCGTCATCTCACCCATCTACITCGTGTCTCTCGTG 710

RESULT 10  
BU058818  
LOCUS  
DEFINITION  
UI-M-FR0-cak-a-11-0-UI.r1 NIH\_BMAP\_FR0 Mus musculus cDNA clone  
771 bp mRNA linear EST 26-AUG-2002







Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH)."

ORIGIN

Alignment Scores:  
Pred. No.: 4.78e-74 Length: 784  
Score: 1212.50 Matches: 243  
Percent Similarity: 95.40% Conservative: 6  
Best Local Similarity: 93.10% Mismatches: 10  
Query Match: 10.19% Indels: 2  
DB: 7 Gaps: 1

US-09-611-257A-37 (1-2266) x CF742232 (1-784)

QY	937	SerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPhe	956	
Db	2	TCATCTTGGGCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTACGTGCTCTTT	61	
QY	957	AsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGlu	976	
Db	62	AACCTGCTGTGCGCATCTTCGTGGAGGTTTCCAGGCAGAGAAATCGGCAACGGGAA	121	
QY	977	AspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGln-GlyGlyAspAl	996	
Db	122	GATACGAGTGGACAGTTAAGCTGTATTTCAGTGCCTGTCAACTCCAGGGGNGAGATGC	181	
QY	996	aAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAspAr	1016	
Db	182	CACCAAGTCTGAGTCAGAGCCTGATTCTTTTCGCCCACTGTGGATGGTATGGGACAG	241	
QY	1016	gLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLe	1036	
Db	242	GAAGAAGCGCTTGGCCCTGTGGCTTGGGAGAACACTCGGAACACTACGAAGAGCCTTTT	301	
QY	1036	uProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerTh	1056	
Db	302	GCCACCTCTCATCATCCACACAGCTGTACACCGATGTCACTGCCCAAGAGCTCCAGCAC	361	
QY	1056	rGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGl	1076	
Db	362	AGGTGTGGGGAAGCACTGGGCTCTGGCTCTCGCCGCACAGTAGCAGTGGGTCCGCTGA	421	
QY	1076	uProGlyAlaAla--HisGluMetLysSerProProSerAlaArgSerSerProHisSe	1095	
Db	422	GCCTGGAACTGCCCATCATGAGATGAATCACCGCCCAAGTGCCTCCGAAGCTCCCGCACAG	481	
QY	1095	rProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyAr	1115	
Db	482	TCCCTGGAGCGCAGCAAGCAGCTGGACCAAGCGGCGCTCCAGCCGGAACAGCTGGGCGG	541	
QY	1115	gAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGl	1135	
Db	542	GGCCCCCAGCCTGAAGCGTAGGAGCCCAAGCGGGAGCGGAGGTCCCTGCTGTGGAGA	601	
QY	1135	uGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAlaSerProAlaGl	1155	
Db	602	GGGTCAGGAGAGCCAGGATGAGGAGGAGAGTTTCAGAAAGAGGACCCGGCCAGCCAGCAGG	661	
QY	1155	ySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuPr	1175	
Db	662	CAGTGATCATGCCACAGGGGTTCCTTGGAACTGAGGGCAAGAGTTCTCTTGACCTGCC	721	
QY	1175	oAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGl	1195	
Db	722	TGACACCCTGCAGGTGCCCGGGCTTCATCGAACAGCCAGCGGTGGAGCTCTGCCTCTGA	781	
QY	1195	u	1195	
Db	782	A	782	

RESULT 13  
BU709095  
LOCUS

810 bp mRNA linear EST 15-JUL-2003

DEFINITION	UI-M-EW0-caz-e-20-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone				
	IMAGE:6419323 5', mRNA sequence.				
ACCESSION	BU709095				
VERSION	BU709095.1 GI:23642225				
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 810)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Dr. James Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> This clone was contributed by the Brain Molecular Anatomy Project (BMAP)				
FEATURES	Seq primer: pYX-5.				
source	Location/Qualifiers				
	1. .810				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
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	/db_xref="taxon:10090"				
	/clone="IMAGE:6419323"				
	/tissue_type="whole brain"				
	/dev_stage="embryo 15.5 dpc"				
	/lab_host="DH10B (T1 phage resistant)"				
	/clone_lib="NIH_BMAP_EW0"				
	/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."				
ORIGIN					
Alignment Scores:					
Pred. No.:	2.79e-72	Length:	810		
Score:	1187.50	Matches:	244		
Percent Similarity:	90.77%	Conservative:	2		
Best Local Similarity:	90.04%	Mismatches:	6		
Query Match:	9.98%	Indels:	22		
DB:	5	Gaps:	1		
US-09-611-257A-37 (1-2266) x BU709095 (1-810)					
Qy	1358	ValIleAspIleLeu-ValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLe		1377	
Db	1	GTCATCGACATCCTGTGTGTCCATGGTCTCTGTACAGCGGCACCAAGATTCTCGGCATGCT		60	
Qy	1377	uArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGl		1397	
Db	61	GAGGGTGTCTGGGCTGTCTGGGACCCCTACGTCCACTCAGGGTTCATCAGCCGGGCCAGGG		120	
Qy	1397	yLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValVa		1417	

Db	121	GCTGAAGCTGGTGTAGAGACTCTGATGTATCCCTCAAAACCATTTGGCAACATTTGGT	180
QY	1417	lileCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLy	1437
Db	181	CATCTGCTGTCCTTCTTCATCATTTTGGAAATCTTGGGTGCAGCTCTTCAAGGGAA	240
QY	1437	sphePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGl	1457
Db	241	GTTCTTCGTGTGTCCAGGTGAGGACACCAAGGACATCACTAACAAAGTCCGACTGTGCTGA	300
QY	1457	uAlaSerTyrArgTyrValArgHisLysTyrzhenPheAspAsnLeuGlyGlnAlaLeuMe	1477
Db	301	GGCCAGTTACCGTGGTCCGGCACAAAGTACAACTTTGACAAACCTGGCCAGGCTCTGAT	360
QY	1477	tSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAs	1497
Db	361	GTCCCTGTTGTGTGGCTCCAAAGGATGGCTGGGTGACATCATGTATGATGACTGGA	420
QY	1497	pAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPh	1517
Db	421	TGCTGTGGAGTGGACCAAGAGCCCATCATGAACCAACCTTGGATGCTCTACTT	480
QY	1517	eileSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValVa	1537
Db	481	CATCTCCTTCTCCTCATCGTGGCTTCTTCGTCCTGAAACATGTTTGTGGCGTGGTGGT	540
QY	1537	lGluAsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGl	1557
Db	541	GGAGAACTTCCATAAGTGCAGGCAGCACCAAGAGGAGGAGGCGCGCGGGAGGA	600
QY	1557	uLysArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	601	GAAGCGACTAAAGAGGCTGGAGAAAAGAGAGGAATCTAATGTTGGACGATGAATTGC	660
QY	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTy	1579
Db	661	TTCCGGCAGCTCAGCCAGCGCTGCGTCAGAAAGCCAGTGCANACCTACTACTGACTA	720
QY	1579	rSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIl	1599
Db	721	CTCGCGCTTCCGGCTCCC-TCGTACACCTGTGTACAGC-CACTACCTGNA-CTCTTCAT	777
QY	1599	eThrGlyValIleGlyLeuAsnValThr	1609
Db	778	CACTGGTGTATCGGCTGAATGTGGTCAG	808
RESULT 14			
B1160856			
LOCUS			
DEFINITION			
602864778F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019018 5',			
mRNA sequence.			
B1160856			
ACCESSION			
VERSION			
B1160856.1 GI:14620857			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 736)			
NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>			
Tissue Procurement: ATCC			
cDNA Library Preparation: Ling Hong/Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
<a href="http://image.llnl.gov">http://image.llnl.gov</a>			
Plate: LLCW1833 row: k column: 19			
High quality sequence stop: 710.			

FEATURES		Location/Qualifiers	
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		/db_xref="taxon:9606"	
		/clone="IMAGE:5019018"	
		/tissue_type="epithelioid carcinoma cell line"	
		/lab_host="DH10B (phage-resistant)"	
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		/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.  "	
ORIGIN			
Alignment Scores:			
Pred. No.:		3,56e-72 Length: 736	
Score:		1185.00 Matches: 236	
Percent Similarity:		97.15% Conservative: 3	
Best Local Similarity:		95.93% Mismatches: 5	
Query Match:		9.95% Indels: 2	
DB:		4 Gaps: 0	
US-09-611-257A-37 (1-2266) x B1160856 (1-736)			
QY	1268	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1287
Db	2	CTGTGTACCGGATCATCCACAAAGATGTTCCGACACGTGTCCTTGTTCATCATCTTC	61
QY	1288	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1307
Db	62	CTTAACATGCATCACCATCGCCATGGAGCGCCCCAAATGACCCACAGCGCTGAACGC	121
QY	1308	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1327
Db	122	ATCTTCTGACCTCTCCAATTACATCTTCCCGCAGTCTTTCTGGCTGAAATGACAGTG	181
QY	1328	LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTyrAsn	1347
Db	182	AAGTGTGGTGGCTGGGCTGGTGTCTCATCTCCGTATCGACATTCGCGGACCCCTGCGC	241
QY	1348	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1367
Db	242	GTGCTGGACGGGCTGTTGGTGTCTCATCTCCGTATCGACATTCGCGGACCCCTGCGC	301
QY	1368	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1387
Db	302	GACAGCGGCACCAAGATCTTGGGATGTGAGGGTGTGCGGCTGCTGCGGACCCCTGCGC	361
QY	1388	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1407
Db	362	CCGCTCAGGGTGTATCAGCGGGCGCAGGGGCTGAAGCTGGTGGTGGAGACGCTGATGTC	421
QY	1408	SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly	1427
Db	422	TCACTGAAACCCATCGGCAACATTTAGTATCATCTGCTGTGCTTCTTCATCATTTTCGGC	481
QY	1428	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1447
Db	482	ATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTGTGCCAGGCGGAGATACCAGG	541
QY	1448	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyr	1467
Db	542	AACATCACCAATAATCGGACTGTGCCGAGGCCAGTTACCGTGGTGGTCCGGCACAGTAC	601
QY	1468	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheVal-LeuAlaSerLysAspGl	1487
Db	602	AACCTTTGACAAACCTTGGCCAGGCCCTGATGTCCCTGTACGCATATGGCCTCCCAAGGATGG	661

QY 1487 yTrpValAspIleMetTyrAspGly-LeuAspAlaValGlyValAspGlnGlnProIleM 1507  
Db 662 TAGGGTGGACATCATGTACGATGGCGCTGGATGCTGTGGGGCGTGGACCAGAGCCCATCA 721

QY 1507 etAsnHisAsnPro 1511  
Db 722 TGAACCACAAACCT 735

RESULT 15  
BI736618  
LOCUS  
DEFINITION BI736618 939 bp mRNA linear EST 20-SEP-2001  
603361089F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5367862 5',  
mRNA sequence.

ACCESSION BI736618  
VERSION BI736618.1 GI:15713631  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 939)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

REFERENCE  
AUTHORS Contact: Robert Strausberg, Ph.D.  
TITLE Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
JOURNAL Tissue Procurement: The Cepko Laboratory  
COMMENT cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1936 row: b column: 23  
High quality sequence stop: 853.

FEATURES  
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1..939  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/clone="IMAGE:5367862"  
/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 94"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 7.31e-72 Length: 939  
Score: 1183.00 Matches: 247  
Percent Similarity: 84.69% Conservative: 13  
Best Local Similarity: 80.46% Mismatches: 41  
Query Match: 9.94% Indels: 9  
DB: 4 Gaps: 3

US-09-611-257A-37 (1-2266) x BI736618 (1-939)

QY 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948  
Db 3 GGTGTACGGGACACACTCTCTGCCCAATGACAGCTACATGTGCCCAATGGGAGCACT 62

QY 1949 AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerVal 1968  
Db 63 GCCGAGAGATCCCTAGGACACAGGGGCTGGGGCTCCCAAGCCAGTCAGGCTCCATC 122

QY 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988  
Db 123 TTGTCTGTCTCACTCCCAACCAGCAGACACCAGCTGCATCTTACAGCTTCCCAAGATGCA 182

QY 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2008  
Db 183 CACTATCTGTCTCCAGCCTCATGGGGCTCCCACCTGGGGCGCCCATCCCTAAACTACCCCA 242

QY 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp 2028  
Db 243 CCTGGCCGCTCCCTCTGGCTCAGAGGCCTCTCAGGGCCAGGCAGCAATAAGGACTGAC 302

QY 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyPro 2048  
Db 303 TCCCTGGACGTGCAGGGCCTGGGTAGCCGGGAAGACCTGTGTTCAGAGGTGAGTGGGCC 362

QY 2049 SerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068  
Db 363 TCCTGCCCTCTGACCCGCTCCTCATCTTCTGGGGCGGGTCGAGCATCCAGGTGAGCAG 422

QY 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088  
Db 423 CGCTCCGGCAGCCAGAGCAAAAGTCTCCAAGCACATCCGCCTGCCAGCCCTTGCCAGGC 482

QY 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108  
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QY 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlnGluGluProProSer 2128  
Db 543 GAGCTGAGCTGGATTTTCAGGAGACCTCCTG---CCCAGAGTCAGGAAGAACCCCTGTCC 599

QY 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148  
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QY 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAla-ValSerCysLeuAspSerGlySe 2168  
Db 660 TCCTGGCTAGACGAACAGAGAGAGACACTCCATCGCTTGTTCAGCTGCCTGGACAGCGGCTC 719

QY 2168 rGlnProHisLeuGlyThrAspProSerAsnLeu-GlyGlyGlnProLeuGlyGlyProG 2188  
Db 720 CCAGCCCCGCTATGTCCAAGCCCTCAAGCCTCGGGGGGCCAACCTCTGGGGGGCCCTGG 779

QY 2188 LysSerArgProLysLysLeuSerProProSerIleThrIleAspProProGluSerG 2208  
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QY 2208 LngLysProArgThrProProSerProGlyIleCysLeuArgArgAlaPro-SerSer 2227  
Db 838 --GGACCTCGGCCCATGCAGTCT-GGCGTCTGCCC-AGGAGGAGG---CCGCGGCAAG 890

QY 2228 AspSerLysAspPro 2232  
Db 891 GACTCGAAGGATCCT 905

Search completed: April 16, 2005, 13:08:47  
Job time : 14407 secs

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